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<110> Dumas Milne Edwards, Jean Baptiste
Bougueleret, Lydie
Jobert, Severin

<120> FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED PROTEINS

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<150> US 09/731,872

<151> 2000-12-07

<150> US 60/187,470

<151> 2000-03-06

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His	Ser	Thr	Leu	Ser	Val	Asn	Trp	Ser	Leu	Leu	Leu	Ser	Pro	Glu	Pro	
		55				60					65					
gat	ggg	ggc	ctg	atg	gtg	ctc	cct	aag	gac	agc	att	cag	ttt	tct	tct	390
Asp	Gly	Gly	Leu	Met	Val	Leu	Pro	Lys	Asp	Ser	Ile	Gln	Phe	Ser	Ser	
					75					80					85	
gcc	ctt	gtt	ttt	acc	agg	ctg	ctt	gag	ttt	gac	agc	acc	aac	gtg	tcc	438
Ala	Leu	Val	Phe	Thr	Arg	Leu	Leu	Glu	Phe	Asp	Ser	Thr	Asn	Val	Ser	
				90					95					100		
gat	acg	gca	gca	aag	cct	ttg	gga	aga	cca	tat	cct	cca	tac	tcc	ttg	486
Asp	Thr	Ala	Ala	Lys	Pro	Leu	Gly	Arg	Pro	Tyr	Pro	Pro	Tyr	Ser	Leu	
			105					110					115			
gcc	gat	ttc	tct	tgg	aac	aac	atc	act	gat	tca	ttg	gat	cct	gcc	acc	534
Ala	Asp	Phe	Ser	Trp	Asn	Asn	Ile	Thr	Asp	Ser	Leu	Asp	Pro	Ala	Thr	
		120					125					130				
ctg	agt	gcc	aca	ttt	caa	ggc	cac	ccc	atg	aac	gac	cct	acc	agg	act	582
Leu	Ser	Ala	Thr	Phe	Gln	Gly	His	Pro	Met	Asn	Asp	Pro	Thr	Arg	Thr	
		135				140					145					
ttt	gcc	aat	ggc	agc	ctg	gcc	ttc	agg	gtc	cag	gcc	ttt	tcc	agg	tcc	630
Phe	Ala	Asn	Gly	Ser	Leu	Ala	Phe	Arg	Val	Gln	Ala	Phe	Ser	Arg	Ser	
					155					160					165	
agc	cga	cca	gcc	caa	ccc	cct	cgc	ctc	ctg	cac	aca	gca	gac	acc	tgt	678
Ser	Arg	Pro	Ala	Gln	Pro	Pro	Arg	Leu	Leu	His	Thr	Ala	Asp	Thr	Cys	
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cag	cta	gag	gtg	gcc	ctg	att	gga	gcc	tct	ccc	cgg	gga	aac	cgt	tcc	726
Gln	Leu	Glu	Val	Ala	Leu	Ile	Gly	Ala	Ser	Pro	Arg	Gly	Asn	Arg	Ser	
			185					190					195			
ctg	ttt	ggg	ctg	gag	gta	gcc	aca	ttg	ggc	cag	ggc	cct	gac	tgc	ccc	774
Leu	Phe	Gly	Leu	Glu	Val	Ala	Thr	Leu	Gly	Gln	Gly	Pro	Asp	Cys	Pro	
		200					205					210				
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Ser	Met	Gln	Glu	Gln	His	Ser	Ile	Asp	Asp	Glu	Tyr	Ala	Pro	Ala	Val	
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ttc	cag	ttg	gac	cag	cta	ctg	tgg	ggc	tcc	ctc	cca	tca	ggc	ttt	gca	870
Phe	Gln	Leu	Asp	Gln	Leu	Leu	Trp	Gly	Ser	Leu	Pro	Ser	Gly	Phe	Ala	
		230			235					240					245	
cag	tgg	cga	cca	gtg	gct	tac	tcc	cag	aag	ccg	ggg	ggc	cga	gaa	tca	918
Gln	Trp	Arg	Pro	Val	Ala	Tyr	Ser	Gln	Lys	Pro	Gly	Gly	Arg	Glu	Ser	
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gcc	ctg	ccc	tgc	caa	gct	tcc	cct	ctt	cat	cct	gcc	tta	gca	tac	tct	966
Ala	Leu	Pro	Cys	Gln	Ala	Ser	Pro	Leu	His	Pro	Ala	Leu	Ala	Tyr	Ser	
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ctt	ccc	cag	tca	ccc	att	gtc	cga	gcc	ttc	ttt	ggg	tcc	cag	aat	aac	1014
Leu	Pro	Gln	Ser	Pro	Ile	Val	Arg	Ala	Phe	Phe	Gly	Ser	Gln	Asn	Asn	
		280					285					290				
ttc	tgt	gcc	ttc	aat	ctg	acg	ttc	ggg	gct	tcc	aca	ggc	cct	ggc	tat	1062
Phe	Cys	Ala	Phe	Asn	Leu	Thr	Phe	Gly	Ala	Ser	Thr	Gly	Pro	Gly	Tyr	

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tgg gac caa cac tac ctc agc tgg tgc atg ctc	ctg ggt gtg ggc ttc	1110	
Trp Asp Gln His Tyr Leu Ser Trp Ser Met Leu	Leu Gly Val Gly Phe		
310	315	320	325
cct cca gtg gac ggc ttg tcc cca cta gtc ctg	ggc atc atg gca gtg	1158	
Pro Pro Val Asp Gly Leu Ser Pro Leu Val Leu	Gly Ile Met Ala Val		
330	335	340	
gcc ctg ggt gcc cca ggg ctc atg ctg cta ggg	ggc ggc ttg gtt ctg	1206	
Ala Leu Gly Ala Pro Gly Leu Met Leu Leu Gly	Gly Gly Leu Val Leu		
345	350	355	
ctg ctg cac cac aag aag tac tca gag tac cag	tcc ata aat	1248	
Leu Leu His His Lys Lys Tyr Ser Glu Tyr Gln	Ser Ile Asn		
360	365	370	
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aaaaaaaaa aaaaa		1623	

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 <222> 72..119
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 seq LGMLLGLLMAACT/PS

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Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala	
-15 -10 -5	
gcc tgc aca cct tct gcc tca gtc atc aga acc tgaaggagtt	tgccctgacc 163
Ala Cys Thr Pro Ser Ala Ser Val Ile Arg Thr	

1	5	
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gggcaggctg tccctgcagg atcccacgta cggctgaatc	ttcagactgg ggaaagagag	343
gcaaaaactcc aatatgagga caagttccga aataatttga	aaggcaaaaag gctggatatc	403
aacaccaaca cctacacatc tcaggatctc aagagtgcac	tggcaaaatt caaggagggg	463
gcagagatgg agagttcaaa ggaagacaag gcaaggcagg	ctgaggtaaa gcggctcttc	523
cgccccattg aggaactgaa gaaagacttt gatgagctga	atgttgatc tgaagactgac	583
atgcagatca tggtagggct gatcaacaag ttcaatagtt	ccagctccag tttggaagag	643
aagattgctg cgctctttga tcttgaatat tatgtccatc	agatggacaa tgccgaggac	703
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gtgaaggagt atgtgctggt tgtgctgggc gctgcctttt	ccagcaaccc caaggtccag	823
gtggaggcca tcgaaggggg agccctgcag aagctgctgg	tcatcctggc cacggagcag	883
ccgctcactg caaaggaggg tgctcaccgt gcgcgtggtc	acactgctct acgacctggt	943

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cacggagaag atgttcgccg aggaggagggc tgagctgacc caggagatgt ccccagagaa 1003
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                                     Met Ala
ccc cag agc ctg cct tca tct agg atg gct cct ctg ggc atg ctg ctt 164
Pro Gln Ser Leu Pro Ser Ser Arg Met Ala Pro Leu Gly Met Leu Leu
      -25                                -20                                -15
ggg ccg ctg atg gcc gcc tgc ttc acc ttc tgc ctc agt cat cag aac 212
Gly Pro Leu Met Ala Ala Cys Phe Thr Phe Cys Leu Ser His Gln Asn
      -10                                -5                                1                                5
ctg aag gag ttt gcc ctg acc aac cca gag aag agc agc acc aaa gaa 260
Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr Lys Glu
      10                                15                                20
aca gag aga aaa gaa acc aaa gcc gag gag gag ctg gat gcc gaa gtc 308
Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala Glu Val
      25                                30                                35
ctg gag gtg ttc cac ccg acg cat gag tgg cag gcc ctt cag cca ggg 356
Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln Pro Gly
      40                                45                                50
cag gct gtc cct gca gga tcc cac gta cgg ctg aat ctt cag act ggg 404
Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln Thr Gly
      55                                60                                65
gaa aga gag gca aaa ctc caa tat gag gac aag ttc cga aat aat ttg 452
Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn Asn Leu
      70                                75                                80                                85
aaa ggc aaa agg ctg gat atc aac acc aac acc tac aca tct cag gat 500
Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser Gln Asp
      90                                95                                100
ctc aag agt gca ctg gca aaa ttc aag gag ggg gca gag atg gag agt 548
Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met Glu Ser
      105                                110                                115
tca aag gaa gac aag gca agg cag gct gag gta aag cgg ctc ttc cgc 596

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Pro	Ile	Glu	Glu	Leu	Lys	Lys	Asp	Phe	Asp	Glu	Leu	Asn	Val	Val	Ile		
	135					140					145						
gag	act	gac	atg	cag	atc	atg	gta	cgg	ctg	atc	aac	aag	ttc	aat	agt	692	
Glu	Thr	Asp	Met	Gln	Ile	Met	Val	Arg	Leu	Ile	Asn	Lys	Phe	Asn	Ser		
150				155					160					165			
tcc	agc	tcc	agt	ttg	gaa	gag	aag	att	gct	gcg	ctc	ttt	gat	ctt	gaa	740	
Ser	Ser	Ser	Ser	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Leu	Phe	Asp	Leu	Glu		
				170				175						180			
tat	tat	gtc	cat	cag	atg	gac	aat	gcg	cag	gac	ctg	ctt	tcc	ttt	ggg	788	
Tyr	Tyr	Val	His	Gln	Met	Asp	Asn	Ala	Gln	Asp	Leu	Leu	Ser	Phe	Gly		
			185				190						195				
ggg	ctt	caa	gtg	gtg	atc	aat	ggg	ctg	aac	agc	aca	gag	ccc	ctc	gtg	836	
Gly	Leu	Gln	Val	Val	Ile	Asn	Gly	Leu	Asn	Ser	Thr	Glu	Pro	Leu	Val		
		200					205					210					
aag	gag	tat	gct	gcg	ttt	gtg	ctg	ggc	gct	gcc	ttt	tcc	agc	aac	ccc	884	
Lys	Glu	Tyr	Ala	Ala	Phe	Val	Leu	Gly	Ala	Ala	Phe	Ser	Ser	Asn	Pro		
	215				220				225								
aag	gtc	cag	gtg	gag	gcc	atc	gaa	ggg	gga	gcc	ctg	cag	aag	ctg	ctg	932	
Lys	Val	Gln	Val	Glu	Ala	Ile	Glu	Gly	Gly	Ala	Leu	Gln	Lys	Leu	Leu		
230				235				240						245			
gtc	atc	ctg	gcc	acg	gag	cag	ccg	ctc	act	gca	aag	aag	aag	gtc	ctg	980	
Val	Ile	Leu	Ala	Thr	Glu	Gln	Pro	Leu	Thr	Ala	Lys	Lys	Lys	Val	Leu		
			250					255						260			
ttt	gca	ctg	tgc	tcc	ctg	ctg	cgc	cac	ttc	ccc	tat	gcc	cag	cgg	cag	1028	
Phe	Ala	Leu	Cys	Ser	Leu	Leu	Arg	His	Phe	Pro	Tyr	Ala	Gln	Arg	Gln		
			265				270					275					
ttc	ctg	aag	ctc	ggg	ggg	ctg	cag	gtc	ctg	agg	acc	ctg	gtg	cag	gag	1076	
Phe	Leu	Lys	Leu	Gly	Gly	Leu	Gln	Val	Leu	Arg	Thr	Leu	Val	Gln	Glu		
		280					285					290					
aag	ggc	acg	gag	gtg	ctc	gcc	gtg	cgc	gtg	gtc	aca	ctg	ctc	tac	gac	1124	
Lys	Gly	Thr	Glu	Val	Leu	Ala	Val	Arg	Val	Val	Thr	Leu	Leu	Tyr	Asp		
	295					300				305							
ctg	gtc	acg	gag	aag	atg	ttc	gcc	gag	gag	taggctgagc	tgacccagga					1174	
Leu	Val	Thr	Glu	Lys	Met	Phe	Ala	Glu	Glu								
310				315													
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<222> 66..173

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score 4.89555877630516

seq LLLLRLNDAALRA/LQ

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Met Glu Glu Leu Gln Glu Pro Leu Arg Gly Gln Leu Arg Leu Cys
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Phe Thr Gln Ala Ala Arg Thr Ser Leu Leu Leu Leu Arg Leu Asn Asp
-20 -15 -10
gct gcc ctg cgg gcg ctg caa gag tgt cag cgg caa cag gta cgg ccg 206
Ala Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro
-5 1 5 10
gtg att gct ttc caa ggc cac cga ggg tat ctg aga ctc cca ggc cct 254
Val Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro
15 20 25
ggg tgg tcc tgc ctc ttc tcc ttc ata gtg tcc cag tgt tgt cag gag 302
Gly Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu
30 35 40
ggc gct ggt ggt agc ttg gac ctt gtg tgc caa cgc ttc ctc agg tct 350
Gly Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser
45 50 55
ggg cct aac agc ctc cac tgc ctg ggc tca ctc agg gag cgc ctc att 398
Gly Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile
60 65 70 75
att tgg gca gcc atg gat tct atc cca gcc cca tca tca gtt cag gga 446
Ile Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly
80 85 90
cac aac ctg act gaa gat gcc aga cat cct gag agt tgg cag aac aca 494
His Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr
95 100 105
gga ggc tat tct gaa gga gat gca gta tca cag cca cag atg gca cta 542
Gly Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu
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gag gag gtg tca gtg tca gat cca ctg gca agc aac caa gga cag tca 590
Glu Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser
125 130 135
ctc cca gga tcc tca agg gag cac atg gca cag tgg gaa gtg aga agc 638
Leu Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser
140 145 150 155
cag acc cat gtt cca aac aga gaa cct gtt cag gca ctg cct tcc tct 686
Gln Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser
160 165 170
gcc agc cgg aaa cgt ctg gac aag aaa cgt tca gtg cct gta gcc act 734
Ala Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr
175 180 185
gta gaa ctg gaa gaa aag agg ttc aga act ctg cct tta gtg cca agc 782
Val Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Ser
190 195 200
ccc cta caa ggc ctg acc aat cag gat tta caa gag gga gaa gat tgg 830
Pro Leu Gln Gly Leu Thr Asn Gln Asp Leu Gln Glu Gly Glu Asp Trp
205 210 215
gag caa gaa gat gag gac atg gac ccc aga tta gaa cac agt tcc tca 878
Glu Gln Glu Asp Glu Asp Met Asp Pro Arg Leu Glu His Ser Ser Ser
220 225 230 235

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Leu Leu Gln Tyr Arg Ala Ile His Ser Ala Glu Gln Gln His Ala Tyr
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gag cag gac ttt gag aca gat tat gct gaa tac cgc atc ctg cat gcc      1022
Glu Gln Asp Phe Glu Thr Asp Tyr Ala Glu Tyr Arg Ile Leu His Ala
                270                275                280
cgt gtt ggg act gca agc caa agg ttc ata gag ctg gga gca gag att      1070
Arg Val Gly Thr Ala Ser Gln Arg Phe Ile Glu Leu Gly Ala Glu Ile
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aaa aga gtt cgg cga gga act cca gaa tac aag gtc ctg gaa gac aag      1118
Lys Arg Val Arg Arg Gly Thr Pro Glu Tyr Lys Val Leu Glu Asp Lys
                300                305                310                315
ata atc cag gaa tat aaa aag ttc agg aag cag tac cca agt tac aga      1166
Ile Ile Gln Glu Tyr Lys Lys Phe Arg Lys Gln Tyr Pro Ser Tyr Arg
                320                325                330
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Glu Glu Lys Arg Arg Cys Glu Tyr Leu His Gln Lys Leu Ser His Ile
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Lys Gly Leu Ile Leu Glu Phe Glu Glu Lys Asn Arg Gly Ser
                350                355                360
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cgtccagggtg gcagagcagc taggaacgca aggcctgaac ctggggccag acaccctgct      180
ctcccgggcc atg gtc aac gac cct cca gta cct gcc tta ctg tgg gcc cag      231
      Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln
                -20                -15                -10
gag gtg ggc caa gtc ttg gca ggc cgt gcc cgc agg ctg ctg ctg cag      279

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Phe	Gly	Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Leu	Trp	Val	Ser	Val	
10				15						20					25	
ttc	ctc	tat	ggc	tcc	ttc	tac	tat	tcc	tat	atg	ccg	aca	gtc	agc	cac	375
Phe	Leu	Tyr	Gly	Ser	Phe	Tyr	Tyr	Ser	Tyr	Met	Pro	Thr	Val	Ser	His	
				30						35					40	
ctc	agc	cct	gtg	cat	ttc	tac	tac	agg	acc	gac	tgt	gat	tcc	tcc	acc	423
Leu	Ser	Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	
				45						50					55	
acc	tca	ctc	tgc	tcc	ttc	cct	gtt	gcc	aat	gtc	tgc	ctg	act	aag	ggc	471
Thr	Ser	Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	
				60						65					70	
gga	cgt	gat	cgg	gtg	ctg	atg	tat	gga	cag	ccg	tat	cgt	gtt	acc	tta	519
Gly	Arg	Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	
75										80						
gag	ctt	gag	ctg	cca	gag	tcc	cct	gtg	aat	caa	gat	ttg	ggc	atg	ttc	567
Glu	Leu	Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	
90										100					105	
ttg	gtc	acc	att	tcc	tgc	tac	acc	aga	ggc	ggc	cga	atc	atc	tcc	act	615
Leu	Val	Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	
				110						115					120	
tct	tgc	cgt	tgc	gtg	atg	ctg	cat	tac	cgc	tca	gac	ctg	ctc	cag	atg	663
Ser	Ser	Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	
				125						130					135	
ctg	gac	aca	ctg	gtc	ttc	tct	agc	ctc	ctg	cta	ttt	ggc	ttt	gca	gag	711
Leu	Asp	Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	
				140						145					150	
cag	aag	cag	ctg	ctg	gag	gtg	gaa	ctc	tac	gca	gac	tat	aga	gag	aac	759
Gln	Lys	Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	
155										160					165	
tgc	gtg	agt	gag	tac	gtg	ccg	acc	act	gga	gcg	atc	att	gag	atc	cac	807
Ser	Val	Ser	Glu	Tyr	Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	
170										180					185	
agc	aag	cgc	atc	cag	ctg	tat	gga	gcc	tac	ctc	cgc	atc	cac	gcg	cac	855
Ser	Lys	Arg	Ile	Gln	Leu	Tyr	Gly	Ala	Tyr	Leu	Arg	Ile	His	Ala	His	
				190						195					200	
ttc	act	ggg	ctc	aga	tac	ctg	cta	tac	aac	ttc	ccg	atg	acc	tgc	gcc	903
Phe	Thr	Gly	Leu	Arg	Tyr	Leu	Leu	Tyr	Asn	Phe	Pro	Met	Thr	Cys	Ala	
				205						210					215	
ttc	ata	ggc	gtt	gcc	agc	aac	ttc	acc	ttc	ctc	agc	gtc	atc	gtg	ctc	951
Phe	Ile	Gly	Val	Ala	Ser	Asn	Phe	Thr	Phe	Leu	Ser	Val	Ile	Val	Leu	
				220						225					230	
ttc	agc	tac	atg	cag	tgg	gtg	tgg	ggg	ggc	atc	tgg	ccc	cga	cac	cgc	999
Phe	Ser	Tyr	Met	Gln	Trp	Val	Trp	Gly	Gly	Ile	Trp	Pro	Arg	His	Arg	
				235						240					245	
ttc	tct	ttg	cag	gtt	aac	atc	cga	aaa	aga	gac	aat	tcc	cgg	aag	gaa	1047
Phe	Ser	Leu	Gln	Val	Asn	Ile	Arg	Lys	Arg	Asp	Asn	Ser	Arg	Lys	Glu	
250										260					265	
gtc	caa	cga	agg	atc	tct	gct	cat	cag	cca	ggc	gca	ggg	cct	gaa	ggc	1095
Val	Gln	Arg	Arg	Ile	Ser	Ala	His	Gln	Pro	Gly	Ala	Gly	Pro	Glu	Gly	
				270						275					280	
cag	gag	gag	tca	act	ccg	caa	tca	gat	gtt	aca	gag	gat	ggc	gag	agc	1143
Gln	Glu	Glu	Ser	Thr	Pro	Gln	Ser	Asp	Val	Thr	Glu	Asp	Gly	Glu	Ser	
				285						290					295	
cct	gaa	gat	ccc	tca	ggg	aca	gag	ggc	cag	ctg	tcc	gag	gag	gag	aaa	1191
Pro	Glu	Asp	Pro	Ser	Gly	Thr	Glu	Gly	Gln	Leu	Ser	Glu	Glu	Glu	Lys	


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gct tgg ctg ttc tgagagctcc gctgagcacc tggccttgaa gtttgtgttc      450
Ala Trp Leu Phe
      85
ttccctctgg caatggctcc cttcagcact tctgctttcc actccaattc acacaggctt      510
ggtattaaca gaatcaaggc caggctaggt taggaaaagg gaagagcttt caccttcttt      570
aaaactctcg gctgggcgca gtggctcatg cctgtaatcc cagcattttg ggaggctgag      630
gcagggtgat cacctgaggt cagcagttca aatcagcct ggccaaaatg ctgaaactcc      690
gtctctacta aaaatacaaa aattagccag gcatggtgac aggcgcctgt aatcccagct      750
actcgggagg ccaaggcagg agaattgctc gaactcaggg ggtggagggt gcagtgaagt      810
gagattgtgc cattgcactc cagcctgggc aacagagcaa gactctgtct caggcaaaaa      870
aaaaaaaaaa aa      882

<210> 10
<211> 1849
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..299

<220>
<221> sig_peptide
<222> 84..134
<223> Von Heijne matrix
      score 3.86022363031904
      seq GFVAALVAGGVAG/VS

<400> 10
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gccttgacga ggtctgagcg acc atg gac cgg ccg ggg ttc gtg gca gcg ctg      113
      Met Asp Arg Pro Gly Phe Val Ala Ala Leu
      -15 -10
gtg gct ggt ggg gta gca ggt gtt tct gtt gac ttg ata tta ttt cct      161
Val Ala Gly Gly Val Ala Gly Val Ser Val Asp Leu Ile Leu Phe Pro
      -5 1 5
ctg gat acc att aaa acc agg ctg cag agt ccc caa gga ttt aat aag      209
Leu Asp Thr Ile Lys Thr Arg Leu Gln Ser Pro Gln Gly Phe Asn Lys
10 15 20 25
gct ggt ggt ttt cat gga ata tat gct ggc gtt cct tct gct gct att      257
Ala Gly Gly Phe His Gly Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile
30 35 40
gga tcc ttt cct aat ggt tgc ctg cct gat tcg agt tcc atc      299
Gly Ser Phe Pro Asn Gly Cys Leu Pro Asp Ser Ser Ser Ile
45 50 55
tgaagtgggt aagcagaggg cacaggtatc tgcttctaca agaacatttc agattttctc      359
taacatctta tatgaagagg gtatccaagg gttgtatcga ggctataaaa gcacagtttt      419
aagagagatt cctttttctt tgggtccaggt tcccttatgg gagtccttaa aagccctctg      479
gtcctggagg caggatcatg tgggtggattc ttggcagtcg gcagtctgtg gagcttttgc      539
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gcggtcacag gggctggcag gattatttgc aggtgtcttc cctcgaatgg cagccatcag      719
tctgggaggt ttcattcttc tgggggctta tgaccgaacg cacagcttgc tgttgggaagt      779
tggcagaaag agtccttgaa gcagagacaa gcctcacctc cacttctgtc aagagagggg      839
cctgcagtgt aaaccctctt ccgctgagca gctgtctgaa ctataggccc cagtgtgtaa      899
gaccagttgt gctaagatac cggcatggag attgtgccat ccgtgggtata ggctggctgg      959
tatgaagtca ttggcctgta tgccagagag ctaagagaag aaaacggggg ctgtggcagt      1019
actctgaaca atttcctcag aacctcttaa taaataagtt tggtaatgct gaggccaggc      1079

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cttttagagc tttcatttga tctgtatctg atcttttcatt tcttgccacc tgatggtgga 1139
ttcagcagaa ggcaagatgg ttataattct aaaagaatag cttggtttgtt tggtttgtttg 1199
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gagcaaacaa acagtatgtg attttgcctt gcctattttt tttttctttt ttggggggaag 1739
ataattaaag gcagaatgac tgcgtttgta aaagaaggac caccaactat actgacattt 1799
ataaatgaac ctttattaaa gacacttcaa tgcaaaaaaa aaaaaaaaaa 1849

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<210> 11
<211> 565
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 55..468

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<220>
<221> sig_peptide
<222> 55..99
<223> Von Heijne matrix
      score 8.96936032049195
      seq FTLLFLAAVAGA/LV

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<400> 11
attccccaga ccttctgcag attctgtggt tatactcact cctcatccca aaga atg 57
Met
-15
aaa ttt acc act ctc ctc ttc ttg gca gct gta gca ggg gcc ctg gtc 105
Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu Val
-10 -5 1
tat gct gaa gat gcc tcc tct gac tcg acg ggt gct gat cct gcc cag 153
Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala Gln
5 10 15
gaa gct ggg acc tct aag cct aat gaa gag atc tca ggt cca gca gaa 201
Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala Glu
20 25 30
cca gct tca ccc cca gag aca acc aca aca gcc cag gag act tcg gcg 249
Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Thr Ala Gln Glu Thr Ser Ala
35 40 45 50
gca gca gtt cag ggg aca gcc aag gtc acc tca agc agg cag gaa cta 297
Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu Leu
55 60 65
aac ccc ctg aaa tcc ata gtg gag aaa agt atc tta cta aca gaa caa 345
Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu Gln
70 75 80
gcc ctt gca aaa gca gga aaa gga atg cac gga ggc gtg cca ggt gga 393
Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly Gly
85 90 95
aaa caa ttc atc gaa aat gga agt gaa ttt gca caa aaa tta ctg aag 441
Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu Lys
100 105 110

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aaa ttc agt cta tta aaa cca tgg gca tgagaagctg aataatggga      488
Lys Phe Ser Leu Leu Lys Pro Trp Ala
115                      120
tcattgggact taaagcctta aatacccttg tagcccagag ctattaaaac gaaagcatcc      548
aaaaaaaaaaaa aaaaaaaa      565

<210> 12
<211> 1663
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 152..475

<220>
<221> sig_peptide
<222> 152..244
<223> Von Heijne matrix
      score 10.0910253445132
      seq LVLVVTRSPVNA/CL

<400> 12
atgtgtctgc tgccgccatt gtgcggcgct ggtccctca gaggggttcct gctgctgccg      60
gtgccttgga ccctccccc cgtttctcgt tctactgcc caggagcccg gcgggtccgg      120
gactcccgtc cgtgccggtg cgggcgcggg c atg tgg ctg tgg gag gac cag      172
                               Met Trp Leu Trp Glu Asp Gln
                               -30          -25

ggc ggc ctc ctg ggc cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg      220
Gly Gly Leu Leu Gly Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu
                               -20          -15          -10

gtg acg cgg agc ccg gtc aat gcc tgc ctc ctc acc ggc agc ctc ttc      268
Val Thr Arg Ser Pro Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe
                               -5          1          5

gtt cta ctg cgc gtc ttc agc ttt gag ccg gtg ccc tct tgc agg gcc      316
Val Leu Leu Arg Val Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala
10          15          20

ctg cag gtg ctc aag ccc cgg gac cgc att tct gcc atc gcc cac cgt      364
Leu Gln Val Leu Lys Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg
25          30          35          40

ggc ggc agc aam sag gcg ccc gag aac acg ctg gcg gcc att cgg cag      412
Gly Gly Ser Xaa Xaa Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln
45          50          55

cta aga atg gag caa cag gcg tgg agt tgg aca ttg agt tta ctt ctg      460
Leu Arg Met Glu Gln Gln Ala Trp Ser Trp Thr Leu Ser Leu Leu Leu
60          65          70

acg gga ttc ctg tct taatgcacga taacacagta gataggacga ctgatgggac      515
Thr Gly Phe Leu Ser
75

tgggcgattg tgtgatttga catttgaaca aattaggaag ctgaatcctg cagcaaacca      575
cagactcagg aatgatttcc ctgatgaaaa gatccctacc ctaaggggaag ctgttgacga      635
gtgcctaaac cataacctca caatcttctt tgatgtcaaa ggccatgcac acaaggctac      695
tgaggctcta aagaaaatgt atatggaatt tcttcaactg tataataata gtgtgggtctg      755
ttctttcttg ccagaagtta tctacaaggt aacattcggg atttttcttg tacatattag      815
atgagacaaa cagatcggga tgtaataaca gcattaactc acagaccttg gagcctaagc      875
catacaggag atgggaaacc acgctatgat actttctgga aacattttat atttgttatg      935
atggacattt tgctcgattg gagcatgcat aatatcttgt ggtacctgtg tggaatttca      995
gctttcctca tgcaaaaagga ttttgtatcc cgggcctact tgaagaagtg gtcagctaaa      1055

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ggaatccagg ttgttggttg gactgttaat acctttgatg aaaagagtta ctacgaatcc 1115
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actttcacgg tgggacgaaa cgggttcaga aactgccagg ggcctcatalc agggatatca 1235
aaataccctt tgtgctagcc caggccctgg ggaatcaggt gactcacaca aatgcaatag 1295
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gcatgccaga gttcaacact gttgctcttg aaaatctggg tctgaaaaaa cgcacaagag 1415
cccctgccct gccctagctg aggcacacag ggagaccag tgaggataag cacagattga 1475
attgtacaat ttgcagatgc agatgtaaat gcatgggaca tgcattgataa ctcagagttg 1535
acattttaaa acttgccaca cttatttcaa atatttgtac tcagctatgt taacatgtac 1595
tgtagacatc aaacttgtgg ccatactaata aaaattatta aaaggagcac taaaaaaaaa 1655
aaaaaaaaa 1663

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<210> 13
<211> 744
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 112..552

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<220>
<221> sig_peptide
<222> 112..183
<223> Von Heijne matrix
      score 11.7298925418815
      seq FVLGLGLTPPTLA/QD

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<400> 13
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actgccagat ttttgtaaga ttcttctctc tgggagcctg tgttggaaga g atg gtg 117
                                     Met Val
atg ggc ctg ggc gtt ttg ttg ttg gtc ttc gtg ctg ggt ctg ggt ctg 165
Met Gly Leu Gly Val Leu Leu Leu Val Phe Val Leu Gly Leu Gly Leu
      -20                      -15                      -10
acc cca ccg acc ctg gct cag gat aac tcc agg tac aca cac ttc ctg 213
Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His Phe Leu
      -5                      1                      5                      10
acc cag cac tat gat gcc aaa cca cag ggc cgg gat gac aga tac tgt 261
Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg Tyr Cys
      15                      20                      25
gaa agc atc atg agg aga cgg ggc ctg acc tca ccc tgc aaa gac atc 309
Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys Asp Ile
      30                      35                      40
aac aca ttt att cat ggc aac aag cgc acg atc aag gcc atc tgt gaa 357
Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile Cys Glu
      45                      50                      55
aac aag aat gga aac cct cac aga gaa aac cta aga ata agc aag tct 405
Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser Lys Ser
      60                      65                      70
tct ttc cag gtc acc act tgc aag cta cat gga ggt tcc ccc tgg cct 453
Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro Trp Pro
      75                      80                      85                      90
cca tgc cag tac cga gcc aca gcg ggg ttc aga aac gtt gtt gtt gct 501
Pro Cys Gln Tyr Arg Ala Thr Ala Gly Phe Arg Asn Val Val Val Ala
      95                      100                      105
tgt gaa aat ggc tta cct gtc cac ttg gat cag tca att ttc cgt cgt 549
Cys Glu Asn Gly Leu Pro Val His Leu Asp Gln Ser Ile Phe Arg Arg

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110      115      120
ccg taaccagcgg gcccttggtc aagtgtgtggc tctgtgtgcc ttgccttcca 602
Pro
tttccccctct gcaccagaaa cagtgggtggc aacattcatt gccaaagggcc caaagaaaaga 662
gctacctgga cctttttgttt tctgtttgac aacatgttta ataaataaaa atgtcttgat 722
atcagcaaaaa aaaaaaaaaa aa 744

<210> 14
<211> 1759
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 101..1243

<220>
<221> sig_peptide
<222> 101..199
<223> Von Heijne matrix
      score 3.57142340200611
      seq FLCLGMALCPRQA/TR

<400> 14
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ttttttccat tctctctctc cacttcttca gtgagcagcc atg agt tgg act gtg 115
                        Met Ser Trp Thr Val
                        -30
cct gtt gtg cgg gcc agc cag aga gtg agc tcg gtg gga gcg aat ttc 163
Pro Val Val Arg Ala Ser Gln Arg Val Ser Ser Val Gly Ala Asn Phe
      -25      -20      -15
cta tgc ctg ggg atg gcc ctg tgt ccg cgt caa gca acg cgc atc ccg 211
Leu Cys Leu Gly Met Ala Leu Cys Pro Arg Gln Ala Thr Arg Ile Pro
      -10      -5      1
ctc aac ggc acc tgg ctc ttc acc ccc gtg agc aag atg gcg act gtg 259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val
5      10      15      20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac 307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
      25      30      35
agt aag gtc tcc atc ata gga act gga tcg gtg ggc atg gcc tgc gct 355
Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
      40      45      50
atc agc atc tta tta aaa ggc ttg agt gat gaa ctt gcc ctt gtg gat 403
Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
      55      60      65
ctt gat gaa gac aaa ctg aag ggt gag acg atg gat ctt caa cat ggc 451
Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
70      75      80
agc cct ttc acg aaa atg cca aat att gtt tgt agc aaa gat tac ttt 499
Ser Pro Phe Thr Lys Met Pro Asn Ile Val Cys Ser Lys Asp Tyr Phe
85      90      95      100
gtc aca gca aac tcc aac cta gtg att atc aca gca ggt gca cgc caa 547
Val Thr Ala Asn Ser Asn Leu Val Ile Ile Thr Ala Gly Ala Arg Gln
      105      110      115
gaa aag gga gaa acg cgc ctt aat tta gtc cag cga aat gtg gcc atc 595
Glu Lys Gly Glu Thr Arg Leu Asn Leu Val Gln Arg Asn Val Ala Ile
120      125      130

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ttc aag tta atg att tcc agt att gtc cag tac agc ccc cac tgc aaa	643
Phe Lys Leu Met Ile Ser Ser Ile Val Gln Tyr Ser Pro His Cys Lys	
135 140 145	
ctg att att gtt tcc aat cca gtg gat atc tta act tat gta gct tgg	691
Leu Ile Ile Val Ser Asn Pro Val Asp Ile Leu Thr Tyr Val Ala Trp	
150 155 160	
aag ttg agt gca ttt ccc aaa aac cgt att att gga agc ggc tgt aat	739
Lys Leu Ser Ala Phe Pro Lys Asn Arg Ile Ile Gly Ser Gly Cys Asn	
165 170 175 180	
ctg gat act gct cgt ttt cgt ttc ttg att gga caa aag ctt ggt atc	787
Leu Asp Thr Ala Arg Phe Arg Phe Leu Ile Gly Gln Lys Leu Gly Ile	
185 190 195	
cat tct gaa agc tgc cat gga tgg atc ctc gga gag cat gga gac tca	835
His Ser Glu Ser Cys His Gly Trp Ile Leu Gly Glu His Gly Asp Ser	
200 205 210	
agt gtt cct gtg tgg agt gga gtg aac ata gct ggt gtc cct ttg aag	883
Ser Val Pro Val Trp Ser Gly Val Asn Ile Ala Gly Val Pro Leu Lys	
215 220 225	
gat ctg aac tct gat ata gga act gat aaa gat cct gag caa tgg aaa	931
Asp Leu Asn Ser Asp Ile Gly Thr Asp Lys Asp Pro Glu Gln Trp Lys	
230 235 240	
aat gtc cac aaa gaa gtg act gca act gcc tat gag att att aaa atg	979
Asn Val His Lys Glu Val Thr Ala Thr Ala Tyr Glu Ile Ile Lys Met	
245 250 255 260	
aaa ggt tat act tct tgg gcc att ggc cta tct gtg gcc gat tta aca	1027
Lys Gly Tyr Thr Ser Trp Ala Ile Gly Leu Ser Val Ala Asp Leu Thr	
265 270 275	
gaa agt att ttg aag aat ctt agg aga ata cat cca gtt tcc acc ata	1075
Glu Ser Ile Leu Lys Asn Leu Arg Arg Ile His Pro Val Ser Thr Ile	
280 285 290	
att aag ggc ctc tat gga ata gat gaa gaa gta ttc ctc agt att cct	1123
Ile Lys Gly Leu Tyr Gly Ile Asp Glu Glu Val Phe Leu Ser Ile Pro	
295 300 305	
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Cys Ile Leu Gly Glu Asn Gly Ile Thr Asn Leu Ile Lys Ile Lys Leu	
310 315 320	
acc cct gaa gaa gag gcc cat ctg aaa aaa agt gca aaa aca ctc tgg	1219
Thr Pro Glu Glu Glu Ala His Leu Lys Lys Ser Ala Lys Thr Leu Trp	
325 330 335 340	
gaa att cag aat aag ctt aag ctt taaagttgcc taaaactacc attccgaat	1273
Glu Ile Gln Asn Lys Leu Lys Leu	
345	
tattgaagag atcatagata caggattata taacgaaatt ttgaataaac ttgaattcct	1333
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ttttattgag catccacgtg ctggacgata cttattttaca attcctaagt attttttgta	1453
cctctgatgt agcagcactt gccatgttat atatattgtat ttggcatttg gttcccaaaa	1513
agtaggatgt aggtatttat tgtgttctag aaattccgac tcttttcatt agatatatgc	1573
tatttctttc attcttgctg gttttacacct atgttcattt atatgctgta aaaaagtagt	1633
agcttcttct acaatgtaaa aataaatgta catacaaaaa aatgcagtag tatatacaat	1693
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aaaaaa	1759

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Met Ser Trp Thr Val
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cct gtt gtg cgg gcc agc cag aga atg agc tcg gtg gga gcg aat ttc 163
Pro Val Val Arg Ala Ser Gln Arg Met Ser Ser Val Gly Ala Asn Phe
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Leu Cys Leu Gly Met Ala Leu Cys Leu Arg Gln Ala Thr Arg Ile Pro
-10 -5 1
ctc aac ggc acc tgg ctc ttc aca ccc gtg agc aag atg gcg act gtg 259
Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser Lys Met Ala Thr Val
5 10 15 20
aag agt gag ctt att gag cgt ttc act tcc gag aag ccc gtt cat cac 307
Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu Lys Pro Val His His
25 30 35
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Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val Gly Met Ala Cys Ala
40 45 50
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Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu Leu Ala Leu Val Asp
55 60 65
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Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met Asp Leu Gln His Gly
70 75 80
agc cct ttc acg aaa atg cca ata ttg ttt gta gca aag att act ttg 499
Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val Ala Lys Ile Thr Leu
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Ser Gln Gln Thr Pro Thr
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gtagctttctt ctacaatgta aaaataaatg tacatacaaa aaaatgcagt agtatataca 1687
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      -10      -5      1
agt agc act ttg aag cct act att gaa gca ttg cct aat gtg cta cct 154
Ser Ser Thr Leu Lys Pro Thr Ile Glu Ala Leu Pro Asn Val Leu Pro
      5      10      15
tta aat gaa gat gtt aat aag cag gaa gaa aag aat gaa gat cat act 202
Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr
      20      25      30
ccc aat tat gct cct gct aat gag aaa aat ggc aat tat tat aaa gat 250
Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp
      35      40      45      50
ata aaa caa tat gtg ttc aca aca caa aat cca aat ggc act gag tct 298
Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser
      55      60      65
gaa ata tct gtg aga gcc aca act gac ctg aat ttt gct cta aaa aac 346
Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn
      70      75      80
gga tca acc cca aac gtg cct gca ttt tgg aca atg tta gct aaa gct 394
Gly Ser Thr Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala
      85      90      95
ata aat gga aca gca gtg gtc atg gat gat aaa gat caa tta ttt cac 442
Ile Asn Gly Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His
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cca att cca gag tct gat gtg aat gct aca cag gga gaa aat cag cca 490
Pro Ile Pro Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro
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gat cta gag gat ctg aag atc aaa ata atg ctg gga atc tcg ttg atg 538
Asp Leu Glu Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met
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acc ctc ctc ctc ttt gtg gtc ctc ttg gca ttc tgt agt gct aca ctg 586
Thr Leu Leu Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu
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tac aaa ctg agg cat ctg agt tat aaa agt tgt gag agt cag tac tct 634

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Val	Asn	Pro	Glu	Leu	Ala	Thr	Met	Ser	Tyr	Phe	His	Pro	Ser	Glu	Gly		
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Val	Ser	Asp	Thr	Ser	Phe	Ser	Lys	Ser	Ala	Glu	Ser	Ser	Thr	Phe	Leu		
195				200					205					210			
ggg	acc	act	tct	tca	gat	atg	aga	aga	tca	ggc	aca	aga	aca	tca	gaa	778	
Gly	Thr	Thr	Ser	Ser	Asp	Met	Arg	Arg	Ser	Gly	Thr	Arg	Thr	Ser	Glu		
			215					220					225				
tct	aag	ata	atg	acg	gat	atc	att	tcc	ata	ggc	tca	gat	aat	gag	atg	826	
Ser	Lys	Ile	Met	Thr	Asp	Ile	Ile	Ser	Ile	Gly	Ser	Asp	Asn	Glu	Met		
		230				235						240					
cat	gaa	aac	gat	gag	tcg	gtt	acc	cgg	tgaagaaatc	aaggaacccg						873	
His	Glu	Asn	Asp	Glu	Ser	Val	Thr	Arg									
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ttt cct cca	gaa atc act	gct tca gaa	tat gag tcc	aca gaa	ctt tca											159	
Phe Pro Pro	Glu Ile Thr	Ala Ser Glu	Tyr Glu Ser	Thr Glu	Leu Ser												
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gcc acg acc	ttt tca act	caa agc ccc	ttg caa aaa	tta ttt	gct aga											207	
Ala Thr Thr	Phe Ser Thr	Gln Ser Pro	Leu Gln Lys	Leu Phe	Ala Arg												
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aaa atg aaa	atc tta ggg	act atc cag	atc ctg ttt	gga att	atg acc											255	
Lys Met Lys	Ile Leu Gly	Thr Ile Gln	Ile Leu Phe	Gly Ile	Met Thr												
	30		35		40												
ttt tct ttt	gga gtt atc	ttc ctt ttc	act ttg tta	aaa cca	tat cca											303	
Phe Ser Phe	Gly Val Ile	Phe Leu Phe	Thr Leu Leu	Lys Pro	Tyr Pro												
	45		50		55												
agg ttt ccc	ttt ata ttt	ctt tca gga	tat cca ttc	tgg ggc	tct gtt											351	
Arg Phe Pro	Phe Ile Phe	Leu Ser Gly	Tyr Pro Phe	Trp Gly	Ser Val												
	60		65		70												
ttg ttc att	aat tct gga	gcc ttc cta	att gca gtg	aaa aga	aaa acc											399	
Leu Phe Ile	Asn Ser Gly	Ala Phe Leu	Ile Ala Val	Lys Arg	Lys Thr												

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      75              80              85
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Thr Glu Thr Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala
90              95              100              105
ctg gga gca ata gct gga atc att ctc ctc aca ttt ggt ttc atc cta      495
Leu Gly Ala Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu
      110              115              120
gat caa aac tac att tgt ggt tat tct cac caa aat agt cag tgt aag      543
Asp Gln Asn Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys
      125              130              135
gct gtt act gtc ctg ttc ttg gga att ttg att aca ttg atg act ttc      591
Ala Val Thr Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe
      140              145              150
agc att att gaa tta ttc att tct ctg cct ttc tca att ttg ggg tgc      639
Ser Ile Ile Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys
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cac tca gag gat tgt gat tgt gaa caa tgt tgt tgactagcac tgtgagaata      692
His Ser Glu Asp Cys Asp Cys Glu Gln Cys Cys
170              175              180
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      Met Ala Thr Ala Gln Leu Gln
      -35
agg act ccc atg agt gca ctg gta ttt ccc aat aag ata tca act gaa      162
Arg Thr Pro Met Ser Ala Leu Val Phe Pro Asn Lys Ile Ser Thr Glu
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cac cag tct ttg gtg tta gtg aag agg ctt cta gca gtt tca gta tcc      210
His Gln Ser Leu Val Leu Val Lys Arg Leu Leu Ala Val Ser Val Ser
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tgt atc acg tat ttg agg gga ata ttc cca gaa tgc gct tat gga aca      258
Cys Ile Thr Tyr Leu Arg Gly Ile Phe Pro Glu Cys Ala Tyr Gly Thr
1              5              10              15
aga tat cta gat gat ctt tgt gtc aaa ata ctg aga gaa gat aaa aat      306
Arg Tyr Leu Asp Asp Leu Cys Val Lys Ile Leu Arg Glu Asp Lys Asn
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tgc cca gga tct aca cag tta gtg aaa tgg att cta gga tgt tat gat      354
Cys Pro Gly Ser Thr Gln Leu Val Lys Trp Ile Leu Gly Cys Tyr Asp
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Lys	Tyr	Thr	Asn	Asn	Gly	Pro	Leu	Met	Asp	Phe	Ile	Ser	Lys	Asn	Gln	
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Ser	Asn	Glu	Ser	Ser	Met	Leu	Ser	Thr	Asp	Thr	Lys	Lys	Ala	Ser	Ile	
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ctc	ctc	att	cgc	aag	att	tat	atc	cta	atg	caa	aat	ctg	ggg	cct	tta	594
Leu	Leu	Ile	Arg	Lys	Ile	Tyr	Ile	Leu	Met	Gln	Asn	Leu	Gly	Pro	Leu	
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cct	aat	gat	gtt	tgt	ttg	acc	atg	aaa	ctt	ttt	tac	tat	gat	gaa	gtt	642
Pro	Asn	Asp	Val	Cys	Leu	Thr	Met	Lys	Leu	Phe	Tyr	Tyr	Asp	Glu	Val	
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Thr	Pro	Pro	Asp	Tyr	Gln	Pro	Pro	Gly	Phe	Lys	Asp	Gly	Asp	Cys	Glu	
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Gly	Val	Ile	Phe	Glu	Gly	Glu	Pro	Met	Tyr	Leu	Asn	Val	Gly	Glu	Val	
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Arg	Met	Glu	Asn	Ile	Asp	Ser	Thr	Ile	Leu	Ser	Pro	Lys	Gln	Ile	Lys	
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Thr	Pro	Phe	Gln	Lys	Ile	Leu	Arg	Asp	Lys	Asp	Val	Glu	Asp	Glu	Gln	
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Glu	His	Tyr	Thr	Ser	Asp	Asp	Leu	Asp	Ile	Glu	Thr	Lys	Met	Glu	Glu	
	225				230					235				240		
cag	gaa	aaa	aac	cct	gca	tct	tct	gaa	ctt	gaa	gaa	cca	agt	tta	gtt	978
Gln	Glu	Lys	Asn	Pro	Ala	Ser	Ser	Glu	Leu	Glu	Glu	Pro	Ser	Leu	Val	
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Cys	Glu	Glu	Asp	Glu	Ile	Met	Arg	Ser	Lys	Glu	Ser	Pro	Asp	Leu	Ser	
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Ile	Ser	His	Ser	Gln	Val	Glu	Gln	Leu	Val	Asn	Lys	Thr	Ser	Glu	Leu	
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Asp	Met	Ser	Glu	Ser	Lys	Thr	Arg	Ser	Gly	Lys	Val	Phe	Gln	Asn	Lys	
		290				295					300					
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Met	Ala	Asn	Gly	Asn	Gln	Pro	Val	Lys	Ser	Ser	Lys	Glu	Asn	Arg	Lys	
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Arg	Ser	Gln	His	Glu	Ser	Gly	Arg	Ile	Val	Leu	His	His	Phe	Asp	Ser	
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Ser	Ser	Gln	Glu	Ser	Val	Pro	Lys	Arg	Arg	Lys	Phe	Ser	Glu	Pro	Lys	
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Glu	His	Ile														

355
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Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly Ala Glu Asn Leu His
-10 -5 1
gtg aaa ata agt tgc tct ctg gac tgg ttg atg gtc tca gtt atc cca 152
Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met Val Ser Val Ile Pro
5 10 15 20
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Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala Asp Glu Leu His Leu
25 30 35
gga atg ggc tgc cct gca aat cgg ata cat aca tat gta tat gag ttt 248
Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr Tyr Val Tyr Glu Phe
40 45 50
ata tat ctt gtt cgt gat tgt ggc atc agg aca agg gta gtt tct gag 296
Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr Arg Val Val Ser Glu
55 60 65
gaa act ctc ctt ttt caa acc gag ctg tac ttt acc cca agg aat ata 344
Glu Thr Leu Leu Phe Gln Thr Glu Leu Tyr Phe Thr Pro Arg Asn Ile
70 75 80
gat cat gac cct cag gaa atc cat ttg gag tgt tcc acc tct agg aaa 392
Asp His Asp Pro Gln Glu Ile His Leu Glu Cys Ser Thr Ser Arg Lys
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Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn Glu Ile Lys Leu Asp
105 110 115
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Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr Ala Glu Glu Leu Gly

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Leu Leu Ser Ser Ser Pro Asn Leu Leu

135      140
aacttgaagc tgggtgttatg tatttttcag gaaaacagtt tcatttttttc atagcaaaaa 595
tatagttggg gtatatctct ccttaagtct ctggtttcta aaaaccctac ttcagtaaag 655
gtcctgatta gttgattagc gaaaaaaaaa aaaaaa 691

<210> 20
<211> 1138
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 271..969

<220>
<221> sig_peptide
<222> 271..366
<223> Von Heijne matrix
      score 5.6680378526706
      seq WMGLACFRSLAAS/SP

<220>
<221> misc_feature
<222> 989
<223> n=a, g, c or t

<400> 20
aaaaaccttt caagtgccccc ctccctttcct taaagtcttt tatagggggtc cccttcttgg 60
ccatctccat cctgtgagtc aggactgaaa gggcacagac aggtcactgc cagcattggt 120
ggggcaagcc tgcaagcacg catcactggg gatctgacat gacaatggcc gcctgcccc 180
tctgaggggt acaggactta ccccagtggt aagcagctaa gcaggtctga ccagccgacc 240
tggacctggc caagggtcct gtcacccctc atg gcc acc ccg cca ttc cgg ctg 294
                                Met Ala Thr Pro Pro Phe Arg Leu
                                -30                                -25
ata agg aag atg ttt tcc ttc aag gtg agc aga tgg atg ggg ctt gcc 342
Ile Arg Lys Met Phe Ser Phe Lys Val Ser Arg Trp Met Gly Leu Ala
                                -20                                -15                                -10
tgc ttc cgg tcc ctg gcg gca tcc tct ccc agt att cgc cag aag aaa 390
Cys Phe Arg Ser Leu Ala Ala Ser Ser Pro Ser Ile Arg Gln Lys Lys
                                -5                                1                                5
cta atg cac aag ctg cag gag gaa aag gct ttt cgc gaa gag atg aaa 438
Leu Met His Lys Leu Gln Glu Glu Lys Ala Phe Arg Glu Glu Met Lys
                                10                                15                                20
att ttt cgt gaa aaa ata gag gac ttc agg gaa gag atg tgg act ttc 486
Ile Phe Arg Glu Lys Ile Glu Asp Phe Arg Glu Glu Met Trp Thr Phe
25                                30                                35                                40
cga ggc aag atc cat gct ttc cgg ggc cag atc ctg ggt ttt tgg gaa 534
Arg Gly Lys Ile His Ala Phe Arg Gly Gln Ile Leu Gly Phe Trp Glu
                                45                                50                                55
gag gag aga cct ttc tgg gaa gag gag aaa acc ttc tgg aaa gag gaa 582
Glu Glu Arg Pro Phe Trp Glu Glu Lys Thr Phe Trp Lys Glu Glu
                                60                                65                                70
aaa tcc ttc tgg gaa atg gaa aag tct ttc agg gag gaa gag aaa act 630
Lys Ser Phe Trp Glu Met Glu Lys Ser Phe Arg Glu Glu Glu Lys Thr
75                                80                                85

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ttc tgg aaa aag tac cgc act ttc tgg aag gag gat aag gcc ttc tgg      678
Phe Trp Lys Lys Tyr Arg Thr Phe Trp Lys Glu Asp Lys Ala Phe Trp
90 95 100
aaa gag gac aat gcc tta tgg gaa aga gac cgg aac ctt ctt cag gag      726
Lys Glu Asp Asn Ala Leu Trp Glu Arg Asp Arg Asn Leu Leu Gln Glu
105 110 115 120
gac aag gcc ctg tgg gag gaa gaa aag gcc ctg tgg gta gag gaa aga      774
Asp Lys Ala Leu Trp Glu Glu Glu Lys Ala Leu Trp Val Glu Glu Arg
125 130 135
gcc ctc ctt gag ggg gag aaa gcc ctg tgg gaa gat aaa acg tcc ctc      822
Ala Leu Leu Glu Gly Glu Lys Ala Leu Trp Glu Asp Lys Thr Ser Leu
140 145 150
tgg gag gaa gag aat gcc ctc tgg gag gaa gag agg gcc ttc tgg atg      870
Trp Glu Glu Glu Asn Ala Leu Trp Glu Glu Glu Arg Ala Phe Trp Met
155 160 165
gag aac aat ggc cac att gcc gga gag cag atg ctc gaa gat ggg ccc      918
Glu Asn Asn Gly His Ile Ala Gly Glu Gln Met Leu Glu Asp Gly Pro
170 175 180
cac aac gcc aac aga ggg cag cgc ttg ctg gcc ttc tcc cga ggc agg      966
His Asn Ala Asn Arg Gly Gln Arg Leu Leu Ala Phe Ser Arg Gly Arg
185 190 195 200
gcg tagccagcat gcaggtgcan gggccctgtg gtccagactc ccctggggtg      1019
Ala
ggattcaagt ccagggtgag cccatgtgct ggagaaaata cacactcatt ggtctccttg      1079
ctttgaaaga tccaataaag tcctgaggca aggtttggaa aaccaaaaaa aaaaaaaaaa      1138

<210> 21
<211> 468
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 76..276

<220>
<221> sig_peptide
<222> 76..135
<223> Von Heijne matrix
      score 5.21332530399231
      seq SPVFLVFPPEITA/SE

<400> 21
agcacaagaa aagaacatgg tctagactga agtaccaact aaatcatctc ctttcaaatt      60
atcaccgaca ccatac atg gat tca agc acc gca cac agt ccg gtg ttt ctg      111
      Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu
      -20 -15 -10
gta ttt cct cca gaa atc act gct tca gaa tat gag tcc aca gaa ctt      159
Val Phe Pro Pro Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu
      -5 1 5
tca gcc acg acc ttt tca act caa agc ccc ttg caa aaa tta ttt gct      207
Ser Ala Thr Thr Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala
10 15 20
aga aaa atg aaa atc tta ggg gat atc cat tct ggg gct ctg ttt tgt      255
Arg Lys Met Lys Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys
25 30 35 40
tca tta att ctg gag cct tcc taattgcagt gaaaagaaaa accacagaaa      306
Ser Leu Ile Leu Glu Pro Ser

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45
ctctgggaat tttgattaca ttgatgactt tcagcattat tgaattattc atttctctgc 366
ctttctcaat tttgggtgc cactcagagg attgtgattg tgaacaatgt tgttgactag 426
cactgtgaga ataaagatgt gttaaaataa aaaaaaaaaa aa 468

<210> 22
<211> 720
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 6..287

<220>
<221> sig_peptide
<222> 6..80
<223> Von Heijne matrix
score 4.17710408129886
seq ISLSHLFLDLRS/LW

<400> 22
atttg atg tgc ttc tta gtc tcg ttt aac ttg ccg att cat ata tcc ctg 50
Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu
-25 -20 -15
tct cat ttg ttc tta gat ttg tca cga agc ctc tgg ttt ttg gct tgt 98
Ser His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys
-10 -5 1 5
cct ggt ttg aac ttg gtg tat ctg gct ctt gac tca ttt tct gac ctc 146
Pro Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu
10 15 20
aga cca tcc tta aat ctg ctt ttc tac ttt gta cca ggc ttt ggc gtc 194
Arg Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val
25 30 35
tcc aag tac ctg acc tca gct caa cct gtc ttg ggt ttt ctt ctc ctc 242
Ser Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu
40 45 50
cct gac att gac aac cca gcc ctc cta ggc aca gag aga tgg agc 287
Pro Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser
55 60 65
tgagtgtggt tttcctgaaa taaagcttgc attatgagag ggaataaaca gaagaaaaaa 347
atagtaagta aaatcttgct tgcctctcag taaaataaag ctctattttt cgtttttttt 407
ttttccaact tcctgtacaa aaaagggaaa acttttagctt ttgggggaaa tttggagcta 467
gcctgttggt actgttgagc ttagtgtatc tataactata tattattcca caatatctta 527
aatactttat aaagataattt tcataaatta cagcaatcct ggcttttagat gattgatggc 587
cattttttaa caattaaagc taatttctag ctttttatga gtttggtatt aagcacagta 647
gtttcttaga aagtctccag ggaatgcatt ttgcaaaata aaaatcagct aatgacccaa 707
aaaaaaaaaa aaa 720

<210> 23
<211> 727
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 171..692

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<220>
<221> sig_peptide
<222> 171..227
<223> Von Heijne matrix
      score 4.17573075349936
      seq LLLGQRCSLKVSG/QE

<400> 23
attgtgacat caccgtgcac tagccaatgg ctgcctgcct aagctgggtc cctgggtctcc      60
tgggactact agccctttgt tgatagggag aagccaacat ctcccgcagg accccctaat      120
cttcagggca gctcccagag catggatccc tcctgattcc actcagcccg atg ttc      176
                               Met Phe
ctc aca gtc aag ctg ctc ctg ggc cag aga tgc agt ctg aag gtg tca      224
Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys Val Ser
      -15                               -10                               -5
ggg caa gag agt gta gcc acg ctg aag aga ctg gtg tcc agg cgg ctg      272
Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg Arg Leu
      1                               5                               10                               15
aag gtg cct gag gag cag cag cac ctg ctt ttc cgt ggc cag ctc ctg      320
Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln Leu Leu
      20                               25                               30
gag gat gac aag cac ctc tct gac tac tgc att ggg ccc aat gcc tct      368
Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn Ala Ser
      35                               40                               45
atc aat gtc atc atg cag ccc ttg gag aag atg gcg cta aag gag gcc      416
Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys Glu Ala
      50                               55                               60
cac cag ccg cag acc cag ccc ctg tgg cac cag ctg gga ctg gtc cta      464
His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu Val Leu
      65                               70                               75
gct aaa cac ttt gaa cca cag gat gcc aag gcc gtg ctg cag ctg cta      512
Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln Leu Leu
      80                               85                               90                               95
agg cag gag cac gag gag cgc ctg cag aag ata agc ctg gag cac ctg      560
Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu His Leu
      100                               105                               110
gag cag ctg gcc cag tac ctc ctg gca gag gag cct cac gtg gag cca      608
Glu Gln Leu Ala Gln Tyr Leu Leu Ala Glu Glu Pro His Val Glu Pro
      115                               120                               125
gct gga gag agg gag ctt gag gcg aag gca cgg cct cag agc tcc tgt      656
Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser Ser Cys
      130                               135                               140
gac atg gag gag aag gag gag gca gca gct gat cag taaacggggcc      702
Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln
      145                               150                               155
atcctaccgg aaaaaaaaaa aaaaaa      727

<210> 24
<211> 470
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 137..454

<220>
<221> sig_peptide

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<222> 137..187

<223> Von Heijne matrix

score 10.7019149919754

seq VLMLLAVLIWTGA/EN

<400> 24

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atcctgtgaa ctacccaaaa ggaggaaaac gaacgcagct gagcatggga tgccatataa      60
aaatcactta aaccagtcgc cactccttgt ttcctgagtt gtcctgtgct ggaggtctgc      120
tcagacgaag gtctcc atg gcg tta gaa gtc ttg atg ctc ctc gct gtc ttg      172
          Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu
                    -15                      -10
att tgg acc ggt gct gag aac ctc cat gtg aaa ata agt tgc tct ctg      220
Ile Trp Thr Gly Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu
-5                      1                      5                      10
gac tgg ttg atg gtc tca gtt atc cca gtt gca gaa agc aga aat ctg      268
Asp Trp Leu Met Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu
          15                      20                      25
tat ata ttt gcg gat gaa tta cat ctg gga atg ggc tgc cct gca aat      316
Tyr Ile Phe Ala Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn
          30                      35                      40
cgg ata cat aca tat gta tat gag ttt ata tat ctt gtt cgt gat tgt      364
Arg Ile His Thr Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys
          45                      50                      55
ggc atc agg aca agg gta aga aca gtg att gtc tgt aaa aaa tac tgc      412
Gly Ile Arg Thr Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys
60                      65                      70                      75
atg ttt tgt cag act ttt atg cct agt att aaa att gtc ttt      454
Met Phe Cys Gln Thr Phe Met Pro Ser Ile Lys Ile Val Phe
          80                      85
taaaaaaaaa aaaaaa      470

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<210> 25

<211> 987

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 238..609

<220>

<221> sig_peptide

<222> 238..291

<223> Von Heijne matrix

score 10.0374888212272

seq LLLLVMALPPGTT/GV

<400> 25

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attccattca cagactcttg ttgggcagca gccacccgct cacctccatc cccaggactt      60
agagggacgc agggcggttg gaacagagga cactccaggc gctgaccctg ggaggccagg      120
accagggcca aagtcctctg ggcaagagga gtcctcagag gtccttcatt cagcggttcc      180
gggaggtctg ggaagcccac ggcttggtg gggcagggtc aacgccgccca ggccgcc      237
atg gtc ctg tgc tgg ctg ctg ctt ctg gtg atg gct ctg ccc cca ggc      285
Met Val Leu Cys Trp Leu Leu Leu Val Met Ala Leu Pro Pro Gly
          -15                      -10                      -5
acg acg ggc gtc aag gac tgc gtc ttc tgt gag ctc acc gac tcc atg      333
Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
          1                      5                      10

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45	50	55	
ttg ggg gac acc cag cac gga gag aag ctg agg cgg aac tgc act atc			352
Leu Gly Asp Thr Gln His Gly Glu Lys Leu Arg Arg Asn Cys Thr Ile			
60	65	70	75
tac cgg ccc tgg ttc tcc ccc tac agc tac ttc gtg tgt gca gac aaa			400
Tyr Arg Pro Trp Phe Ser Pro Tyr Ser Tyr Phe Val Cys Ala Asp Lys			
80	85	90	
gag agc cag ctg gag gcc tat gac ttc cca gag gtg cag cag gat gag			448
Glu Ser Gln Leu Glu Ala Tyr Asp Phe Pro Glu Val Gln Gln Asp Glu			
95	100	105	
ggc aag tgg gac aac tgc ctt tct gag gac atg gct gag aac atc tgt			496
Gly Lys Trp Asp Asn Cys Leu Ser Glu Asp Met Ala Glu Asn Ile Cys			
110	115	120	
tcg tcc tct tcc tcc cca gag aac act tgc cct cga gaa gcc acc aag			544
Ser Ser Ser Ser Ser Pro Glu Asn Thr Cys Pro Arg Glu Ala Thr Lys			
125	130	135	
aaa tcc agg cat ggc ctg gac tcc atc aca tcc cag gac atc cta atg			592
Lys Ser Arg His Gly Leu Asp Ser Ile Thr Ser Gln Asp Ile Leu Met			
140	145	150	155
gct tcc aga tgg cac cca gca cag cag aat ggc tac aag tgc gtg gcc			640
Ala Ser Arg Trp His Pro Ala Gln Gln Asn Gly Tyr Lys Cys Val Ala			
160	165	170	
tgc tgc cgc atg tac ccc acc ctg gac ttc ctc aag agc cac atc aag			688
Cys Cys Arg Met Tyr Pro Thr Leu Asp Phe Leu Lys Ser His Ile Lys			
175	180	185	
agg ggc ttc agg gag ggc ttc agc tgc aag gtg tac tac cgc aag ctc			736
Arg Gly Phe Arg Glu Gly Phe Ser Cys Lys Val Tyr Tyr Arg Lys Leu			
190	195	200	
aaa gcc ctc tgg agc aag gag cag aag gcc cgg ctg gga gac agg ctc			784
Lys Ala Leu Trp Ser Lys Glu Gln Lys Ala Arg Leu Gly Asp Arg Leu			
205	210	215	
tcc tcc ggc agc tgc cag gcc ttc aat agt cct gct gaa cac ctt agg			832
Ser Ser Gly Ser Cys Gln Ala Phe Asn Ser Pro Ala Glu His Leu Arg			
220	225	230	235
caa att ggc ggt gaa gcc tac tta tgt ctc tagagagatg ccaataaagt			882
Gln Ile Gly Gly Glu Ala Tyr Leu Cys Leu			
240	245		
tagtcacagc caaaaaaaaa aaaaaa			908

<210> 27
 <211> 762
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..310

<220>
 <221> sig_peptide
 <222> 83..157
 <223> Von Heijne matrix
 score 4.72955689475746
 seq LCALLSNFCPSTT/VK

<400> 27	
ttttttctac tacaaacgcc atgggggatgc ggggtctggga acagcggaaa accctaccct	60
gccctgaaaa gtccttggt ca atg tgc atg tcc ctt tct atg aaa gtt cct	112


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          35          40          45
agc ctc agc atg tcc aag gat gat atg tct tcc aca tta ctg aca ttc      543
Ser Leu Ser Met Ser Lys Asp Asp Met Ser Ser Thr Leu Leu Thr Phe
          50          55          60
aga agt tta cat tat aat gac ccc aag gga aac agt tcg ggt aat gac      591
Arg Ser Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp
          65          70          75
aaa gag tgt tgc aat gac atg aca gtc tgg aga aaa gtt tca gaa gca      639
Lys Glu Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala
          80          85          90
aac gga tcg tgc aag tgg agc aat aac ttc atc cgc agc tcc aca gaa      687
Asn Gly Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu
          95          100          105          110
gtg atg cgc agg gtc cac agg gcc ccc agc tgc aag ttt gta cag aat      735
Val Met Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn
          115          120          125
cct ggc ata agc tgc tgt gag agc cta gaa ctg gaa aat aca gtg tgc      783
Pro Gly Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys
          130          135          140
cag ttc act aca ggc aaa caa ttc ccc agg tgc caa tac cat agt gtt      831
Gln Phe Thr Thr Gly Lys Gln Phe Pro Arg Cys Gln Tyr His Ser Val
          145          150          155
acc tca tta gag aag ata ttg aca gtg ctg aca ggt cat tct ctg atg      879
Thr Ser Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met
          160          165          170
agc tgg tta gtt tgt ggc tct aag ttg taaatccac agagctttag      926
Ser Trp Leu Val Cys Gly Ser Lys Leu
          175          180
gactagggtc ttactaaaga aggacctctt cttgttcatt cttgtttaaa cctttcctta      986
atatctactc tttagcacta tagtgaactc ctgattatct attctaactg gaggagtga      1046
aaatccaaaa ttgtggataa ttcaattaaa agttatgact gaaaaaaaaa aaaaaa      1102

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<210> 29
 <211> 436
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..287

<220>
 <221> sig_peptide
 <222> 24..131
 <223> Von Heijne matrix
 score 3.79790641648006
 seq ILMRDFSPSGIFG/AF

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<400> 29
acagcggaca ccaggactcc aaa atg gcg tca gtt gta cca gtg aag gac aag      53
          Met Ala Ser Val Val Pro Val Lys Asp Lys
          -35          -30
aaa ctt ctg gag gtc aaa ctg ggg gag ctg cca agc tgg atc ttg atg      101
Lys Leu Leu Glu Val Lys Leu Gly Glu Leu Pro Ser Trp Ile Leu Met
          -25          -20          -15
cgg gac ttc agt cct agt ggc att ttc gga gcg ttt caa aga ggt tac      149
Arg Asp Phe Ser Pro Ser Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr
          -10          -5          1          5

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tac cgg tac tac aac aag tac atc aat gtg aag aag ggg agc atc tcg      197
Tyr Arg Tyr Tyr Asn Lys Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser
          10          15          20
ggg att acc atg gtg ctg gca tgc tac gtg ctc ttt agc tac tcc ttt      245
Gly Ile Thr Met Val Leu Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe
          25          30          35
tcc tac aag cat ctc aag cac gag cgg ctc cgc aaa tac cac      287
Ser Tyr Lys His Leu Lys His Glu Arg Leu Arg Lys Tyr His
          40          45          50
tgaagaggac acactctgca cccccccacc ccacgacctt ggcccgagcc cctccgtgag      347
gaacacaatc tcaatcggtg ctgaatcctt tcatatccta ataggaatta acctccaaat      407
aaaacatgac tggtaaaaaa aaaaaaaaaa      436

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<210> 30
<211> 1938
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 132..1574

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<220>
<221> sig_peptide
<222> 132..206
<223> Von Heijne matrix
      score 11.1130239236827
      seq LALLLTSTPEALG/AN

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<400> 30
ctcccccttcc cgctcccagg aaccccatcca gcctcaggaa ctgccccccag ccacgagcc      60
ttggctactt aagggacctg ggcccaatcc acagctggga cagtcctggc ccaactgcact      120
gggaatctag g atg ggg gcc ttg gcc aga gcc ctg ccg tcc ata ctg ctg      170
      Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu
          -25          -20          -15
gca ttg ctg ctt acg tcc acc cca gag gct ctg ggt gcc aac ccc ggc      218
Ala Leu Leu Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly
          -10          -5          1
ttg gtc gcc agg atc acc gac aag gga ctg cag tat gcg gcc cag gag      266
Leu Val Ala Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu
      5          10          15          20
ggg cta ttg gct ctg cag agt gag ctg ctc agg atc acg ctg cct gac      314
Gly Leu Leu Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp
          25          30          35
ttc acc ggg gac ttg agg atc ccc cac gtc ggc cgt ggg cgc tat gag      362
Phe Thr Gly Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu
          40          45          50
ttc cac agc ctg aac atc cac agc tgt gag ctg ctt cac tct gcg ctg      410
Phe His Ser Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu
          55          60          65
agg cct gtc cct ggc cag ggc ctg agt ctc agc atc tcc gac tcc tcc      458
Arg Pro Val Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser
          70          75          80
atc cgg gtc cag ggc agg tgg aag gtg cgc aag tca ttc ttc aaa cta      506
Ile Arg Val Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu
      85          90          95          100
cag ggc tcc ttt gat gtc agt gtc aag ggc atc agc att tcg gtc aac      554
Gln Gly Ser Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn

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ctc	ctg	ttg	ggc	agc	gat	tcc	tcc	ggg	agg	ccc	aca	ggt	act	gcc	tcc	602
Leu	Leu	Leu	Gly	Ser	Asp	Ser	Ser	Gly	Arg	Pro	Thr	Val	Thr	Ala	Ser	
			120					125					130			
agc	tgc	agc	agt	gac	atc	gct	gac	gtg	gag	gtg	gac	atg	tcg	gga	gac	650
Ser	Cys	Ser	Ser	Asp	Ile	Ala	Asp	Val	Glu	Val	Asp	Met	Ser	Gly	Asp	
		135					140					145				
ttg	ggg	tgg	ctg	ttg	aac	ctc	ttc	cac	aac	cag	att	gag	tcc	aag	ttc	698
Leu	Gly	Trp	Leu	Leu	Asn	Leu	Phe	His	Asn	Gln	Ile	Glu	Ser	Lys	Phe	
	150				155					160						
cag	aaa	gta	ctg	gag	agc	agg	att	tgc	gaa	atg	atc	cag	aaa	tcg	gtg	746
Gln	Lys	Val	Leu	Glu	Ser	Arg	Ile	Cys	Glu	Met	Ile	Gln	Lys	Ser	Val	
165					170				175						180	
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Ser	Ser	Asp	Leu	Gln	Pro	Tyr	Leu	Gln	Thr	Leu	Thr	Val	Thr	Thr	Glu	
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att	gac	agt	ttc	gcc	gac	att	gat	tat	agc	tta	gtg	gaa	gcc	cct	cgg	842
Ile	Asp	Ser	Phe	Ala	Asp	Ile	Asp	Tyr	Ser	Leu	Val	Glu	Ala	Pro	Arg	
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Arg	Asn	His	Arg	Ser	Pro	Val	Thr	Leu	Leu	Ala	Ala	Val	Met	Ser	Leu	
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Pro	Glu	Glu	His	Asn	Lys	Met	Val	Tyr	Phe	Ala	Ile	Ser	Asp	Tyr	Val	
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Phe	Asn	Thr	Ala	Ser	Leu	Val	Tyr	His	Glu	Glu	Gly	Tyr	Leu	Asn	Phe	
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Thr	Lys	Ser	Phe	Arg	Pro	Phe	Val	Pro	Arg	Leu	Ala	Arg	Leu	Tyr	Pro	
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Asn	Met	Asn	Leu	Glu	Leu	Gln	Gly	Ser	Val	Pro	Ser	Ala	Pro	Leu	Leu	
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Asn	Phe	Ser	Pro	Gly	Asn	Leu	Ser	Val	Asp	Pro	Tyr	Met	Glu	Ile	Asp	
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Ser	Val	Ala	Thr	Asn	Val	Ser	Ala	Thr	Leu	Thr	Phe	Asn	Thr	Ser	Lys	
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Ile	Thr	Gly	Phe	Leu	Lys	Pro	Gly	Lys	Val	Lys	Val	Glu	Leu	Lys	Glu	
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tcc	aaa	ggt	gga	cta	ttc	aat	gca	gag	ctg	ttg	gaa	gcg	ctc	ctc	aac	1418
Ser	Lys	Val	Gly	Leu	Phe	Asn	Ala	Glu	Leu	Leu	Glu	Ala	Leu	Leu	Asn	
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tat	tac	atc	ctt	aac	acc	ttc	tac	ccc	aag	ttc	aat	gat	aag	ttg	gcc	1466
Tyr	Tyr	Ile	Leu	Asn	Thr	Phe	Tyr	Pro	Lys	Phe	Asn	Asp	Lys	Leu	Ala	
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Gly Leu Gln Ile His Lys Asp Phe Leu Phe Leu Gly Ala Asn Val Gln
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Tyr Met Arg Val
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                                   Met

gcc aaa tat caa ggt gaa gtt caa agt ttg aaa ctg gat gat gat tca 167
Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp Ser
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gtt ata gaa gga gta agc gac caa gta ctt gtg gca gtt gtg gtc agt 215
Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val Ser
      -25          -20          -15
ttc gct ttg att gct acc ctg gta tat gca ctt ttc aga aat gta cat 263
Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val His
      -10          -5          1          5
caa aac att cac cca gaa aac cag gag cta gta agg gta ctt cga gaa 311
Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg Glu
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cag ctt caa aca gaa cag gat gca cct gct gcc act cga cag cag ttc 359
Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Ala Thr Arg Gln Gln Phe
          25          30          35
tac act gac atg tac tgt ccc atc tgc ctg cac caa gcc tcc ttc ccg 407
Tyr Thr Asp Met Tyr Cys Pro Ile Cys Leu His Gln Ala Ser Phe Pro
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gtg gag acc aac tgt gga cat ctt ttt tgt ggt gcc tgc att att gct 455
Val Glu Thr Asn Cys Gly His Leu Phe Cys Gly Ala Cys Ile Ile Ala
55          60          65          70
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1114

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acgtctcttc ggagagcgcg cac atg gcg act cag gcg cac tcc ctc agc tac 173
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ggc ctc cga gat ttt gaa gcc agc ttc ata agg cta ttg gac aaa ata 317
Gly Leu Arg Asp Phe Glu Ala Ser Phe Ile Arg Leu Leu Asp Lys Ile
20 25 30
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Thr Asn Gly Ser Arg Ile Glu Ile Asn Gln Thr Gly Thr Thr Leu Tyr
35 40 45
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Tyr Gln Pro Gly Leu Leu Tyr Gly Gly Ser Val Glu His Asp Cys Ser
50 55 60
gtc ctt cgt ggc att ggg tat tac ctg gag agt ctt ctt tgc ttg gct 461
Val Leu Arg Gly Ile Gly Tyr Tyr Leu Glu Ser Leu Leu Cys Leu Ala
65 70 75
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Pro Phe Met Lys His Pro Leu Lys Ile Val Leu Arg Gly Val Thr Asn
80 85 90 95
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Asp Gln Ile Asp Pro Ser Val Asp Val Leu Lys Ala Thr Ala Leu Pro
100 105 110
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Val Arg Arg Gly Met Pro Pro Gly Gly Gly Glu Val Val Phe Ser
130 135 140
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Cys Pro Val Arg Lys Val Leu Lys Pro Ile Gln Leu Thr Asp Pro Gly
145 150 155
aaa atc aaa cgt att aga gga atg gcg tac tct gta cgt gtg tca cct 749

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Gln	Met	Ala	Asn	Arg	Ile	Val	Asp	Ser	Ala	Arg	Ser	Ile	Leu	Asn	Lys	
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Phe	Ile	Pro	Asp	Ile	Tyr	Ile	Tyr	Thr	Asp	His	Ile	Lys	Gly	Val	Asn	
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Ser	Gly	Lys	Ser	Pro	Gly	Phe	Gly	Leu	Ser	Leu	Val	Ala	Glu	Thr	Thr	
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Ser	Gly	Thr	Phe	Leu	Ser	Ala	Glu	Leu	Ala	Ser	Asn	Pro	Gln	Gly	Gln	
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Gly	Ala	Ala	Val	Leu	Pro	Glu	Asp	Leu	Gly	Arg	Asn	Cys	Ala	Arg	Leu	
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Leu	Leu	Glu	Glu	Ile	Tyr	Arg	Gly	Gly	Cys	Val	Asp	Ser	Thr	Asn	Gln	
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Ser	Leu	Ala	Leu	Leu	Leu	Met	Thr	Leu	Gly	Gln	Gln	Asp	Val	Ser	Lys	
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Val	Leu	Leu	Gly	Pro	Leu	Ser	Pro	Tyr	Thr	Ile	Glu	Phe	Leu	Arg	His	
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Leu	Lys	Ser	Phe	Phe	Gln	Ile	Met	Phe	Lys	Ile	Glu	Thr	Lys	Pro	Cys	
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Gly	Glu	Glu	Leu	Lys	Gly	Gly	Asp	Lys	Val	Leu	Met	Thr	Cys	Val	Gly	
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Ile	Gly	Phe	Ser	Asn	Leu	Ser	Arg	Thr	Leu	Lys						
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 -15 -10 -5
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 Thr Ala Leu Ala Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser
 1 5 10
 aaa aac ctc ggt gga aag tca tca ggc aga cgc caa ggc att aag aaa 199
 Lys Asn Leu Gly Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys
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 Met Glu Gly His Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg
 35 40 45
 cat ttc cgc tgg cac cca ggt gcc cat gtg agt tgc tcc gtt gct gcc 295
 His Phe Arg Trp His Pro Gly Ala His Val Ser Cys Ser Val Ala Ala
 50 55 60
 ccc ctt ttt cct ttt cta ggt tgacctctcc ttgccctaa gcatggtaat 346
 Pro Leu Phe Pro Phe Leu Gly
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 ctctctgaca aagaaatcca gatgatgcga gacctgatga agacaatata tggaaa atg 179
 Met
 -20
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 Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly Leu
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Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu Leu
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gac tat gag gat ggt aga gga tcc cga cat gca tat tca aca caa agt 371
Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln Ser
      30      35      40      45
gag aga tcc aaa aga gat tac aca cca tca acc aac tct cta gca ctg 419
Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala Leu
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tct cga tca agt att gct tta cct caa gga tcc atg agt agt ata aaa 467
Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile Lys
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Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala Met
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atg caa ttc aca gcc cct att ccc gga gct aca gga cct atc aag ctc 563
Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys Leu
      95      100      105
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Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr Pro
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Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn Ser
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His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser Leu
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Val	His	Arg	Asn	Ile	His	Ser	His	Gly	Leu	Arg	Ser	Asn	Leu	Gln	Glu	
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Ile	Phe	Leu	Pro	Ala	Phe	Pro	Cys	His	Glu	Arg	Lys	Lys	Gln	Glu		
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Val Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu							
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Ala Phe Arg Arg Ala Cys Leu Ser Gly Gly Thr Gln Arg Asp Trp Ser							
40	45	50					
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Gln Thr Leu Asn Leu Leu Trp Leu Thr Val Pro Leu Gly Val Phe Trp							
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Ser Leu Phe Leu Gly Trp Ile Trp Leu Gln Leu Leu Glu Val Pro Asp							
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cct aat gtt gtc cct cac tat gca act gga gtg gtg ctg ttt ggt ctc							443
Pro Asn Val Val Pro His Tyr Ala Thr Gly Val Val Leu Phe Gly Leu							
85	90	95	100				
tcg gca gtg gtg gag ctt cta gga gag ccc ttt tgg gtc ttg gca caa							491
Ser Ala Val Val Glu Leu Leu Gly Glu Pro Phe Trp Val Leu Ala Gln							
105	110	115					
gca cat atg ttt gtg aag ctc aag gtg att gca gag agc ctg tcg gta							539
Ala His Met Phe Val Lys Leu Lys Val Ile Ala Glu Ser Leu Ser Val							

att	ctt	aag	acc	ggt	ctg	aca	gct	ttt	ctc	gtg	ctg	tgg	ttg	cct	cac	587
Ile	Leu	Lys	Thr	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His	
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tgg	gga	ttg	tac	att	ttc	tct	ttg	gcc	cag	ctt	ttc	tat	acc	aca	ggt	635
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val	
	150					155				160						
ctg	gtg	ctc	tgc	tat	ggt	att	tat	ttc	aca	aag	tta	ctg	ggt	tcc	cca	683
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro	
165					170					175					180	
gaa	tca	acc	aag	ctt	caa	act	ctt	cct	gtc	tcc	aga	ata	aca	gat	ctg	731
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	
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tta	ccc	aat	att	aca	aga	aat	gga	gcg	ttt	ata	aac	tgg	aaa	gag	gct	779
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	
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aaa	ctg	act	tgg	agt	ttt	ttc	aaa	cag	tct	ttc	ttg	aaa	cag	att	ttg	827
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu	
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aca	gaa	ggc	gag	cga	tat	gtg	atg	aca	ttt	ttg	aat	gta	ttg	aac	ttt	875
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	
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ggt	gat	cag	ggt	gtg	tat	gat	ata	gtg	aat	aat	ctt	ggc	tcc	ctt	gtg	923
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val	
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gcc	aga	tta	att	ttc	cag	cca	ata	gag	gaa	agt	ttt	tat	ata	ttt	ttt	971
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe	
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gct	aag	gtg	ctg	gag	agg	gga	aag	gat	gcc	aca	ctt	cag	aag	cag	gag	1019
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu	
		280					285					290				
gac	gtt	gct	gtg	gct	gct	gca	gtc	ttg	gag	tcc	ctg	ctc	aag	ctg	gcc	1067
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala	
		295					300					305				
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Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln	
	310					315				320						
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Leu	Ala	Leu	Asp	Ile	Tyr	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly	
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cct	gtt	ttg	ctg	cgt	tcc	tac	tgt	ctc	tat	gtt	ctc	ctg	ctt	gcc	atc	1211
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile	
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aat	gga	gtg	aca	gag	tgt	ttc	aca	ttt	gct	gcc	atg	agc	aaa	gag	gag	1259
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Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu	
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Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile	
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ttg	gcc	aac	tgc	ttt	aac	atg	ggc	att	cgg	atc	acg	cag	agc	ctt	tgc	1403
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys	
405				410					415					420		
ttc	atc	cac	cgc	tac	tac	cga	agg	agc	ccc	cac	agg	ccc	ctg	gct	ggc	1451
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly	
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Leu His Leu Ser Pro Val Leu Leu Gly Thr Phe Ala Leu Ser Gly Gly
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ggt act gct gtt tgc gag gta ttc ctc tgc tgt gag cag ggc tgg cca      1547
Val Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro
      455      460      465

gcc aga ctg gca cac att gct gtg ggg gcc ttc tgt ctg gga gca act      1595
Ala Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr
      470      475      480

ctc ggg aca gca ttc ctc aca gag acc aag ctg atc cat ttc ctc agg      1643
Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg
      485      490      495      500

act cag tta ggt gtg ccc aga cgc act gac aaa atg aca tgacttcagg      1692
Thr Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
      505      510

gaagcctgga caccgcaggc acctggacca gctatgggta gttctgtggg tggaacacat      1752
tctgtgtaag agccccactg agggctctgc agcggagtga cagcaacccc agagatgagg      1812
caccagagag tgccactgca tgagacacct gtgaccattc gaagtctgaa atgcgggggg      1872
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atcgatggta gctataagag tcgtgtctga acccggtctt tccaattggc ctgctccatc      180
cgaacagcgt caactcc atg gcg cgg ttc ctg aca ctt tgc act tgg ctg      230
      Met Ala Arg Phe Leu Thr Leu Cys Thr Trp Leu
      -20      -15

ctg ttg ctc ggc ccc ggg ctc ctg gcg acc gtg cgg gcc gaa tgc agc      278
Leu Leu Leu Gly Pro Gly Leu Leu Ala Thr Val Arg Ala Glu Cys Ser
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cag gat tgc gcg acg tgc agc tac cgc cta gtg cgc ccg gcc gac atc      326
Gln Asp Cys Ala Thr Cys Ser Tyr Arg Leu Val Arg Pro Ala Asp Ile
      5      10      15

aac ttc ctg gct tgc gta atg gaa tgt gaa ggt aaa ctg cct tct ctg      374
Asn Phe Leu Ala Cys Val Met Glu Cys Glu Gly Lys Leu Pro Ser Leu
      20      25      30      35

aaa att tgg gaa acc tgc aag gag ctc ctg cag ctg tcc aaa cca gat      422
Lys Ile Trp Glu Thr Cys Lys Glu Leu Leu Gln Leu Ser Lys Pro Asp
      40      45      50

ctt cct caa gat ggc acc agc acc ctc aga gaa aat agc aaa ccg gaa      470
Leu Pro Gln Asp Gly Thr Ser Thr Leu Arg Glu Asn Ser Lys Pro Glu

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Glu Ser His Leu Leu Ala Lys Arg Tyr Gly Gly Phe Met Lys Arg Tyr			
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Gly Gly Phe Met Lys Lys Met Asp Glu Leu Tyr Pro Met Glu Pro Glu			
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gaa gag gcc aat gga agt gag atc ctc gcc aag cgg tat ggg ggc ttc			614
Glu Glu Ala Asn Gly Ser Glu Ile Leu Ala Lys Arg Tyr Gly Gly Phe			
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atg aag aag gat gca gag gag gac gac tcg ctg gcc aat tcc tca gac			662
Met Lys Lys Asp Ala Glu Glu Asp Asp Ser Leu Ala Asn Ser Ser Asp			
120	125	130	
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Leu Leu Lys Glu Leu Leu Glu Thr Gly Asp Asn Arg Glu Arg Ser His			
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His Gln Asp Gly Ser Asp Asn Glu Glu Val Ser Lys Arg Tyr Gly			
150	155	160	
ggc ttc atg aga ggc tta aag aga agc ccc caa ctg gaa gat gaa gcc			806
Gly Phe Met Arg Gly Leu Lys Arg Ser Pro Gln Leu Glu Asp Glu Ala			
165	170	175	
aaa gag ctg cag aag cga tat ggg ggc ttc atg aga aga gta ggt cgc			854
Lys Glu Leu Gln Lys Arg Tyr Gly Gly Phe Met Arg Arg Val Gly Arg			
180	185	190	195
cca gag tgg tgg atg gac tac cag aaa cgg tat gga ggt ttc ctg aag			902
Pro Glu Trp Trp Met Asp Tyr Gln Lys Arg Tyr Gly Gly Phe Leu Lys			
200	205	210	
cgc ttt gcc gag gct ctg ccc tcc gac gaa gaa ggc gaa agt tac tcc			950
Arg Phe Ala Glu Ala Leu Pro Ser Asp Glu Glu Gly Glu Ser Tyr Ser			
215	220	225	
aaa gaa gtt cct gaa atg gaa aaa aga tac gga gga ttt atg aga ttt			998
Lys Glu Val Pro Glu Met Glu Lys Arg Tyr Gly Gly Phe Met Arg Phe			
230	235	240	
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aaactgttga tgggtgttta ttgtcatgtg ttgcttgcc tgtatagttg acttcattgt			1118
ctggataact atacaacctg aaaactgtca ttccaggttc tgtgctcttt ttggagtctt			1178
taagctcagt attagtctat tgcagctatc tcgttttcat gctaaaatag tttttgttat			1238
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 seq VVMLMLLTLLVLG/MV

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			Met	Pro	Phe	Ala	Tyr	Phe	Phe	Thr	Glu					
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Ser	Glu	Gly	Phe	Ala	Gly	Ser	Arg	Lys	Gly	Val	Leu	Gly	Arg	Val	Tyr	
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Glu	Thr	Val	Val	Met	Leu	Met	Leu	Leu	Thr	Leu	Leu	Val	Leu	Gly	Met	
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Ser	Leu	Tyr	Asp	Phe	Trp	Glu	Tyr	Tyr	Leu	Pro	Tyr	Leu	Tyr	Ser	Cys	
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Ile	Ser	Phe	Leu	Gly	Val	Leu	Leu	Leu	Val	Cys	Thr	Pro	Leu	Gly		
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ctc	gcc	cgc	atg	ttc	tcc	gtc	act	ggg	aag	ctg	cta	gtc	aag	ccc	cgg	819
Leu	Ala	Arg	Met	Phe	Ser	Val	Thr	Gly	Lys	Leu	Leu	Val	Lys	Pro	Arg	
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Leu	Leu	Glu	Asp	Leu	Glu	Glu	Gln	Leu	Tyr	Cys	Ser	Ala	Phe	Glu	Glu	
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gca	gcc	ctg	acc	cgc	agg	atc	tgt	aat	cct	act	tcc	tgc	tgg	ctg	cct	915
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Leu	Asp	Met	Glu	Leu	Leu	His	Arg	Gln	Val	Leu	Ala	Leu	Gln	Thr	Gln	
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Arg	Val	Leu	Leu	Glu	Lys	Arg	Arg	Lys	Ala	Ser	Ala	Trp	Gln	Arg	Asn	
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Leu	Gly	Tyr	Pro	Leu	Ala	Met	Leu	Cys	Leu	Leu	Val	Leu	Thr	Gly	Leu	
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Ser	Val	Leu	Ile	Val	Ala	Ile	His	Ile	Leu	Glu	Leu	Leu	Ile	Asp	Glu	
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Ala	Ala	Met	Pro	Arg	Gly	Met	Gln	Gly	Thr	Ser	Leu	Gly	Gln	Val	Ser	
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Phe	Tyr	Leu	Met	Val	Ser	Ser	Val	Val	Gly	Phe	Tyr	Ser	Ser	Pro	Leu	
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Pro	Leu	Pro	Val	Ser	Gly	Phe	Pro	Gln	Ala	Ser	Arg	Lys	Thr	Gln	His																									
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                               Met Ser Arg Ser Ser Lys Val Val Leu Gly
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ctc tcg gtg ctg ctg acg gcg gcc aca gtg gcc ggc gta cat gtg aag           161
Leu Ser Val Leu Leu Thr Ala Ala Thr Val Ala Gly Val His Val Lys
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cag cag tgg gac cag cag agg ctt cgt gac gga gtt atc aga gac att           209
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[illegible]

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Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser Gly																
-25 -20 -15																
ctc ctc ctg cag gtg ttg ttt cgg ttg atc acc ttt gtc ttg aat gca																154
Leu Leu Leu Gln Val Leu Phe Arg Leu Ile Thr Phe Val Leu Asn Ala																
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Phe Ile Leu Arg Phe Leu Ser Lys Glu Ile Val Gly Val Val Asn Val																
10 15 20																
aga cta acg ctg ctt tac tca acc acc ctc ttc ctg gcc aga gag gcc																250
Arg Leu Thr Leu Leu Tyr Ser Thr Thr Leu Phe Leu Ala Arg Glu Ala																
25 30 35																
ttc cgc aga gca tgt ctc agt ggg ggc acc cag cga gac tgg agc cag																298
Phe Arg Arg Ala Cys Leu Ser Gly Thr Gln Arg Asp Trp Ser Gln																
40 45 50																

acc	ctc	aac	ctg	ctg	tgg	cta	aca	gtc	ccc	ctg	ggg	gtg	ttt	tgg	tcc	346
Thr	Leu	Asn	Leu	Leu	Trp	Leu	Thr	Val	Pro	Leu	Gly	Val	Phe	Trp	Ser	
55						60				65						
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Leu	Phe	Leu	Gly	Trp	Ile	Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp	Pro	
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aat	gtt	gtc	cct	cac	tat	gca	act	gga	gtg	gtg	ctg	ttt	ggg	ctc	tcg	442
Asn	Val	Val	Pro	His	Tyr	Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu	Ser	
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gca	gtg	gtg	gag	ctt	cta	gga	gag	ccc	ttt	tgg	gtc	ttg	gca	caa	gca	490
Ala	Val	Val	Glu	Leu	Leu	Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln	Ala	
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cat	atg	ttt	gtg	aag	ctc	aag	gtg	att	gca	gag	agc	ctg	tcg	gta	att	538
His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val	Ile	
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ctt	aag	agc	gtt	ctg	aca	gct	ttt	ctc	gtg	ctg	tgg	ttg	cct	cac	tgg	586
Leu	Lys	Ser	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His	Trp	
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gga	ttg	tac	att	ttc	tct	ttg	gcc	cag	ctt	ttc	tat	acc	aca	gtt	ctg	634
Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val	Leu	
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Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro	Glu	
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tca	acc	aag	ctt	caa	act	ctt	cct	gtc	tcc	aga	ata	aca	gat	ctg	tta	730
Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	Leu	
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ccc	aat	att	aca	aga	aat	gga	gcg	ttt	ata	aac	tgg	aaa	gag	gct	aaa	778
Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	Lys	
		200					205					210				
ctg	act	tgg	agt	ttt	ttc	aaa	cag	tct	ttc	ttg	aaa	cag	att	ttg	aca	826
Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu	Thr	
		215				220					225					
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Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	Gly	
230					235				240						245	
gat	cag	ggg	gtg	tat	gat	ata	gtg	aat	aat	ctt	ggc	tcc	ctt	gtg	gcc	922
Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Leu	Gly	Ser	Leu	Val	Ala		
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aga	tta	att	ttc	cag	cca	ata	gag	gaa	agt	ttt	tat	ata	ttt	ttt	gct	970
Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe	Ala	
			265				270						275			
aag	gtg	ctg	gag	agg	gga	aag	gat	gcc	aca	ctt	cag	aag	cag	gag	gac	1018
Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu	Asp	
			280				285					290				
gtt	gct	gtg	gct	gct	gca	gtc	ttg	gag	tcc	ctg	ctc	aag	ctg	gcc	ctg	1066
Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala	Leu	
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ctg	gcc	ggc	ctg	acc	atc	act	gtt	ttt	ggc	ttt	gcc	tat	tct	cag	ctg	1114
Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln	Leu	
310					315				320						325	
gct	ctg	gat	atc	aac	gga	ggg	acc	atg	ctt	agc	tca	gga	tcc	ggg	cct	1162
Ala	Leu	Asp	Ile	Asn	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly	Pro	
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Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile	Asn	
			345				350						355			
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Gly	Val	Thr	Glu	Cys	Phe	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu	Val		
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Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu	Val		
		375				380					385						
tta	tcc	tat	ctc	ttg	acc	cgt	tgg	tgt	ggc	agc	gtg	ggc	ttc	atc	ttg	1354	
Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile	Leu		
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gcc	aac	tgc	ttt	aac	atg	ggc	att	cgg	atc	acg	cag	agc	ctt	tgc	ttc	1402	
Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys	Phe		
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atc	cac	cgc	tac	tac	cga	agg	agc	ccc	cac	agg	ccc	ctg	gct	ggc	ctg	1450	
Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly	Leu		
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cac	cta	tcg	cca	gtc	ctg	ctc	ggg	aca	ttt	gcc	ctc	agt	ggg	ggg	gtt	1498	
His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly	Val		
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Thr	Ala	Val	Ser	Glu	Val	Phe	Leu	Cys	Cys	Glu	Gln	Gly	Trp	Pro	Ala		
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Arg	Leu	Ala	His	Ile	Ala	Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr	Leu		
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ggg	aca	gca	ttc	ctc	aca	gag	acc	aag	ctg	atc	cat	ttc	ctc	agg	act	1642	
Gly	Thr	Ala	Phe	Leu	Thr	Glu	Thr	Lys	Leu	Ile	His	Phe	Leu	Arg	Thr		
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cag	tta	ggt	gtg	ccc	aga	cgc	act	gac	aaa	atg	acg	tgacttcagg				1688	
Gln	Leu	Gly	Val	Pro	Arg	Arg	Thr	Asp	Lys	Met	Thr						
		505					510										
gaagcctgga	cacccgaggc	acctggacca	gctatgggta	gttctgtggg	tggaacacat											1748	
tctgtgtaag	agccccactg	agggctctgc	agcggagtga	cagcaacccc	agagatgagg											1808	
caccagagag	tgccactgca	tgagacacct	gtgaccattc	gaagtctgaa	atgcggggggg											1868	
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score 11.6921972463885

seq LLLCLALSGAAET/KP

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atg ggc aca	cag gag ggc	tgg tgc ctg	ctc ctg	tgc ctg	gct cta tct	166	
Met Gly Thr	Gln Glu Gly	Trp Cys	Leu Leu Leu	Cys Leu	Ala Leu Ser		
-20		-15		-10			
gga gca gca	gaa acc aag	ccc cac	cca gca	gag ggg	cag tgg	cgg gca	214

Gly	Ala	Ala	Glu	Thr	Lys	Pro	His	Pro	Ala	Glu	Gly	Gln	Trp	Arg	Ala		
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Val	Asp	Val	Val	Leu	Asp	Cys	Phe	Leu	Val	Lys	Asp	Gly	Ala	His	Arg		
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Gly	Ala	Leu	Ala	Ser	Ser	Glu	Asp	Arg	Ala	Arg	Ala	Ser	Leu	Val	Leu		
		30					35					40					
aag	cag	gtg	cca	gtg	ctg	gac	gat	ggc	tcc	ctg	gag	gac	ttc	acc	gat		358
Lys	Gln	Val	Pro	Val	Leu	Asp	Asp	Gly	Ser	Leu	Glu	Asp	Phe	Thr	Asp		
	45					50					55						
ttc	caa	ggg	ggc	aca	ctg	gcc	caa	gat	gac	cca	cct	att	atc	ttt	gag		406
Phe	Gln	Gly	Gly	Thr	Leu	Ala	Gln	Asp	Asp	Pro	Pro	Ile	Ile	Phe	Glu		
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gcc	tca	gtg	gac	ctg	gtc	cag	att	ccc	cag	gcc	gag	gcc	ttg	ctc	cat		454
Ala	Ser	Val	Asp	Leu	Val	Gln	Ile	Pro	Gln	Ala	Glu	Ala	Leu	Leu	His		
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gct	gac	tgc	agt	ggg	aag	gag	gtg	acc	tgt	gag	atc	tcc	cgc	tac	ttt		502
Ala	Asp	Cys	Ser	Gly	Lys	Glu	Val	Thr	Cys	Glu	Ile	Ser	Arg	Tyr	Phe		
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ctc	cag	atg	aca	gag	acc	act	gtt	aag	aca	gca	gct	tgg	ttc	atg	gcc		550
Leu	Gln	Met	Thr	Glu	Thr	Thr	Val	Lys	Thr	Ala	Ala	Trp	Phe	Met	Ala		
		110					115					120					
aac	gtg	cag	gtc	tct	gga	ggg	gga	cct	agc	atc	tcc	ttg	gtg	atg	aag		598
Asn	Val	Gln	Val	Ser	Gly	Gly	Gly	Pro	Ser	Ile	Ser	Leu	Val	Met	Lys		
	125					130					135						
act	ccc	agg	gtc	gcc	aag	aat	gag	gtg	ctc	tgg	cac	cca	acg	ctg	aac		646
Thr	Pro	Arg	Val	Ala	Lys	Asn	Glu	Val	Leu	Trp	His	Pro	Thr	Leu	Asn		
					145				150					155			
ttg	cca	ctg	agc	ccc	cag	ggg	act	gtg	cga	act	gca	gtg	gag	ttc	cag		694
Leu	Pro	Leu	Ser	Pro	Gln	Gly	Thr	Val	Arg	Thr	Ala	Val	Glu	Phe	Gln		
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gtg	atg	aca	cag	acc	caa	tcc	ctg	agc	ttc	ctg	ctg	ggg	tcc	tca	gcc		742
Val	Met	Thr	Gln	Thr	Gln	Ser	Leu	Ser	Phe	Leu	Leu	Gly	Ser	Ser	Ala		
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tcc	ttg	gac	tgt	ggc	ttc	tcc	atg	gca	ccg	ggc	ttg	gac	ctc	atc	agt		790
Ser	Leu	Asp	Cys	Gly	Phe	Ser	Met	Ala	Pro	Gly	Leu	Asp	Leu	Ile	Ser		
		190					195					200					
gtg	gag	tgg	cga	ctg	cag	cac	aag	ggc	agg	ggg	cag	ttg	gtg	tac	agc		838
Val	Glu	Trp	Arg	Leu	Gln	His	Lys	Gly	Arg	Gly	Gln	Leu	Val	Tyr	Ser		
	205					210					215						
tgg	acc	gca	ggg	cag	ggg	cag	gct	gtg	cgg	aag	ggc	gct	acc	ctg	gag		886
Trp	Thr	Ala	Gly	Gln	Gly	Gln	Ala	Val	Arg	Lys	Gly	Ala	Thr	Leu	Glu		
				225					230					235			
cct	gca	caa	ctg	ggc	atg	gcc	agg	gat	gcc	tcc	ctc	acc	ctg	ccc	ggc		934
Pro	Ala	Gln	Leu	Gly	Met	Ala	Arg	Asp	Ala	Ser	Leu	Thr	Leu	Pro	Gly		
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ctc	act	ata	cag	gac	gag	ggg	acc	tac	att	tgc	cag	atc	acc	acc	tct		982
Leu	Thr	Ile	Gln	Asp	Glu	Gly	Thr	Tyr	Ile	Cys	Gln	Ile	Thr	Thr	Ser		
			255					260					265				
ctg	tac	cga	gct	cag	cag	atc	atc	cag	ctc	aac	atc	caa	gct	tcc	cct		1030
Leu	Tyr	Arg	Ala	Gln	Gln	Ile	Ile	Gln	Leu	Asn	Ile	Gln	Ala	Ser	Pro		
		270					275					280					
aaa	gta	cga	ctg	agc	ttg	gca	aac	gaa	gct	ctg	ctg	ccc	acc	ctc	atc		1078
Lys	Val	Arg	Leu	Ser	Leu	Ala	Asn	Glu	Ala	Leu	Leu	Pro	Thr	Leu	Ile		
	285					290					295						
tgc	gac	att	gct	ggc	tat	tac	cct	ctg	gat	gtg	gtg	gtg	acg	tgg	acc		1126
Cys	Asp	Ile	Ala	Gly	Tyr	Tyr	Pro	Leu	Asp	Val	Val	Val	Thr	Trp	Thr		

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Arg Glu Glu Leu Gly Ser Pro Ala Gln Val Ser Gly Ala Ser Phe

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tcc agc ctc agg caa agc gtg gca ggc acc tac agc atc tcc tcc tct      1222
Ser Ser Leu Arg Gln Ser Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser

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ctc acc gca gaa cct ggc tct gca ggt gcc act tac acc tgc cag gtc      1270
Leu Thr Ala Glu Pro Gly Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val

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aca cac atc tct ctg gag gag ccc ctt ggg gcc agc acc cag gtt gtc      1318
Thr His Ile Ser Leu Glu Glu Pro Leu Gly Ala Ser Thr Gln Val Val

          365          370          375
cca cca gag cgg aga aca gcc ttg gga gtc atc ttt gcc agc agt ctc      1366
Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu

380          385          390          395
ttc ctt ctt gca ctg atg ttc ctg ggg ctt cag aga cgg caa gca cct      1414
Phe Leu Leu Ala Leu Met Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro

          400          405          410
aca gga ctt ggg ctg ctt cag gct gaa cgc tgg gag acc act tcc tgt      1462
Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys

          415          420          425
gct gac aca cag agc tcc cat ctc cat gaa gac cgc aca gcg cgt gta      1510
Ala Asp Thr Gln Ser Ser His Leu His Glu Asp Arg Thr Ala Arg Val

          430          435          440
agc cag ccc agc tgacctaaag cgacatgaga ctactagaaa gaaacgacac      1562
Ser Gln Pro Ser

          445
ccttcccaa gcccccacag ctactccaac ccaaacaaca accaagccag tttaatggta      1622
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agactgcatg ctgcttcttc tcatgccaa gccagaccct ctcacaacct cggatctcag      180
tccttcatgg agacctgggc ccagcaggaa tggcagtgca ggaaattggc gccagatgg      240
ttcttccatg tgaagtgtc tcgggctctg ggctgacgag agaacacctg gtaaccagg      300
tagccctctg tcagtcaccc agggcagggc agc atg gtg cgg att cag agg agg      354
                        Met Val Arg Ile Gln Arg Arg
                        -30          -25
aag ctt ttg gca tct tgc ctg tgc gtc aca gcc acc gtc ttt ctg ctt      402

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Val	Thr	Leu	Gln	Ala	Leu	Asp	Thr	Val	Glu	Asn	Leu	Met	Lys	Val	Thr	
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ggc	cct	ccc	cag	gga	gtt	aca	gac	tcc	atg	caa	tgc	ttc	aat	gat	cag	498
Gly	Pro	Pro	Gln	Gly	Val	Thr	Asp	Ser	Met	Gln	Cys	Phe	Asn	Asp	Gln	
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Trp	Pro	Leu	Ser	Asn	Thr	Arg	Ser	Ser	Glu	His	Ile	Lys	Glu	Val	Met	
	25				30					35					40	
gtt	gag	ctg	ggg	aag	ttt	gaa	agg	aag	gag	ttt	aaa	agt	tcc	agt	ttg	594
Val	Glu	Leu	Gly	Lys	Phe	Glu	Arg	Lys	Glu	Phe	Lys	Ser	Ser	Ser	Leu	
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caa	gat	gga	cat	aca	aaa	atg	gag	gaa	gca	cct	acg	cat	ctt	aat	tca	642
Gln	Asp	Gly	His	Thr	Lys	Met	Glu	Glu	Ala	Pro	Thr	His	Leu	Asn	Ser	
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Phe	Leu	Lys	Lys	Glu	Gly	Leu	Thr	Phe	Asn	Arg	Lys	Arg	Lys	Trp	Glu	
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Leu	Asp	Ser	Tyr	Pro	Ile	Met	Leu	Trp	Trp	Ser	Pro	Leu	Thr	Gly	Glu	
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Thr	Gly	Arg	Leu	Gly	Gln	Cys	Gly	Ala	Asp	Ala	Cys	Phe	Phe	Thr	Ile	
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Asn	Arg	Thr	Tyr	Leu	His	His	His	Met	Thr	Lys	Ala	Phe	Leu	Phe	Tyr	
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Gly	Thr	Asp	Phe	Asn	Ile	Asp	Ser	Leu	Pro	Leu	Pro	Arg	Lys	Ala	His	
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His	Asp	Trp	Ala	Val	Phe	His	Glu	Glu	Ser	Pro	Lys	Asn	Asn	Tyr	Lys	
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Leu	Phe	His	Lys	Pro	Val	Ile	Thr	Leu	Phe	Asn	Tyr	Thr	Ala	Thr	Phe	
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Ser	Arg	His	Ser	His	Leu	Pro	Leu	Thr	Thr	Gln	Tyr	Leu	Glu	Ser	Ile	
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Glu	Val	Leu	Lys	Ser	Leu	Arg	Tyr	Leu	Val	Pro	Leu	Gln	Ser	Lys	Asn	
				205					210					215		
aag	ctt	aga	aaa	aga	ctt	gct	ccg	ctg	gtg	tat	gta	cag	tca	tac	tgt	1122
Lys	Leu	Arg	Lys	Arg	Leu	Ala	Pro	Leu	Val	Tyr	Val	Gln	Ser	Tyr	Cys	
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Asp	Pro	Pro	Ser	Asp	Arg	Asp	Ser	Tyr	Val	Arg	Glu	Leu	Met	Thr	Tyr	
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atc	gag	gtc	gat	tcc	tat	ggt	gaa	tgt	tta	cga	aac	aaa	gac	ctc	cct	1218
Ile	Glu	Val	Asp	Ser	Tyr	Gly	Glu	Cys	Leu	Arg	Asn	Lys	Asp	Leu	Pro	
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Gln	Gln	Leu	Lys	Asn	Pro	Gla	Ser	Met	Asp	Ala	Asp	Gly	Phe	Tyr	Arg	
	265				270					275					280	
atc	att	gca	cag	tat	aag	ttt	atc	cta	gct	ttt	gag	aat	gca	gtt	tgt	1314
Ile	Ile	Ala	Gln	Tyr	Lys	Phe	Ile	Leu	Ala	Phe	Glu	Asn	Ala	Val	Cys	

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gat gac tac atc act gag aag ttc tgg agg cca ctg aaa ctg ggg gta      1362
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gtc cct gta tat tac gga tcc ccc agc atc aca gac tgg ctt cca agt      1410
Val Pro Val Tyr Tyr Gly Ser Pro Ser Ile Thr Asp Trp Leu Pro Ser
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aac aaa agt gct att ctt gta tca gaa ttt tct cac ccc agg gaa ctg      1458
Asn Lys Ser Ala Ile Leu Val Ser Glu Phe Ser His Pro Arg Glu Leu
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gca agt tac atc aga cga ctg gat tct gat gac aga ttg tat gag gcc      1506
Ala Ser Tyr Ile Arg Arg Leu Asp Ser Asp Asp Arg Leu Tyr Glu Ala
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tat gta gaa tgg aag ctg aag ggt aga tct cta acc agc gac ttc      1551
Tyr Val Glu Trp Lys Leu Lys Gly Arg Ser Leu Thr Ser Asp Phe
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tgacagctct caggggaacgg aaatggggag tgcaagacgt caaccaggac aattacatcg      1611
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gcttaccacc caaaagatgg gaggcagaag ataccacact gagttgccc gagcccacag      1731
tgtttgcttt ctcaccactc cggactccac ctttgagctc tttgcgagag atgtggattt      1791
ccagctttga acaatccaag aaagaagccc aggcactaag gtggctggtt gataggaatc      1851
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 seq GVGLVTLLGLAVG/SY

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ggg gtg ggg ctg gtc act ctg ctc ggc ctg gct gtg ggc tcc tac ttg      158
Gly Val Gly Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu
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Val Arg Arg Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu
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aag tac ctg cta cga ctg cta gac aag acg act gtg agc cac aac acc      254
Lys Tyr Leu Leu Arg Leu Leu Asp Lys Thr Val Ser His Asn Thr
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Lys Arg Phe Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu
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Val	Asp	Leu	Val	Ile	Lys	Val	Tyr	Leu	Lys	Gly	Val	His	Pro	Lys	Phe		
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cct	gag	gga	ggg	aag	atg	tct	cag	tac	ctg	gat	agc	ctg	aag	gtt	ggg	494	
Pro	Glu	Gly	Gly	Lys	Met	Ser	Gln	Tyr	Leu	Asp	Ser	Leu	Lys	Val	Gly		
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Pro	Met	Leu	Gln	Leu	Ile	Arg	Ala	Ile	Leu	Lys	Val	Pro	Glu	Asp	Pro		
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Lys	Gly	Phe	Val	Thr	Ala	Asp	Met	Ile	Arg	Glu	His	Leu	Pro	Ala	Pro		
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Gly	Asp	Asp	Val	Leu	Val	Leu	Leu	Cys	Gly	Pro	Pro	Pro	Met	Val	Gln		
	245					250				255							
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Leu	Ala	Cys	His	Pro	Asn	Leu	Asp	Lys	Leu	Gly	Tyr	Ser	Gln	Lys	Met		
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Arg	Phe	Thr	Tyr														
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score 11.6921972463885

seq LLLCLALSGAAET/KP

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ggcgggtgggc aaggagggaa ctcgagagca gcctcc atg ggc aca cag gag ggc      174
                               Met Gly Thr Gln Glu Gly
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tgg tgc ctg ctg ctc tgc ctg gct cta tct gga gca gca gaa acc aag      222
Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser Gly Ala Ala Glu Thr Lys
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ccc cac cca gca gag ggg cag ttg cgg gca gtg gac gtg gtc cta gac      270
Pro His Pro Ala Glu Gly Gln Leu Arg Ala Val Asp Val Val Leu Asp
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Cys Phe Leu Ala Lys Asp Gly Ala His Arg Gly Ala Leu Ala Ser Ser
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gag gac agg gca agg gcc tcc ctt gtg ctg aag cag gtg cca gtg ctg      366
Glu Asp Arg Ala Arg Ala Ser Leu Val Leu Lys Gln Val Pro Val Leu
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Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu Ala Ser Val Asp Leu Val
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cag att ccc cag gcc gag gcc ttg ctc cat gct gac tgc agt ggg aag      510
Gln Ile Pro Gln Ala Glu Ala Leu Leu His Ala Asp Cys Ser Gly Lys
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Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe Leu Gln Met Thr Glu Thr
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Thr Val Lys Thr Ala Ala Trp Phe Met Ala Asn Met Gln Val Ser Gly
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Gly Gly Xaa Ser Ile Ser Leu Val Met Lys Thr Pro Arg Val Thr Lys
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Asn Glu Ala Leu Trp His Pro Thr Leu Asn Leu Pro Leu Ser Pro Gln
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Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala Ser Leu Asp Cys Gly Phe
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His Lys Gly Arg Gly Gln Leu Val Tyr Ser Trp Thr Ala Gly Gln Gly	
210 215 220 225	
cag gct gtg cgg aag ggc gct acc ctg gag cct gca caa ctg ggc atg	942
Gln Ala Val Arg Lys Gly Ala Thr Leu Glu Pro Ala Gln Leu Gly Met	
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Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly Leu Thr Ile Gln Asp Glu	
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Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser Leu Tyr Arg Ala Gln Gln	
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Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro Lys Val Arg Leu Ser Leu	
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Ser Pro Ala Gln Val Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser	
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Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser Leu Thr Ala Glu Pro Gly	
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Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val Thr His Ile Ser Leu Glu	
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Glu Pro Leu Gly Ala Ser Thr Gln Val Val Pro Pro Glu Arg Arg Thr	
370 375 380 385	
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Ala Leu Gly Val Ile Phe Ala Ser Ser Leu Phe Leu Leu Ala Leu Met	
390 395 400	
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Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro Thr Gly Leu Gly Leu Leu	
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Gln Ala Glu Arg	
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 Lys Val Phe Trp Asp Leu Ala Ala Thr Arg Ala Val Phe Gly Val Gln
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 Gly Leu Val Ser Ser Leu Tyr Leu Pro His Leu Thr Leu Phe Leu Val
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Arg Pro
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Val Pro Ala Leu Leu Trp Ala Gln Glu Val Gly Gln Val Leu Ala Gly
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Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly Val Leu Phe Cys Thr Ile
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ctc ctt ttg ctc tgg gtg tct gtc ttc ctc tat ggc tcc ttc tac tat 378
Leu Leu Leu Leu Trp Val Ser Val Phe Leu Tyr Gly Ser Phe Tyr Tyr
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Ser Tyr Met Pro Thr Val Ser His Leu Ser Pro Val His Phe Tyr Tyr

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Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	Gly	Arg	Asp	Arg	Val	Leu	Met	Tyr	
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gga	cag	ccg	tat	cgt	gtt	acc	tta	gag	ctt	gag	ctg	cca	gag	tcc	cct	570
Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	Glu	Leu	Glu	Leu	Pro	Glu	Ser	Pro	
			85					90					95			
gtg	aat	caa	gat	ttg	ggc	atg	ttc	ttg	gtc	acc	att	tcc	tgc	tac	acc	618
Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	Leu	Val	Thr	Ile	Ser	Cys	Tyr	Thr	
			100				105					110				
aga	ggg	ggc	cga	atc	atc	tcc	act	tct	tcg	cgt	tcg	gtg	atg	ctg	cat	666
Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	Ser	Ser	Arg	Ser	Val	Met	Leu	His	
	115					120					125					
tac	cgc	tca	gac	ctg	ctc	cag	atg	ctg	gac	aca	ctg	gtc	ttc	tct	agc	714
Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	Leu	Asp	Thr	Leu	Val	Phe	Ser	Ser	
130					135					140					145	
ctc	ctg	cta	ttt	ggc	ttt	gca	gag	cag	aag	cag	ctg	ctg	gag	gtg	gaa	762
Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	Gln	Lys	Gln	Leu	Leu	Glu	Val	Glu	
				150					155					160		
ctc	tac	gca	gac	tat	aga	gag	aac	tcg	tac	gtg	ccg	acc	act	gga	gcg	810
Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	Ser	Tyr	Val	Pro	Thr	Thr	Gly	Ala	
			165					170					175			
atc	att	gag	atc	cac	agc	aag	cgc	atc	cag	ctg	tat	gga	gcc	tac	ctc	858
Ile	Ile	Glu	Ile	His	Ser	Lys	Arg	Ile	Gln	Leu	Tyr	Gly	Ala	Tyr	Leu	
			180				185					190				
cgc	atc	cac	gcg	cac	ttc	act	ggg	ctc	aga	tac	ctg	cta	tac	aac	ttc	906
Arg	Ile	His	Ala	His	Phe	Thr	Gly	Leu	Arg	Tyr	Leu	Leu	Tyr	Asn	Phe	
			195			200					205					
ccg	atg	acc	tgc	gcc	ttc	ata	ggg	gtt	gcc	agc	aac	ttc	acc	ttc	ctc	954
Pro	Met	Thr	Cys	Ala	Phe	Ile	Gly	Val	Ala	Ser	Asn	Phe	Thr	Phe	Leu	
210					215					220					225	
agc	gtc	atc	gtg	ctc	ttc	agc	tac	atg	cag	tgg	gtg	tgg	ggg	ggc	atc	1002
Ser	Val	Ile	Val	Leu	Phe	Ser	Tyr	Met	Gln	Trp	Val	Trp	Gly	Gly	Ile	
				230					235					240		
tgg	ccc	cga	cac	cgc	ttc	tct	ttg	cag	gtt	aac	atc	cga	aaa	aga	gac	1050
Trp	Pro	Arg	His	Arg	Phe	Ser	Leu	Gln	Val	Asn	Ile	Arg	Lys	Arg	Asp	
			245					250					255			
aat	tcc	cgg	aag	gaa	gtc											

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gtc cta gag act ctg ggc agc tct gaa cct gct ggg ggt gct ctc cga      1386
Val Leu Glu Thr Leu Gly Ser Ser Glu Pro Ala Gly Gly Ala Leu Arg
      355                      360                      365
cag cgc ccc acc tgc tct agt tcc tgaagaaaag gggcagactc ctcacattcc      1440
Gln Arg Pro Thr Cys Ser Ser Ser
370                      375
agcactttcc cacctgactc ctctcccctc gtttttcctt caataaaacta ttttgtgtca      1500
gcttcgaaaa aaaaaaaaaa aaa      1523

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ctctccaag gtctagtac ggagcccgcg cgcggcgcca cc atg cgg cag aag      114
                               Met Arg Gln Lys
                               -20
gcg gta tcg ctt ttc ttc tgc tac ctg ctg ctc ttc act tgc agt ggg      162
Ala Val Ser Leu Phe Phe Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly
      -15                      -10                      -5
gtg gag gca ggt aag aaa aag tgc tcg gag agc tcg gac agc ggc tcc      210
Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser
      1                      5                      10                      15
ggg ttc tgg aag gcc ctg acc ttc atg gcc gtc gga gga gga ctc gca      258
Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala
      20                      25                      30
gtc gcc ggg ctg ccc gcg ctg ggc ttc acc ggc gcc ggc atc gcg gcc      306
Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala
      35                      40                      45
aac tcg gtg gct gcc tcg ctg atg agc tgg tct gcg atc ctg aat ggg      354
Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly
      50                      55                      60
ggc ggc gtg ccc gcc ggg ggg cta gtg gcc acg ctg cag agc ctc ggg      402
Gly Gly Val Pro Ala Gly Gly Leu Val Ala Thr Leu Gln Ser Leu Gly
      65                      70                      75                      80
gct ggt ggc agc agc gtc gtc ata ggt aat att ggt gcc ctg atg ggc      450
Ala Gly Gly Ser Ser Val Val Ile Gly Asn Ile Gly Ala Leu Met Gly
      85                      90                      95
tac gcc acc cac aag tat ctc gat agt gag gag gat gag gag      492
Tyr Ala Thr His Lys Tyr Leu Asp Ser Glu Glu Asp Glu Glu
      100                      105                      110
tagccagcag ctcccagaac ctcttcttcc ttcttggcct aactcttcca gttaggatct      552
agaactttgc cttttttttt tttttttttt tttttttgag atgggttctc actatattgt      612
ccaggctaga gtgcagtggc tattcacaga tgcgaacata gtacactgca gcttccaact      672
cctagcctca agtgatctc ctgtctcaac ctcccaagta ggattacaag catgcgccga      732

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cgatgcccag aatccagaac tttgtctatc actctcccca acaacctaga tgtgaaaaca 792
gaataaaactt cacccagaaa gcaaaaaaaaa aaaaaaaaaa 832

<210> 49
<211> 831
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 234..491

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<221> sig_peptide
<222> 234..293
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seq AVAGLPALGFTGA/GI

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ctcctccaag gtctagtac ggagcccgcg cgcggcgcca ccatgcggca gaaggcggtta 120
tcgcttttct ctgctacctg ctgctcttca cttgcagtgg ggtggaggca ggtaagaaaa 180
agtgtctcga gagctcggac agcggctccg ggttctggaa ggcctgacc ttc atg 236

Met

-20

gcc gtc gga gga gga ctc gca gtc gcc ggg ctg ccc gcg ctg ggc ttc 284
Ala Val Gly Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe
-15 -10 -5

acc ggc gcc ggc atc gcg gcc aac tcg gtg gct gcc tcg ctg atg agc 332
Thr Gly Ala Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser
1 5 10

tgg tct gcg atc ctg aat ggg ggc ggc gtg ccc gcc ggg ggg cta gtg 380
Trp Ser Ala Ile Leu Asn Gly Gly Gly Val Pro Ala Gly Gly Leu Val
15 20 25

gcc acg ctg cag agc ctc ggg gct ggt ggc agc agc gtc gtc ata ggt 428
Ala Thr Leu Gln Ser Leu Gly Ala Gly Gly Ser Ser Val Val Ile Gly
30 35 40 45

aat att ggt gcc ctg atg ggc tac gcc acc cac aag tat ctc gat agt 476
Asn Ile Gly Ala Leu Met Gly Tyr Ala Thr His Lys Tyr Leu Asp Ser
50 55 60

gag gag gat gag gag tagccagcag ctcccagaac ctcttcttcc ttcttggcct 531
Glu Glu Asp Glu Glu
65

aactcttcca gttaggatct agaactttgc cttttttttt tttttttttt tttttttgag 591
atgggttctc actatatgt ccaggctaga gtgcagtggc tattcacaga tgcgaacata 651
gtacactgca gctccaact cctagcctca agtgatcctc ctgtctcaac ctccaagta 711
ggattacaag catgcgccga cgatgcccag aatccagaac tttgtctatc actctcccca 771
acaacctaga tgtgaaaaca gaataaactt cacccagaaa gcaaaaaaaaa aaaaaaaaaa 831

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<212> DNA
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 seq ILLLLWLIAPSRA/CT

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 ctgtgggttc cgcacccgct gccacccccg cccctagcgt ggacatttat cctctagcgc 120
 tcaggccctg cgcgccatgc cgcagatcca gcgcccagag agacaccaga gaaccacc 179
 atg gcc ccc ttt gag ccc ctg gct tct ggc atc ctg ttg ttg ctg tgg 227
 Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
 -20 -15 -10
 ctg ata gcc ccc agc agg gcc tgc acc tgt gtc cca ccc cac cca cag 275
 Leu Ile Ala Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln
 -5 1 5
 acg gcc ttc tgc aat tcc gac ctc gtc atc agg gcc aag ttc gtg ggg 323
 Thr Ala Phe Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly
 10 15 20 25
 aca cca gaa gtc aac cag acc acc tta tac cag cgt tat gag atc aag 371
 Thr Pro Glu Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys
 30 35 40
 atg acc aag atg tat aaa ggg ttc caa gcc tta ggg gat gcc gct gac 419
 Met Thr Lys Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp
 45 50 55
 atc cgg ttc gtc tac acc ccc gcc atg gag agt gtc tgc gga tac ttc 467
 Ile Arg Phe Val Tyr Thr Pro Ala Met Glu Ser Val Cys Gly Tyr Phe
 60 65 70
 cac agg tcc cac aac cgc agc gag gag ttt ctc att gct gga aaa ctg 515
 His Arg Ser His Asn Arg Ser Glu Glu Phe Leu Ile Ala Gly Lys Leu
 75 80 85
 cag gat gga ctc ttg cac atc act acc tgc agt ttt gtg gct ccc tgg 563
 Gln Asp Gly Leu Leu His Ile Thr Thr Cys Ser Phe Val Ala Pro Trp
 90 95 100 105
 aac agc ctg agc tta gct cag cgc cgg ggc ttc acc aag acc tac act 611
 Asn Ser Leu Ser Leu Ala Gln Arg Arg Gly Phe Thr Lys Thr Tyr Thr
 110 115 120
 gtt ggc tgt gag gaa tgc aca gtg ttt ccc tgt tta tcc ttc ccc tgc 659
 Val Gly Cys Glu Glu Cys Thr Val Phe Pro Cys Leu Ser Phe Pro Cys
 125 130 135
 aaa ctg cag agt ggc act cat tgc ttg tgg acg gac cag ctc ctc caa 707
 Lys Leu Gln Ser Gly Thr His Cys Leu Trp Thr Asp Gln Leu Leu Gln
 140 145 150
 ggc tct gaa aag ggc ttc cag tcc cgt cac ctt gcc tgc ctg cct cgg 755
 Gly Ser Glu Lys Gly Phe Gln Ser Arg His Leu Ala Cys Leu Pro Arg
 155 160 165
 gag cca ggg ctg tgc acc tgg cag tcc ctg cgg tcc cag ata gcc 800
 Glu Pro Gly Leu Cys Thr Trp Gln Ser Leu Arg Ser Gln Ile Ala
 170 175 180
 tgaatcctgc ccggagtgga agctgaagcc tgcacagtgt ccaccctgtt cccactccca 860
 tctttcttcc ggacaatgaa ataaagagtt accaccacgc aaaaaaaaaa aaaaaaa 917

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 seq FVVFSLEFLICAMA/GD

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 aagtgggtcta taggagaaa atg aaa tat gat tgt ccc ttc agt ggg aca tca 172
 Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser
 -20 -15
 ttt gtg gtc ttc tct ctc ttt ttg atc tgt gca atg gct gga gat gta 220
 Phe Val Val Phe Ser Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val
 -10 -5 1
 gtc tac gct gac atc aaa act gtt cgg act tcc ccg tta gaa ctc gcg 268
 Val Tyr Ala Asp Ile Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala
 5 10 15
 ttt cca ctt cag aga tct gtt tct ttc aac ttt tct act gtc cat aaa 316
 Phe Pro Leu Gln Arg Ser Val Ser Phe Asn Phe Ser Thr Val His Lys
 20 25 30 35
 tca tgt cct gcc aaa gac tgg aag gtg cat aag gga aaa tgt tac tgg 364
 Ser Cys Pro Ala Lys Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp
 40 45 50
 att gct gaa act aag aaa tct tgg aac aaa agt caa aat gac tgt gcc 412
 Ile Ala Glu Thr Lys Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala
 55 60 65
 ata aac aat tca tat ctc atg gtg att caa gac att act gct atg gtg 460
 Ile Asn Asn Ser Tyr Leu Met Val Ile Gln Asp Ile Thr Ala Met Val
 70 75 80
 aga ttt aac att tagaggtgac agcatccccc acactggcag ttaatttttt 512
 Arg Phe Asn Ile
 85
 gtctacaaac ttggcaaaag tctgtgaaaa gaagtttcaa cttcatgtgt tattaactat 572
 acaaataatta gttgaatgaa ttgttgaatt acaaaaaaaaa aaaaaaaaaa 621

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 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> 68..484

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 <222> 68..112
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 seq AVVFVFSLLDCCA/LI

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gaggagg atg gag gcg gtg gtg ttc gtc ttc tct ctc ctc gat tgt tgc 109
      Met Glu Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys
      -15                -10                -5
gcg ctc atc ttc ctc tcg gtc tac ttc ata att aca ttg tct gat tta 157
Ala Leu Ile Phe Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu
      1                5                10                15
gaa tgt gat tac att aat gct aga tca tgt tgc tca aaa tta aac aag 205
Glu Cys Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys
      20                25                30
tgg gta att cca gaa ttg att ggc cat acc att gtc act gta tta ctg 253
Trp Val Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu
      35                40                45
ctc atg tca ttg cac tgg ttc atc ttc ctt ctc aac tta cct gtt gcc 301
Leu Met Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala
      50                55                60
act tgg aat ata tat cga tac att atg gtg ccg agt ggt aac atg gga 349
Thr Trp Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly
      65                70                75
gtg ttt gat cca aca gaa ata cac aat cga ggg cag ctg aag tca cac 397
Val Phe Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His
      80                85                90                95
atg aaa gaa gcc atg atc aag ctt ggt ttc cac ttg ctc tgc ttc ttc 445
Met Lys Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe
      100                105                110
atg tat ctt tat agt atg atc tta gct ttg ata aat gac tgaagctgga 494
Met Tyr Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp
      115                120
gaagccgtgg ttgaagtcag cctacactac agtgcacagt tgaggagcca gagacttctt 554
aaatcatcct tagaaccgtg accatagcag tatatatattt cctcttgga caaaaaacta 614
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<213> Homo sapiens

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<220>
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<222> 38..517

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<220>
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<223> Von Heijne matrix
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      -25
ctg ctc tcc tgg acg ctg agc aga gtc ctg tgg ctc tcc ggc ctc tct 103
Leu Leu Ser Trp Thr Leu Ser Arg Val Leu Trp Leu Ser Gly Leu Ser
      -20                -15                -10
gag ccg gga gct gcc cgg cag ccc cgg atc atg gaa gag aaa gcg cta 151
Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile Met Glu Glu Lys Ala Leu

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-5          1          5          10
gag gtt tat gat ttg att aga act atc cgg gac cca gaa aag ccc aat 199
Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg Asp Pro Glu Lys Pro Asn
          15          20          25
act tta gaa gaa ctg gaa gtg gtc tcg gaa agt tgt gtg gaa gtt cag 247
Thr Leu Glu Glu Leu Glu Val Val Ser Glu Ser Cys Val Glu Val Gln
          30          35          40
gag ata aat gaa gaa gaa tat ctg gtt att atc agg ttc acg cca aca 295
Glu Ile Asn Glu Glu Glu Tyr Leu Val Ile Ile Arg Phe Thr Pro Thr
          45          50          55
gta cct cat tgc tct ttg gcg act ctt att ggg ctg tgc tta aga gta 343
Val Pro His Cys Ser Leu Ala Thr Leu Ile Gly Leu Cys Leu Arg Val
          60          65          70          75
aaa ctt cag cga tgt tta cca ttt aaa cat aag ttg gaa atc tac att 391
Lys Leu Gln Arg Cys Leu Pro Phe Lys His Lys Leu Glu Ile Tyr Ile
          80          85          90
tct gaa gga acc cac tca aca gaa gaa gac atc aat aag cag ata aat 439
Ser Glu Gly Thr His Ser Thr Glu Glu Asp Ile Asn Lys Gln Ile Asn
          95          100          105
gac aaa gag cga gtg gca gct gca atg gaa aac ccc aac tta cgg gaa 487
Asp Lys Glu Arg Val Ala Ala Ala Met Glu Asn Pro Asn Leu Arg Glu
          110          115          120
att gtg gaa cag tgt gtc ctt gaa cct gac tgatagctgt ttttaagagcc 537
Ile Val Glu Gln Cys Val Leu Glu Pro Asp
          125          130
actggcctgt aattgtttga tatatttgta actcttttgta taatgtcaga gactcatggt 597
taatacatag gtgatttgta cctcagagca ttttttaaag gattctttcc aagcgagatt 657
taattataag gtagtaccta atttgttcaa tgtataacat tctcaggatt tgtaacactt 717
aaatgatcag acagaataat atttttctagt tattatgtgt aagatgaggt gctatttttc 777
tgatgctcat tctgatacaa ctattttttcg tgtcaaatat ctactgtgcc caaatgtact 837
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<210> 54
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 <212> DNA
 <213> Homo sapiens

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 <222> 92..139
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 seq FLLLTCLFITGTS/VS

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ttccagtgtt tctggcagtt ggtccagaag g atg cct cca ttc ctg ctt ctc 112
                                Met Pro Pro Phe Leu Leu Leu
                                -15          -10
acc tgc ctc ttc atc aca ggc acc tcc gtg tca ccc gtg gcc cta gat 160
Thr Cys Leu Phe Ile Thr Gly Thr Ser Val Ser Pro Val Ala Leu Asp
          -5          1          5
cct tgt tct gct tac atc agc ctg aat gag ccc tgg agg aac act gac 208
Pro Cys Ser Ala Tyr Ile Ser Leu Asn Glu Pro Trp Arg Asn Thr Asp

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10	15	20	
cac cag ttg gat gag tct	caa ggt cct cct cta	tgt gac aac cat gtg	256
His Gln Leu Asp Glu Ser	Gln Gly Pro Pro Leu	Cys Asp Asn His Val	
25	30	35	
aat ggg gag tgg tac cac	ttc acg ggc atg gcg	gga gat gcc atg cct	304
Asn Gly Glu Trp Tyr His	Phe Thr Gly Met Ala	Gly Asp Ala Met Pro	
40	45	50	55
acc ttc tgc ata cca gaa	aac cac tgt gga acc	cac gca cct gtc tgg	352
Thr Phe Cys Ile Pro Glu	Asn His Cys Gly Thr	His Ala Pro Val Trp	
60	65	70	
ctc aat ggc agc cac ccc	cta gaa ggc gac ggc	att gtg caa cgc cag	400
Leu Asn Gly Ser His Pro	Leu Glu Gly Asp Gly	Ile Val Gln Arg Gln	
75	80	85	
gct tgt gcc agc ttc aat	ggg aac tgc tgt ctc	tgg aac acc acg gtg	448
Ala Cys Ala Ser Phe Asn	Gly Asn Cys Cys Leu	Trp Asn Thr Thr Val	
90	95	100	
gaa gtc aag gct tgc cct	gga ggc tac tat gtg	tat cgt ctg acc aag	496
Glu Val Lys Ala Cys Pro	Gly Tyr Tyr Val Tyr	Arg Leu Thr Lys	
105	110	115	
ccc agc gtc tgc ttc cac	gtc tac tgt ggt cgt	gag tac ctt ccc tgt	544
Pro Ser Val Cys Phe His	Val Tyr Cys Gly Arg	Glu Tyr Leu Pro Cys	
120	125	130	135
gct ctt ttt ctc cac caa	caa ggc cac agg tgg	agt cca aaa gtg ccc	592
Ala Leu Phe Leu His Gln	Gln Gly His Arg Trp	Ser Pro Lys Val Pro	
140	145	150	
aat tat agg ata tgc agt	tac agt ggc aac tat	atc tca atc	634
Asn Tyr Arg Ile Cys Ser	Tyr Ser Gly Asn Tyr	Ile Ser Ile	
155	160	165	
tgaacaacat tgatgtgggg	ctaaagatac tctgatttct	gagatctctt cttagaactt	694
ctgaaaaatt cctgaagaaa	tagaagggga aaggagctat	gactttgac agttcttttt	754
aattttgtct gaattccatt	caaacaaaac attagaaaat	gaaacattgg gccaggcgca	814
gtggctcatg cctgtaatcc	cagcactttg ggaggctgag	gcgggtggat cacaagatca	874
ggagtttaag accagcctgg	ccaatatggt gaaaccctgt	ctctactaga aatacaaaaa	934
ttagacaggc gtgggtggcag	gcaactgtaa ccccagctac	ccgggagggt gaggcaggag	994
aattgcttga acccgggagg	tggacgttgc ggtcaggcga	aaatcgtgcc attgcactcc	1054
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<210> 55
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 27..767

<220>
 <221> sig_peptide
 <222> 27..80
 <223> Von Heijne matrix
 score 8.96664802487992
 seq LFCLAVLAASSFS/KA

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	Met Gly Leu Pro Gly Leu Phe Cys Leu
	-15 -10
gcc gtg ctg gct gcc agc agc	ttc tcc aag gca cgg gag gaa gaa att
	101

Ala	Val	Leu	Ala	Ala	Ser	Ser	Phe	Ser	Lys	Ala	Arg	Glu	Glu	Glu	Ile	
				-5					1				5			
acc	cct	gtg	gtc	tcc	att	gcc	tac	aaa	gtc	ctg	gaa	gtt	ttc	ccc	aaa	149
Thr	Pro	Val	Val	Ser	Ile	Ala	Tyr	Lys	Val	Leu	Glu	Val	Phe	Pro	Lys	
		10					15					20				
ggc	cgc	tgg	gtg	ctc	ata	acc	tgc	tgt	gca	ccc	cag	cca	cca	ccg	ccc	197
Gly	Arg	Trp	Val	Leu	Ile	Thr	Cys	Cys	Ala	Pro	Gln	Pro	Pro	Pro	Pro	
		25					30				35					
atc	acc	tat	tcc	ctc	tgt	gga	acc	aag	aac	atc	aag	gtg	gcc	aag	aag	245
Ile	Thr	Tyr	Ser	Leu	Cys	Gly	Thr	Lys	Asn	Ile	Lys	Val	Ala	Lys	Lys	
		40				45				50					55	
gtg	gtg	aag	acc	cac	gag	ccg	gcc	tcc	ttc	aac	ctc	aac	gtc	aca	ctc	293
Val	Val	Lys	Thr	His	Glu	Pro	Ala	Ser	Phe	Asn	Leu	Asn	Val	Thr	Leu	
				60					65					70		
aag	tcc	agt	cca	gac	ctg	ctc	acc	tac	ttc	tgc	cgg	gcg	tcc	tcc	acc	341
Lys	Ser	Ser	Pro	Asp	Leu	Leu	Thr	Tyr	Phe	Cys	Arg	Ala	Ser	Ser	Thr	
			75					80					85			
tca	ggt	gcc	cat	gtg	gac	agt	gcc	agg	cta	cag	atg	cac	tgg	gag	ctg	389
Ser	Gly	Ala	His	Val	Asp	Ser	Ala	Arg	Leu	Gln	Met	His	Trp	Glu	Leu	
		90					95					100				
tgg	tcc	aag	cca	gtg	tct	gag	ctg	cgg	gcc	aac	ttc	act	ctg	cag	gac	437
Trp	Ser	Lys	Pro	Val	Ser	Glu	Leu	Arg	Ala	Asn	Phe	Thr	Leu	Gln	Asp	
		105					110				115					
aga	ggg	gca	ggc	ccc	agg	gtg	gag	atg	atc	tgc	cag	gcg	tcc	tcg	ggc	485
Arg	Gly	Ala	Gly	Pro	Arg	Val	Glu	Met	Ile	Cys	Gln	Ala	Ser	Ser	Gly	
				125					130						135	
agc	cca	cct	atc	acc	aac	agc	ctg	atc	ggg	aag	gat	ggg	cag	gtc	cac	533
Ser	Pro	Pro	Ile	Thr	Asn	Ser	Leu	Ile	Gly	Lys	Asp	Gly	Gln	Val	His	
				140					145					150		
ctg	cag	cag	aga	cca	tgc	cac	agg	cag	cct	gcc	aac	ttc	tcc	ttc	ctg	581
Leu	Gln	Gln	Arg	Pro	Cys	His	Arg	Gln	Pro	Ala	Asn	Phe	Ser	Phe	Leu	
			155					160					165			
ccg	agc	cag	aca	tcg	gac	tgg	ttc	tgg	tgc	cag	gct	gca	aac	aac	gcc	629
Pro	Ser		Gln	Thr	Ser	Asp	Trp	Phe	Trp	Cys	Gln	Ala	Ala	Asn	Ala	
			170				175					180				
aat	gtc	cag	cac	agc	gcc	ctc	aca	gtg	gtg	ccc	cca	gga	ggg	ttg	ccc	677
Asn	Val	Gln	His	Ser	Ala	Leu	Thr	Val	Val	Pro	Pro	Gly	Gly	Leu	Pro	
						190				195						
agg	gca	ccc	acc	atc	gtg	ctg	gtt	ggc	agc	ctt	gcc	tcc	act	gcg	gcc	725
Arg	Ala	Pro	Thr	Ile	Val	Leu	Val	Gly	Ser		Leu	Ala	Ser	Thr	Ala	
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<211> 925
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 4..399

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<220>
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<222> 4..126
<223> Von Heijne matrix
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      seq RVVSWLFSIVVFG/SI

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acg atg gaa ggg ggt gcg tac gga gcg ggc aaa gcc ggg ggc gcc ttc      48
  Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe
      -40                      -35                      -30
gac ccc tac acc ctg gtc cgg cag ccg cac acc atc ctg cgc gtc gtg      96
Asp Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val
      -25                      -20                      -15
tct tgg ctg ttc tcc ata gtg gtg ttc ggc tcc atc gtg aac gag ggc      144
Ser Trp Leu Phe Ser Ile Val Val Phe Gly Ser Ile Val Asn Glu Gly
      -10                      -5                      1                      5
tac ctc aac agc gcc tcc gag ggg gag cag ttc tgc atc tac aac cgc      192
Tyr Leu Asn Ser Ala Ser Glu Gly Glu Gln Phe Cys Ile Tyr Asn Arg
      10                      15                      20
aac ccc aac gcc tgc agc tat ggc gtg gcc gtg ggc gtg ctc gcc ttc      240
Asn Pro Asn Ala Cys Ser Tyr Gly Val Ala Val Gly Val Leu Ala Phe
      25                      30                      35
ctc acc tgc ctg ctg tac ctg gcc ctg gac gtg tac ttc ccg cag atc      288
Leu Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val Tyr Phe Pro Gln Ile
      40                      45                      50
agc agc gtc aag gac cgc aag aaa gcc gtc ctg tcc gac atc ggt gtc      336
Ser Ser Val Lys Asp Arg Lys Lys Ala Val Leu Ser Asp Ile Gly Val
      55                      60                      65                      70
tcg ggt gag ccc cac cca gca ggt acc ccc tgc aca gag tct aca gag      384
Ser Gly Glu Pro His Pro Ala Gly Thr Pro Cys Thr Glu Ser Thr Glu
      75                      80                      85
ggc tgt ccc ggg cca taggaggcgg ctgccaccct tcttcccatg ttccagatga      439
Gly Cys Pro Gly Pro
      90
gggaaatgag ccttctgggc tttcctctgg ttcgtgggat tctgctacct ggccaaccag      499
tggcaggtct ccaagcccaa ggacaacca ctgaacgaag ggacggacgc agcccgggcc      559
gccatgcct tctccttttt ctccatcttc acctggagcc tgaccgcagc cctggccgtg      619
cggagattca aggacctaa cttccaggag gagtacagca cactgttccc tgcttcggca      679
cagccgtagg cctccccggc ttgcagaggc cggcagccct gtatcacccc tggcagttag      739
gtggcaggag cagcctagt ccagaaatgt ccaagatgcc agggcatgca gggcagtgga      799
aggctggctt gaggaaccaa ttcaggttct ccactgactc attcattcct tcaccgcctc      859
cttcattgat tcttcattgc ttcattcatt cagtaaacad ttattgagta aaaaaaaaaa      919
aaaaaa                                           925

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<212> DNA
<213> Homo sapiens

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<222> 127..879

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<221> sig_peptide
<222> 127..198

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<223> Von Heijne matrix
score 5.38660866264012
seq ALCSVCSMSVLRA/YP

<400> 57

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gccaggagag tcccgcacagg agtgtcaggt ttcaatctca gcaccagcca ctcagagcag      120
ggcacg atg ttg ggg gcc cgc ctc agg ctc tgg gtc tgt gcc ttg tgc      168
      Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys
                -20                                -15
agc gtc tgc agc atg agc gtc ctc aga gcc tat ccc aat gcc tcc cca      216
Ser Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
-10                -5                                1                                5
ctg ctc ggc tcc agc tgg ggt ggc ctg atc cac ctg tac aca gcc aca      264
Leu Leu Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr
                10                                15                                20
gcc agg aac agc tac cac ctg cag atc cac aag aat ggc cat gtg gat      312
Ala Arg Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp
                25                                30                                35
ggc gca ccc cat cag acc atc tac agt gcc ctg atg atc aga tca gag      360
Gly Ala Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu
                40                                45                                50
gat gct ggc ttt gtg gtg att aca ggt gtg atg agc aga aga tac ctc      408
Asp Ala Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu
                55                                60                                65                                70
tgc atg gat ttc aga ggc aac att ttt gga tca cac tat ttc gac ccg      456
Cys Met Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro
                75                                80                                85
gag aac tgc agg ttc caa cac cag acg ctg gaa aac ggg tac gac gtc      504
Glu Asn Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val
                90                                95                                100
tac cac tct cct cag tat cac ttc ctg gtc agt ctg ggc cgg gcg aag      552
Tyr His Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys
                105                                110                                115
aga gcc ttc ctg cca ggc atg aac cca ccc ccg tac tcc cag ttc ctg      600
Arg Ala Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu
                120                                125                                130
tcc cgg agg aac gag atc ccc cta att cac ttc aac acc ccc ata cca      648
Ser Arg Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro
                135                                140                                145                                150
cgg cgg cac acc cgg agc gcc gag gac gac tcg gag cgg gac ccc ctg      696
Arg Arg His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu
                155                                160                                165
aac gtg ctg aag ccc cgg gcc cgg atg acc ccg gcc ccg gcc tcc tgt      744
Asn Val Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys
                170                                175                                180
tca cag gag ctg ccc agc gcc gag gac aac agc ccg atg gcc agt gac      792
Ser Gln Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp
                185                                190                                195
cca tta ggg gtg gtc agg ggc ggt cga gtg aac acg cac gct ggg gga      840
Pro Leu Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly
                200                                205                                210
acg ggc ccg gaa ggc tgc cgc ccc ttc gcc aag ttc atc tagggctcgt      889
Thr Gly Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
                215                                220                                225
ggaagggcac cctctttaac ccattccctca gcaaacgcag ctcttcccaa ggaccaggtc      949
ccttgacgtt ccgaggatgg gaaaggtgac aggggcatgt atggaatttg ctgcttctct      1009
ggggctccctt ccacaggagg tcctgtgaga accaaccctt gaggcccaag tcatgggggt      1069

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tcaccgcctt	cctcactcca	tatagaacac	ctttcccaat	aggaaacccc	aacaggtaaa	1129
ctagaaattt	ccccttcattg	aaggtagaga	gaaggggtct	ctcccaacat	atttctcttc	1189
cttgtgcctc	tcctctttat	cacttttaag	catgaaaaaa	aaaaaaaaaa	a	1240

<210> 58
 <211> 902
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 156..566

<220>
 <221> sig_peptide
 <222> 156..221
 <223> Von Heijne matrix
 score 5.67458379966095
 seq LVSMAGRVCLCQG/SA

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tcctggccct	gagcgggaat cgcagtggcc gaggctgagc ggcaggcgga tcgccccgac 120
cctcactcct	ggcgtctgag tctctggcgt agccc atg ctg agt ggg cgg ctg 173
	Met Leu Ser Gly Arg Leu

	-20	
gtc ctg ggt ctg gtc tcc atg gct ggc cgc gtt tgt ttg tgc cag ggc 221		
Val Leu Gly Leu Val Ser Met Ala Gly Arg Val Cys Leu Cys Gln Gly		
-15 -10 -5		
agc gcg gga tcc ggg gcc atc ggt ccg gtg gag gcc gcc att cgc acg 269		
Ser Ala Gly Ser Gly Ala Ile Gly Pro Val Glu Ala Ala Ile Arg Thr		
1 5 10 15		
aag ttg gag gag gcc ctg agc ccc gag gtg cta gag ctt cgc aac gag 317		
Lys Leu Glu Glu Ala Leu Ser Pro Glu Val Leu Glu Leu Arg Asn Glu		
20 25 30		
agc ggt ggc cac gcg gtc ccg cca ggc agt gag act cac ttc cgc gtg 365		
Ser Gly Gly His Ala Val Pro Pro Gly Ser Glu Thr His Phe Arg Val		
35 40 45		
gct gtg gtg agc tct cgt ttc gag gga ctg agc ccc cta caa cga cac 413		
Ala Val Val Ser Ser Arg Phe Glu Gly Leu Ser Pro Leu Gln Arg His		
50 55 60		
cgg ctg gtc cac gca gcg ctg gcc gag gag ctg gga ggt ccg gtc cat 461		
Arg Leu Val His Ala Ala Leu Ala Glu Glu Leu Gly Gly Pro Val His		
65 70 75 80		
gcg ctg gcc atc cag gca cgg acc ccc gcc cag tgg aga gag aac tct 509		
Ala Leu Ala Ile Gln Ala Arg Thr Pro Ala Gln Trp Arg Glu Asn Ser		
85 90 95		
cag ctg gac act agc ccc cca tgc ctg ggt ggg aac aag aaa act cta 557		
Gln Leu Asp Thr Ser Pro Pro Cys Leu Gly Gly Asn Lys Lys Thr Leu		
100 105 110		
gga acc ccc tgaaccccaa gagagggagg accaggatcc gaatgggctg 606		
Gly Thr Pro		
115		
ggtgagcag aattaccgag gccttcctt tgatacagtc caggatttgt aagggatgaa 666		
gacccctggg cccattctg ttgggggtcca tacatactct ccgaagatag caacttgctt 726		
caggtcaaag tgaacccgag aaaagagaag aatcactcac tactgtctt gccctggact 786		
attcaggaag ggcagcccg atgttccatg ttaaactctg acagaattgc accagacctg 846		
atgagttgga aacaatccta tacattaaaa gaaattacac taaaaaaaaa aaaaaa 902		

<210> 59
 <211> 1969
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..1657

<220>
 <221> sig_peptide
 <222> 35..118
 <223> Von Heijne matrix
 score 3.75144398608723
 seq SGLLLQVLFRLLIT/FV

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 Met Gly Ser Gln Glu Val Leu
 -25
 ggc cac gcg gcc cgg ctg gcc tcc tcc ggt ctc ctc ctg cag gtg ttg 103
 Gly His Ala Ala Arg Leu Ala Ser Ser Gly Leu Leu Gln Val Leu
 -20 -15 -10
 ttt cgg ttg atc acc ttt gtc ttg aat gca ttt att ctt cgc ttc ctg 151
 Phe Arg Leu Ile Thr Phe Val Leu Asn Ala Phe Ile Leu Arg Phe Leu
 -5 1 5 10
 tca aag gaa atc gtt ggc gta gta aat gta aga cta acg ctg ctt tac 199
 Ser Lys Glu Ile Val Gly Val Val Asn Val Arg Leu Thr Leu Leu Tyr
 15 20 25
 tca acc acc ctc ttc ctg gcc aga gag gcc ttc cgc aga gca tgt ctc 247
 Ser Thr Thr Leu Phe Leu Ala Arg Glu Ala Phe Arg Arg Ala Cys Leu
 30 35 40
 agt ggg ggc acc cag cga gac tgg agc cag acc ctc aac ctg ctg tgg 295
 Ser Gly Gly Thr Gln Arg Asp Trp Ser Gln Thr Leu Asn Leu Leu Trp
 45 50 55
 cta aca gtc ccc ctg ggt gtg ttt tgg tcc tta ttc ctg ggc tgg atc 343
 Leu Thr Val Pro Leu Gly Val Phe Trp Ser Leu Phe Leu Gly Trp Ile
 60 65 70 75
 tgg ttg cag ctg ctt gaa gtg cct gat cct aat gtt gtc cct cac tat 391
 Trp Leu Gln Leu Leu Glu Val Pro Asp Pro Asn Val Val Pro His Tyr
 80 85 90
 gca act gga gtg gtg ctg ttt ggt ctc tcg gca gtg gtg gag ctt cta 439
 Ala Thr Gly Val Val Leu Phe Gly Leu Ser Ala Val Val Glu Leu Leu
 95 100 105
 gga gag ccc ttt tgg gtc ttg gca caa gca cat atg ttt gtg aag ctc 487
 Gly Glu Pro Phe Trp Val Leu Ala Gln Ala His Met Phe Val Lys Leu
 110 115 120
 aag gtg att gca gag agc ctg tcg gta att ctt aag agc gtt ctg aca 535
 Lys Val Ile Ala Glu Ser Leu Ser Val Ile Leu Lys Ser Val Leu Thr
 125 130 135
 gct ttt ctc gtg ctg tgg ttg cct cac tgg gga ttg tac att ttc tct 583
 Ala Phe Leu Val Leu Trp Leu Pro His Trp Gly Leu Tyr Ile Phe Ser
 140 145 150 155
 ttg gcc cag ctt ttc tat acc aca gtt ctg gtg ctc tgc tat gtt att 631
 Leu Ala Gln Leu Phe Tyr Thr Thr Val Leu Val Leu Cys Tyr Val Ile
 160 165 170
 tat ttc aca aag tta ctg ggt tcc cca gaa tca acc aag ctt caa act 679

Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro	Glu	Ser	Thr	Lys	Leu	Gln	Thr	
			175					180					185			
ctt	cct	gtc	tcc	aga	ata	aca	gat	ctg	tta	ccc	aat	att	aca	aga	aat	727
Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu	Leu	Pro	Asn	Ile	Thr	Arg	Asn	
			190				195				200					
gga	gcg	ttt	ata	aac	tgg	aaa	gag	gct	aaa	ctg	act	tgg	agt	ttt	ttc	775
Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala	Lys	Leu	Thr	Trp	Ser	Phe	Phe	
	205					210					215					
aaa	cag	tct	ttc	ttg	aaa	cag	att	ttg	aca	gaa	ggc	gag	cga	tat	gtg	823
Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu	Thr	Glu	Gly	Glu	Arg	Tyr	Val	
220					225					230					235	
atg	aca	ttt	ttg	aat	gta	ttg	aac	ttt	ggg	gat	cag	ggg	gtg	tat	gat	871
Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe	Gly	Asp	Gln	Gly	Val	Tyr	Asp	
				240					245					250		
ata	gtg	aat	aat	ctt	ggc	tcc	ctt	gtg	gcc	aga	tta	att	ttc	cag	cca	919
Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val	Ala	Arg	Leu	Ile	Phe	Gln	Pro	
			255					260					265			
ata	gag	gaa	agt	ttt	tat	ata	ttt	ttt	gct	aag	gtg	ctg	gag	agg	gga	967
Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe	Ala	Lys	Val	Leu	Glu	Arg	Gly	
		270					275					280				
aag	gat	gcc	aca	ctt	cag	aag	cag	gag	gac	gtt	gct	gtg	gct	gct	gca	1015
Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu	Asp	Val	Ala	Val	Ala	Ala	Ala	
	285					290					295					
gtc	ttg	gag	tcc	ctg	ctc	aag	ctg	gcc	ctg	ctg	gcc	ggc	ctg	acc	atc	1063
Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala	Leu	Leu	Ala	Gly	Leu	Thr	Ile	
300					305					310					315	
act	gtt	ttt	ggc	ttt	gcc	tat	tct	cag	ctg	gct	ctg	gat	atc	tac	gga	1111
Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln	Leu	Ala	Leu	Asp	Ile	Tyr	Gly	
				320					325					330		
ggg	acc	atg	ctt	agc	tca	gga	tcc	ggg	cct	gtt	ttg	ctg	cgt	tcc	tac	1159
Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly	Pro	Val	Leu	Leu	Arg	Ser	Tyr	
			335					340					345			
tgt	ctc	tat	gtt	ctc	ctg	ctt	gcc	atc	aat	gga	gtg	aca	gag	tgt	tta	1207
Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile	Asn	Gly	Val	Thr	Glu	Cys	Leu	
			350				355					360				
aca	ttt	gct	gcc	atg	agc	aaa	gag	gag	gtc	gac	agg	tac	aat	ttt	gtg	1255
Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu	Val	Asp	Arg	Tyr	Asn	Phe	Val	
	365					370					375					
atg	ctg	gcc	ctg	tcc	tcc	tca	ttc	ctg	gtg	tta	tcc	tat	ctc	ttg	acc	1303
Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu	Val	Leu	Ser	Tyr	Leu	Leu	Thr	
380					385					390					395	
cgt	tgg	tgt	ggc	agc	gtg	ggc	ttc	atc	ttg	gcc	aac	tgc	ttt	aac	atg	1351
Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile	Leu	Ala	Asn	Cys	Phe	Asn	Met	
				400					405					410		
ggc	att	cgg	atc	acg	cag	agc	ctt	tgc	ttc	atc	cac	cgc	tac	tac	cga	1399
Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys	Phe	Ile	His	Arg	Tyr	Tyr	Arg	
			415					420					425			
agg	agc	ccc	cac	agg	ccc	ctg	gct	ggc	ctg	cac	cta	tcg	cca	gtc	ctg	1447
Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly	Leu	His	Leu	Ser	Pro	Val	Leu	
			430				435					440				
ctc	ggg	aca	ttt	gcc	ctc	agt	ggg	ggg	gtt	act	gct	gtt	tcg	gag	gta	1495
Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly	Val	Thr	Ala	Val	Ser	Glu	Val	
	445					450					455					
ttc	ctc	tgc	tgt	gat	cag	ggc	tgg	cca	gcc	aga	ctg	gca	cac	att	gct	1543
Phe	Leu	Cys	Cys	Asp	Gln	Gly	Trp	Pro	Ala	Arg	Leu	Ala	His	Ile	Ala	
460					465					470					475	
gtg	ggg	gcc	ttc	tgt	ctg	gga	gca	act	ctc	ggg	aca	gca	ttc	ctc	aca	1591
Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr	Leu	Gly	Thr	Ala	Phe	Leu	Thr	


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                                480                                485                                490
gag acc aag ctg atc cat ttc ctc agg act cag tta ggt gtg ccc aga      1639
Glu Thr Lys Leu Ile His Phe Leu Arg Thr Gln Leu Gly Val Pro Arg
                                495                                500                                505
cgc act gac aaa atg aca tgacttcagg gaagcctgga cacccgaggc      1687
Arg Thr Asp Lys Met Thr
                                510
acctggacca gctatgggta gttctgtggg tggaacacat tctgtgtaag agccccactg      1747
agggctctgc agcggagtga cagcaacccc agagatgagg caccagagag tgccactgca      1807
tgagacacct gtgaccattc gaagtctgaa atgcgggggg ggagtttcat ttttaagtga      1867
agaccaaag ccctttaaaa ataatagttt tttatcattt tatagtaatc agcattttct      1927
cttttactaa tatactcatt ccttttgaaa aaaaaaaaaa aa      1969

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..937

<220>
<221> sig_peptide
<222> 77..127
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      seq RIVSAALLAFVQT/HL

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gagcagaaga gagagc atg gag ctg gag agg atc gtc agt gca gcc ctc ctt      112
      Met Glu Leu Glu Arg Ile Val Ser Ala Ala Leu Leu
                                -15                                -10
gcc ttt gtc cag aca cac ctc ccg gag gcc gac ctc agt ggc ttg gat      160
Ala Phe Val Gln Thr His Leu Pro Glu Ala Asp Leu Ser Gly Leu Asp
-5                                1                                5                                10
gag gtc atc ttc tcc tat gtg ctt ggg gtc ctg gag gac ctg ggc ccc      208
Glu Val Ile Phe Ser Tyr Val Leu Gly Val Leu Glu Asp Leu Gly Pro
                                15                                20                                25
tcg ggc cca tca gag gag aac ttc gat atg gag gct ttc act gag atg      256
Ser Gly Pro Ser Glu Glu Asn Phe Asp Met Glu Ala Phe Thr Glu Met
                                30                                35                                40
atg gag gcc tat gtg cct ggc ttc gcc cac atc ccc agg ggc aca ata      304
Met Glu Ala Tyr Val Pro Gly Phe Ala His Ile Pro Arg Gly Thr Ile
                                45                                50                                55
ggg gac atg atg cag aag ctc tca ggg cag ctg agc gat gcc agg aac      352
Gly Asp Met Met Gln Lys Leu Ser Gly Gln Leu Ser Asp Ala Arg Asn
60                                65                                70                                75
aaa gag aac ctg caa ccg cag agc tct ggt gtc caa ggt cag gtg ccc      400
Lys Glu Asn Leu Gln Pro Gln Ser Ser Gly Val Gln Gly Gln Val Pro
                                80                                85                                90
atc tcc cca gag ccc ctg cag cgg ccc gaa atg ctc aaa gaa gag act      448
Ile Ser Pro Glu Pro Leu Gln Arg Pro Glu Met Leu Lys Glu Glu Thr
                                95                                100                                105
agg tct tcg gct gct gct gct gca gac acc caa gat gag gca act ggc      496
Arg Ser Ser Ala Ala Ala Ala Ala Asp Thr Gln Asp Glu Ala Thr Gly
                                110                                115                                120

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gct	gag	gag	gag	gtt	ctg	cca	ggg	gtg	gat	gta	ctc	ctg	gag	gtg	ttc	544	
Ala	Glu	Glu	Glu	Leu	Leu	Pro	Gly	Val	Asp	Val	Leu	Leu	Glu	Val	Phe		
125							130					135					
cct	acc	tgt	tcg	gtg	gag	cag	gcc	cag	tgg	gtg	ctg	gcc	aaa	gct	cgg	592	
Pro	Thr	Cys	Ser	Val	Glu	Gln	Ala	Gln	Trp	Val	Leu	Ala	Lys	Ala	Arg		
140							145					150				155	
ggg	gac	ttg	gaa	gaa	gct	gtg	cag	atg	ctg	gta	gag	gga	aag	gaa	gag	640	
Gly	Asp	Leu	Glu	Glu	Ala	Val	Gln	Met	Leu	Val	Glu	Gly	Lys	Glu	Glu		
160							165					170					
ggg	cct	gca	gcc	tgg	gag	ggc	ccc	aac	cag	gac	ctg	ccc	aga	cgc	ctc	688	
Gly	Pro	Ala	Ala	Trp	Glu	Gly	Pro	Asn	Gln	Asp	Leu	Pro	Arg	Arg	Leu		
175							180					185					
aga	ggc	ccc	caa	aag	gat	gag	ctg	aag	tcc	ttc	atc	ctg	cag	aag	tac	736	
Arg	Gly	Pro	Gln	Lys	Asp	Glu	Leu	Lys	Ser	Phe	Ile	Leu	Gln	Lys	Tyr		
190							195					200					
atg	atg	gtg	gat	agc	gca	gag	gat	cag	aag	att	cac	cgg	ccc	atg	gct	784	
Met	Met	Val	Asp	Ser	Ala	Glu	Asp	Gln	Lys	Ile	His	Arg	Pro	Met	Ala		
205							210					215					
ccc	aag	gag	gcc	ccc	aag	aag	ctg	atc	cga	tac	atc	gac	aac	cag	gta	832	
Pro	Lys	Glu	Ala	Pro	Lys	Lys	Leu	Ile	Arg	Tyr	Ile	Asp	Asn	Gln	Val		
220							225					230				235	
gtg	agc	acc	aaa	ggg	gag	cga	ttc	aaa	gat	gtg	cgg	aac	cct	gag	gcc	880	
Val	Ser	Thr	Lys	Gly	Glu	Arg	Phe	Lys	Asp	Val	Arg	Asn	Pro	Glu	Ala		
240							245					250					
gag	gag	atg	aag	gcc	aca	tac	atc	aac	ctc	aag	cca	gcc	aga	aag	tac	928	
Glu	Glu	Met	Lys	Ala	Thr	Tyr	Ile	Asn	Leu	Lys	Pro	Ala	Arg	Lys	Tyr		
255							260					265					
cgc	ttc	cat	tgaggcactc	gccggactct	gcccgcgcct	tctaggctca										977	
Arg	Phe	His															
270																	
gatccccagag ggatgcagga gccctataacc cctacacagg ggccccctaata ctctgtccc																1037	
ccttctctac tcctttgtct catagtgtta acctactctc ggagctgcct ccatgggcac																1097	
agtaaagggtg gcccaaggaa aaaaaaaaaa aaaaaa																1132	

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<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 9..503

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<223> Von Heijne matrix
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[illegible]

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cag ggc ttc gcc gag tgt ctc atc cgc ttg ggg gac agc atg ggc cgc      194
Gln Gly Phe Ala Glu Cys Leu Ile Arg Leu Gly Asp Ser Met Gly Arg
      15      20      25
gga ggc gag ctg gag acc atc tgc agg tct tgg aat tac ttc cat gcc      242
Gly Gly Glu Leu Glu Thr Ile Cys Arg Ser Trp Asn Tyr Phe His Ala
      30      35      40
tgt gcc tct cag gtc ctg tca ggc tgt ccg gag gag gca gct gca gtg      290
Cys Ala Ser Gln Val Leu Ser Gly Cys Pro Glu Glu Ala Ala Ala Val
      45      50      55
tgg gaa tca cta cag caa gaa gct cgc cag gcc ccc cgt ccg aat aac      338
Trp Glu Ser Leu Gln Gln Glu Ala Arg Gln Ala Pro Arg Pro Asn Asn
      60      65      70      75
ttg cac act ctg tgc ggt gcc ccg gtg cat gtt cgg gag cgc ggc aca      386
Leu His Thr Leu Cys Gly Ala Pro Val His Val Arg Glu Arg Gly Thr
      80      85      90
ggc tcc gaa acc aac cag gag acg ctg cgg gct aca gcg cct gca ctc      434
Gly Ser Glu Thr Asn Gln Glu Thr Leu Arg Ala Thr Ala Pro Ala Leu
      95      100      105
ccc atg gcc cct gcg ccc cca ctg ctg gcg gct gct ctg gct ctg gcc      482
Pro Met Ala Pro Ala Pro Pro Leu Leu Ala Ala Ala Leu Ala Leu Ala
      110      115      120
tac ctc ctg agg cct ctg gcc tagcttggtg gggtgggtag cagcgcccgt      533
Tyr Leu Leu Arg Pro Leu Ala
      125      130
acctccagcc ctgctctggc ggtggttgctc caggctctgc agagcgcagc agggccttttc      593
attaaaggta tttatatattg caaaaaaaaaa aaaaaaaaaa      631

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 seq AVTSLLSPTPATA/LA

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      -25      -20      -15
aca gcc gtt aca tcc ttg cta agc ccc act ccg gct aca gct ctt gct      101
Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala
      -10      -5      1
gtc aga tac gca tcc aag aag tcg ggt ggt agc tcc aaa aac ctc ggt      149
Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly
      5      10      15
gga aag tca tca ggc aga cgc caa ggc att aag aaa atg gaa ggt cac      197
Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His
      20      25      30

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tat gtt cat gct ggg aac atc att gca aca cag cgc cat ttc cgc tgg	245
Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp	
35 40 45 50	
cac cca ggt gcc cat gtg ggt gtt ggg aag aat aaa tgt ctg tat gcc	293
His Pro Gly Ala His Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala	
55 60 65	
ctg gaa gag ggg ata gtc cgc tac act aag gag gtc tac gtg cct cat	341
Leu Glu Glu Gly Ile Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His	
70 75 80	
ccc aga aac acg gag gct gtg gat ctg atc acc agg ctg ccc aag ggt	389
Pro Arg Asn Thr Glu Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly	
85 90 95	
gct gtg ctc tac aag act ttt gtc cac gtg gtt cct gcc aag cct gag	437
Ala Val Leu Tyr Lys Thr Phe Val His Val Val Pro Ala Lys Pro Glu	
100 105 110	
ggc acc ttc aaa ctg gta gct atg ctt tgatgtcctg ttgaggccat	484
Gly Thr Phe Lys Leu Val Ala Met Leu	
115 120	
cggacagaga ctggagccca ggtgacagga gatggtgata ccagaagtca aggggttgggg	544
tggcgacacg gcctcccgag gaagaggtct gcttgatggt gactctgcag gagactctga	604
agtgactgct gggaaaccct ttgggagacc tgacctgggg ccaaaaaataa agtgagccag	664
cgatcatgaac gcatgctatt tagggacaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	722
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gcagagatac agaggcagag gaaaagggca ctcctatgtg acctgttctt agagcaagac	120
aatcaccatc tgaattccag aagccctggt catggttggg gatattttct cgactgc	177
atg gaa tca gaa aga agc aaa agg atg gga aat gcc tgc att ccc ctg	225
Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu	
-30 -25 -20	
aaa aga att gct tat ttc cta tgt ctc tta tct gcg ctt ttg ctg act	273
Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Leu Thr	
-15 -10 -5	
gag ggg aag aaa cca gcg aag cca aaa tgc cct gcc gtg tgt act tgt	321
Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys	
1 5 10	
acc aaa gat aat gct tta tgt gag aat gcc aga tcc att cca cgc acc	369
Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr	
15 20 25 30	
gtt cct cct gat gtt atc tca tta tcc ttt gtg aga tct ggt ttt act	417
Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Gly Phe Thr	
35 40 45	

gaa atc tca gaa ggg agt ttt tta ttc acg cca tcg ctg cag ctc ttg	465
Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu	
50 55 60	
tta ttc aca tcg aac tcc ttt gat gtg atc agt gat gat gct ttt att	513
Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile	
65 70 75	
ggt ctt cca cat cta gag tat tta ttc ata gaa aac aac aac atc aag	561
Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys	
80 85 90	
tca att tca aga cat act ttc cgg gga cta aag tca tta att cac ttg	609
Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu	
95 100 105 110	
agc ctt gca aac aac aat ctc cag aca ctc cca aaa gat att ttc aaa	657
Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys	
115 120 125	
ggc ctg gat tct tta aca aat gtg gac ctg agg ggt aat tca ttt aat	705
Gly Leu Asp Ser Leu Thr Asn Val Asp Leu Arg Gly Asn Ser Phe Asn	
130 135 140	
tgt gac tgt aaa ctg aaa tgg cta gtg gaa tgg ctt ggc cac acc aat	753
Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn	
145 150 155	
gca act gtt gaa gac atc tac tgc gaa ggc ccc cca gaa tac aag aag	801
Ala Thr Val Glu Asp Ile Tyr Cys Glu Gly Pro Pro Glu Tyr Lys Lys	
160 165 170	
cgc aaa atc aat agt ctc tcc tcg aag gat ttc gat tgc atc att aca	849
Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr	
175 180 185 190	
gaa ttt gca aag tct caa gac ctg cct tat caa tca ttg tcc ata gac	897
Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp	
195 200 205	
act ttt tct tat ttg aat gat gag tat gta gtc atc gct cag cct ttt	945
Thr Phe Ser Tyr Leu Asn Asp Glu Tyr Val Val Ile Ala Gln Pro Phe	
210 215 220	
act gga aaa tgc att ttc ctt gaa tgg gac cat gtg gaa aag acc ttc	993
Thr Gly Lys Cys Ile Phe Leu Glu Trp Asp His Val Glu Lys Thr Phe	
225 230 235	
cgg aat tat gac aac att aca gtt tta agg gaa ata cac aga ttt aca	1041
Arg Asn Tyr Asp Asn Ile Thr Val Leu Arg Glu Ile His Arg Phe Thr	
240 245 250	
aac atg tca tagttgactt aagcgcgatga gacaccaa tctgtggctg	1090
Asn Met Ser	
255	
ccatcagaaa ttttctacag tacatgaccc ggatgaactc aatgcatgat gactcttctt	1150
atcacacttg caaatgaatg ccttttcaaac attgagactg ctagaaccaa gcactaccag	1210
tatctccatc cttaactgtc cagtccagtg atgtgggaag ttacctttta taagacaaaa	1270
tttaattgtg taactgttct ttgcagtga gatgtgtaaa taagcgttta atggtatctg	1330
ttactccaaa aagaaatatt aatatgtact tttccattta tttattcatg tgtacagaaa	1390
caactgccaa ataaaatggt tacatttttct ttcagaaaaa aaaaaaaaaa aa	1442

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 <222> 32..274

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<222> 32..178
<223> Von Heijne matrix
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      seq LMVELLKVFVVEA/AV

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                                   Met Glu Gly Ala Gly Ala Gly
                                   -45
tcc ggc ttc cgg aag gag ctg gtg agc agg ctg ctg cac ctg cac ttc      100
Ser Gly Phe Arg Lys Glu Leu Val Ser Arg Leu Leu His Leu His Phe
      -40                               -35                               -30
aag gat gac aag acc aaa gtg agc ggg gac gcg ctg cag ctc atg gtg      148
Lys Asp Asp Lys Thr Lys Val Ser Gly Asp Ala Leu Gln Leu Met Val
      -25                               -20                               -15
gag ttg ctg aag gtc ttc gtt gtg gaa gca gca gtc cgc ggc gtg cgg      196
Glu Leu Leu Lys Val Phe Val Val Glu Ala Ala Val Arg Gly Val Arg
      -10                               -5                               1                               5
cag gcc cag gca gaa gac gcg ctc cgt gtg gac gtg gac cag ctg gag      244
Gln Ala Gln Ala Glu Asp Ala Leu Arg Val Asp Val Asp Gln Leu Glu
      10                               15                               20
aag gtg ctt ccg cag ctg ctc ctg gac ttc tagggatctc agccgtggct      294
Lys Val Leu Pro Gln Leu Leu Leu Asp Phe
      25                               30
gagggcaccc ccagaggagc ccctgggtcca cagaagcagg ccttgtgttt ccagcggcct      354
ctgataagag gcaggggaagg acctgaagga tttggagttg attcaaaca gatctctggg      414
agtctccagc ctgtgcagaa ggggcaggac tgcagtgcac tgcgggcctt ggagtgtcca      474
gtggggacac tgggtgtggga aggggcagca cctggggagt cctgcctct cctccctggg      534
acaatagtgt gcatgccacc cggggtccta caggcaggtg ctgggaaagg cctggccagc      594
aggtagcctg tgtgtttgac aaacagcagc tggcagcgct gcctcctgcc cacattctg      654
ccaccgaca tcaaagctgg cgtgtgacct ttccagccat gcgatattcc ccttgaaga      714
tgcttcccca ggctataaat ttgttctcac aaagcaacat caataaatca aaactgtctc      774
tctcaaaaaa aaaaaaaaaa a      795

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<212> DNA
<213> Homo sapiens

<220>
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<222> 222..920

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<222> 222..311
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      seq VAHALSLPAESYG/ND

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ggaggggagag gcacaggtgg agccgccagt tgagaaggac tctgatccgg ctcagctttc      180
caatcagctg cggaaggagc cacgctttcg ggggttgcaa g atg gcg gcc acc agt      236
                                   Met Ala Ala Thr Ser

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                                -30
gga act gat gag ccg gtt tcc ggg gag ttg gtg tct gtg gca cat gcg      284
Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val Ser Val Ala His Ala
-25                                -20                                -15                                -10
ctt tct ctc cca gca gag tcg tat ggc aac gat cct gac att gag atg      332
Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Asp Pro Asp Ile Glu Met
                                -5                                1                                5
gct tgg gcc atg aga gca atg cag cat gct gaa gtc tat tac aag ctg      380
Ala Trp Ala Met Arg Ala Met Gln His Ala Glu Val Tyr Lys Leu
10                                15                                20
att tca tca gtt gac cca cag ttc ctc aaa ctc acc aaa gta gat gac      428
Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu Thr Lys Val Asp Asp
25                                30                                35
caa att tac tct gag ttc cgg aaa aat ttt gag acc ctt agg ata gat      476
Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu Thr Leu Arg Ile Asp
40                                45                                50                                55
gtg ttg gac cca gaa gaa ctc aag tca gaa tca gcc aaa gag aag tgg      524
Val Leu Asp Pro Glu Glu Leu Lys Ser Glu Ser Ala Lys Glu Lys Trp
60                                65                                70
agg cca ttc tgc ttg aag ttt aat ggg att gtt gaa gac ttc aac tat      572
Arg Pro Phe Cys Leu Lys Phe Asn Gly Ile Val Glu Asp Phe Asn Tyr
75                                80                                85
ggt act ttg ctg cga cta gat tgt tct cag ggc tac act gag gaa aac      620
Gly Thr Leu Leu Arg Leu Asp Cys Ser Gln Gly Tyr Thr Glu Glu Asn
90                                95                                100
acc atc ttt gcc ccc agg ata caa ttc ttt gcc att gaa att gct cgg      668
Thr Ile Phe Ala Pro Arg Ile Gln Phe Phe Ala Ile Glu Ile Ala Arg
105                                110                                115
aac cgg gaa ggc tat aac aaa gct gtt tat atc agt gtt cag gac aaa      716
Asn Arg Glu Gly Tyr Asn Lys Ala Val Tyr Ile Ser Val Gln Asp Lys
120                                125                                130                                135
gaa gga gag aaa gga gtc aac aat gga gga gaa aaa aga gct gac agt      764
Glu Gly Glu Lys Gly Val Asn Asn Gly Gly Glu Lys Arg Ala Asp Ser
140                                145                                150
gga gaa gaa gag aac acc aag aat gga gga gag aaa gga gct gat agt      812
Gly Glu Glu Glu Asn Thr Lys Asn Gly Gly Glu Lys Gly Ala Asp Ser
155                                160                                165
gga gaa gaa aaa gag gaa gga atc aac aga gaa gac aaa act gac aaa      860
Gly Glu Glu Lys Glu Glu Gly Ile Asn Arg Glu Asp Lys Thr Asp Lys
170                                175                                180
gga gga gaa aaa ggg aaa gaa gct gac aaa gaa atc aac aaa agt ggt      908
Gly Gly Glu Lys Gly Lys Glu Ala Asp Lys Glu Ile Asn Lys Ser Gly
185                                190                                195
gaa aaa gct atg taaggatatac agggaacagc actctagaag ctatgactca      960
Glu Lys Ala Met
200
attgagacta caagtaccac ggtgctactt gcacagaccc ctttggttaa atgtaaattc      1020
ttgtacaatt gaaggatacg cagaaggaca tctttctagt ctaacagtca ggagctgctc      1080
tggtcattcc cttgtatgaa ctggtctaaa gactgttagt ggggtgtag ttgatttttc      1140
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ttttggttct tattaaaaaca aaaaaaaaaa aaaaaa      1236

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<210> 66
 <211> 881
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 <213> Homo sapiens

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<221> CDS
<222> 101..355

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<222> 101..160
<223> Von Heijne matrix
score 9.32665652007071
seq LFLCYLLLFTCSG/VE

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cctccaaggt ctagtacgg agcccgcgcg cggcgccacc atg cgg cag aag gcg 115
Met Arg Gln Lys Ala
-20
gta tcg ctt ttc ttg tgc tac ctg ctg ctc ttc act tgc agt ggg gtg 163
Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly Val
-15 -10 -5 1
gag gca ggt aag aaa aag tgc tcg gag agc tcg gac agc ggc tcc ggg 211
Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser Gly
5 10 15
ttc tgg aag gcc ctg acc ttc atg gcc gtc gga gga gga ctc gca gtc 259
Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly Gly Gly Leu Ala Val
20 25 30
gcc ggg ctg ccc gcg ctg ggc ttc acc ggc gcc ggc atc gcg gcc aac 307
Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala Gly Ile Ala Ala Asn
35 40 45
tcg gtg gct gcc tcg ctg atg agc tgg tct gcg atc ctg aat ggg ggc 355
Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala Ile Leu Asn Gly Gly
50 55 60 65
tagtggccac gctgcagagc ctccggggctg gtggcagcag cgtcgtcata ggtaatatgt 415
gtgccctgat gggctacgcc acccacaagt atctcgatag tgaggaggat gaggagtagc 475
cagcagctcc cagaacctct tcttccttct tggcctaact cttccagtta ggatctagaa 535
ctttgccttt tttttttttt tttttttttt ttgagatggg ttctcactat attgtccagg 595
ctagagtga gkggctattc acagatgcga acatagtaca ctgcagcctc caactcctag 655
cctcaagtga tctcctgtc tcaacctccc aagtaggatt acaagcatgc gccgacgatg 715
cccaraatcc araactttgt ctatcactct ccccaacaac ctagatgtga aaacagaata 775
aacttcaccc agaaaaaaaa aaammacaar aaaaaaaaaa aaaaaaaaaa aaaaaaaaaam 835
aaaaaaaaaa rrraaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 881

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<222> 173..301
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seq AGSLVATLQSVGA/AG

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catttcctgg gccaaagtgg gacccggacg gcctcaccat gatgaaacgg gcagctgctg 120
ctgcagtggg aggagccctg gcagtggggg ctgtgccctg gtgctcagtg cc atg ggc 178
Met Gly
ttc act ggg gca gga atc gcc gcg tcc tcc ata gca gcc aag atg atg 226
Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met
-40 -35 -30
tcc gca gca gcc att gcc aac ggg ggt ggt gtt tct gcg ggg agc ctg 274
Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu
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gtg gct act ctg cag tcc gtg ggg gca gct gga ctc tcc aca tca tcc 322
Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser
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Asn Ile Leu Leu Ala Ser Val Gly Ser Val Leu Gly Ala Cys Leu Gly
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aat tca cct tct tct tct ctc cca gct gaa ccc gag gct aaa gaa gat 418
Asn Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp
25 30 35
gag gca aga gaa aat gta ccc caa ggt gaa cct cca aaa ccc cca ctc 466
Glu Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu
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Lys Ser Glu Lys His Glu Glu
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gactcctatg tgacctgttc ttagagcaag acaatcacca tctgaattcc agaagccctg 180
ttcatgggtg gggatatttt ctcgactgc atg gaa tca gaa aga agc aaa agg 233
Met Glu Ser Glu Arg Ser Lys Arg
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Met Gly Asn Ala Cys Ile Pro Leu Lys Arg Ile Ala Tyr Phe Leu Cys
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Leu Leu Ser Ala Leu Leu Leu Thr Glu Gly Lys Lys Pro Ala Lys Pro
-10 -5 1 5
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Lys Cys Pro Ala Val Cys Thr Cys Thr Lys Asp Asn Ala Leu Cys Glu
10 15 20

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Asn Ala Arg Ser Ile Pro Arg Thr Val Pro Pro Asp Val Ile Ser Leu	
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Ser Phe Val Arg Ser Val Phe Thr Glu Ile Ser Glu Gly Ser Phe Leu	
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Phe Thr Pro Ser Leu Gln Leu Leu Leu Phe Thr Ser Asn Ser Phe Asp	
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Val Ile Ser Asp Asp Ala Phe Ile Gly Leu Pro His Leu Glu Tyr Leu	
75 80 85	
ttc ata gaa aac aac aac atc aag tca att tca aga cat act ttc cgg	617
Phe Ile Glu Asn Asn Asn Ile Lys Ser Ile Ser Arg His Thr Phe Arg	
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gga cta aag tca tta att cac ttg agc ctt gca aac aac aat ctc cag	665
Gly Leu Lys Ser Leu Ile His Leu Ser Leu Ala Asn Asn Asn Leu Gln	
105 110 115	
aca ctc cca aaa gat att ttc aaa ggc ctg gat tct tta aca aat gtg	713
Thr Leu Pro Lys Asp Ile Phe Lys Gly Leu Asp Ser Leu Thr Asn Val	
120 125 130	
gac ctg agg ggt aat tca ttt aat tgt gac tgt aaa ctg aaa tgg cta	761
Asp Leu Arg Gly Asn Ser Phe Asn Cys Asp Cys Lys Leu Lys Trp Leu	
135 140 145 150	
gtg gaa tgg ctt ggc cac acc aat gca act gtt gaa gac atc tac tgc	809
Val Glu Trp Leu Gly His Thr Asn Ala Thr Val Glu Asp Ile Tyr Cys	
155 160 165	
gaa ggc ccc cca gaa tac aag aag cgc aaa atc aat agt ctc tcc tcg	857
Glu Gly Pro Pro Glu Tyr Lys Lys Arg Lys Ile Asn Ser Leu Ser Ser	
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Lys Asp Phe Asp Cys Ile Ile Thr Glu Phe Ala Lys Ser Gln Asp Leu	
185 190 195	
cct tat caa tca ttg tcc ata gac act ttt tct tat ttg aat gat gag	953
Pro Tyr Gln Ser Leu Ser Ile Asp Thr Phe Ser Tyr Leu Asn Asp Glu	
200 205 210	
tat gta gtc atc gct cag cct ttt act gga aaa tgc att ttc ctt gaa	1001
Tyr Val Val Ile Ala Gln Pro Phe Thr Gly Lys Cys Ile Phe Leu Glu	
215 220 225 230	
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Trp Asp His Val Glu Lys Thr Phe Arg Asn Tyr Asp Asn Ile Thr Val	
235 240 245	
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Leu Arg Glu Ile His Arg Phe Thr Asn Met Ser	
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aatgcatgat gactcttctt atcacacttg caaatgaatg cctttcaaac attgagactg	1222
ctagaaccaa gcactaccag tatctccatc cttaactgtc cagtccagtg atgtgggaag	1282
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taagcgttta atgggtatctg ttactccaaa aagaaatatt aatatgtact tttccattta	1402
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 gccgctggac tccgctgcct ccccatctc cccgccatct gcgcccggag g atg agc 177
 Met Ser
 cca gcc ttc agg gcc atg gat gtg gag ccc cgc gcc aaa ggc gtc ctt 225
 Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu
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 Phe Asn Glu Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln
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 ttc tac gag acc ctc cct gct gag atg cgc aaa ttc act ccc cag tac 369
 Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro Gln Tyr
 25 30 35
 aaa ggt gtg gta tct gtg cgc ttt gaa gaa gat gaa gac agg aac ttg 417
 Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg Asn Leu
 40 45 50
 tgt cta ata gca tat cca ttg aaa ggg gac cat gga att gtg gac att 465
 Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val Asp Ile
 55 60 65 70
 gta gat aat tca gac tgt gaa cca aaa agt aag ctc cta agg tgg aca 513
 Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg Trp Thr
 75 80 85
 aca aac aaa aaa cat cat gtc tta gaa aca gaa aag acc cct aag gac 561
 Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro Lys Asp
 90 95 100
 tgg gtg cgt cag cac cgt aaa gag gag aaa atg aag agc cat aag tta 609
 Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His Lys Leu
 105 110 115
 gaa gaa gaa ttt gag tgg cta aag aaa tct gaa gtc ttg tac tac act 657
 Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr Tyr Thr
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 Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr Asn Pro
 135 140 145 150
 tgg agc atg aaa tgt cac cag caa cag tta cag aga atg aag gag aat 753
 Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys Glu Asn
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 Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn Leu Thr
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 Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg
 185 190 195

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Gln	His	Gly	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Ala	Ala	Asn	Gln	Ile	Arg	
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Lys	Cys	Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val	Cys	Gly	
215			220			225			230							
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Met	Gln	Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met	Asn	Lys	
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tac	cat	gga	cgg	aag	cta	tcg	atg	cag	ggc	ttc	aag	gag	gca	ctt	ttc	1041
Tyr	His	Gly	Arg	Lys	Leu	Ser	Met	Gln	Gly	Phe	Lys	Glu	Ala	Leu	Phe	
250						255			260							
cag	ttc	ttc	cac	aat	ggg	cgg	tac	ctg	cgc	cgt	gaa	ctc	ctg	ggc	cct	1089
Gln	Phe	Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu	Gly	Pro	
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gtg	ctc	aag	aag	ctg	act	gag	ctc	aag	gca	gtg	ttg	gag	cga	cag	gag	1137
Val	Leu	Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg	Gln	Glu	
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tcc	tac	cgc	ttc	tac	tca	agc	tcc	ctg	ctg	gtc	att	tat	gat	ggc	aag	1185
Ser	Tyr	Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val	Ile	Tyr	Asp	Gly	Lys	
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gag	cgg	ccc	gaa	gtg	gtc	ctg	gac	tca	gat	gct	gag	gat	ttg	gag	gac	1233
Glu	Arg	Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu	Glu	Asp	
315			320			325										
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Leu	Ser	Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala	Tyr	Lys	
330			335			340										
ccc	atc	ggc	gcc	agc	tct	gta	gat	gtg	cgc	atg	atc	gac	ttt	gca	cac	1329
Pro	Ile	Gly	Ala	Ser	Ser	Val	Asp	Val	Arg	Met	Ile	Asp	Phe	Ala	His	
345			350			355										
acc	acc	tgc	agg	ctg	tat	ggc	gag	gac	acc	gtg	gtg	cat	gag	ggc	cag	1377
Thr	Thr	Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu	Gly	Gln	
360			365			370										
gat	gct	ggc	tat	atc	ttc	ggg	ctc	cag	agc	ctg	ata	gac	att	gtc	aca	1425
Asp	Ala	Gly	Tyr	Ile	Phe	Gly	Leu	Gln	Ser	Leu	Ile	Asp	Ile	Val	Thr	
375			380			385			390							
gag	ata	agt	gag	gag	agt	ggg	gag	tgagcttgct	agctgctcca	gtacttgaga						1479
Glu	Ile	Ser	Glu	Glu	Ser	Gly	Glu									
395																
gcgactctgt	gtccccaggca			cagctgtgct			gcgtcaggga			ggaagccagt			atggccaggt			1539
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gtcccagctg	tgcttttgagt			ctttatattat			tttaactatt			tcttcaacat			tccacatttg			1659
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Gly Val Leu Ala Gly Val Glu Ser Arg Gln Gly Ser Ile Lys Gly Leu
-5 1 5
gtg tac tcc agc aac ttc cag aac gtg aag cag ctg tac gcg ctg gtg 149
Val Tyr Ser Ser Asn Phe Gln Asn Val Lys Gln Leu Tyr Ala Leu Val
10 15 20
tgc gaa acg cag cgc tac tcc gcc gtg ctg gat gct gtg atc gcc agc 197
Cys Glu Thr Gln Arg Tyr Ser Ala Val Leu Asp Ala Val Ile Ala Ser
25 30 35 40
gcc ggc ctc ctc cgt gcg gag aag aag ctg cgg ccg cac ctg gcc aag 245
Ala Gly Leu Leu Arg Ala Glu Lys Lys Leu Arg Pro His Leu Ala Lys
45 50 55
gtg cta gtg tat gag ttg ttg ttg gga aag ggc ttt cga ggg ggt ggg 293
Val Leu Val Tyr Glu Leu Leu Leu Gly Lys Gly Phe Arg Gly Gly Gly
60 65 70
ggc cga tgg aag gct ctg ttg ggc cgg cac cag gcg agg ctc aag gct 341
Gly Arg Trp Lys Ala Leu Leu Gly Arg His Gln Ala Arg Leu Lys Ala
75 80 85
gag ttg gct cgg ctc aag gtt cat cgg ggt gtg agc cgg aat gag gac 389
Glu Leu Ala Arg Leu Lys Val His Arg Gly Val Ser Arg Asn Glu Asp
90 95 100
ctg ttg gaa gtg gga tcc agg cct ggt cca gcc tcc cag ctg cct cga 437
Leu Leu Glu Val Gly Ser Arg Pro Gly Pro Ala Ser Gln Leu Pro Arg
105 110 115 120
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Phe Val Arg Val Asn Thr Leu Lys Thr Cys Ser Asp Asp Val Val Asp
125 130 135
tat ttc aag aga caa ggt ttc tcc tat cag ggt cgg gct tcc agc ctc 533
Tyr Phe Lys Arg Gln Gly Phe Ser Tyr Gln Gly Arg Ala Ser Ser Leu
140 145 150
gat gac tta cga gcc ctc aag ggg aag cat ttt ctc ctg gac ccc ttg 581
Asp Asp Leu Arg Ala Leu Lys Gly Lys His Phe Leu Leu Asp Pro Leu
155 160 165
atg ccg gag ctg ctg gtg ttt ccc gcc cag aca gat ctg cat gaa cac 629
Met Pro Glu Leu Leu Val Phe Pro Ala Gln Thr Asp Leu His Glu His
170 175 180
cca ctg tac cgg gcc gga cac ctc att ctg cag gac agg gcc agc tgt 677
Pro Leu Tyr Arg Ala Gly His Leu Ile Leu Gln Asp Arg Ala Ser Cys
185 190 195 200
ctc cca gcc atg ctg ctg gac ccc ccg cca ggc tcc cat gtc atc gat 725
Leu Pro Ala Met Leu Leu Asp Pro Pro Pro Gly Ser His Val Ile Asp
205 210 215
gcc tgt gcc gcc cca ggc aat aag acc agt cac ttg gct gct ctt ctg 773
Ala Cys Ala Ala Pro Gly Asn Lys Thr Ser His Leu Ala Ala Leu Leu
220 225 230
aag aac caa ggg aag atc ttt gcc ttt gac ctg gat gcc aag cgg ctg 821
Lys Asn Gln Gly Lys Ile Phe Ala Phe Asp Leu Asp Ala Lys Arg Leu
235 240 245
gca tcc atg gcc acg ctg ctg gcc cgg gct ggc gtc tct tgc tgt gaa 869
Ala Ser Met Ala Thr Leu Leu Ala Arg Ala Gly Val Ser Cys Cys Glu
250 255 260

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His	Glu	Val	His	Tyr	Ile	Leu	Leu	Asp	Pro	Ser	Cys	Ser	Gly	Ser	Gly		
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Val	Arg	Leu	His	Ala	Leu	Ala	Gly	Phe	Gln	Gln	Arg	Ala	Leu	Cys	His		
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gcg	ctc	act	ttc	cct	tcc	ctg	cag	cgg	ctc	gtc	tac	tcc	acg	tgc	tcc	1109	
Ala	Leu	Thr	Phe	Pro	Ser	Leu	Gln	Arg	Leu	Val	Tyr	Ser	Thr	Cys	Ser		
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Leu	Cys	Gln	Glu	Glu	Asn	Glu	Asp	Val	Val	Arg	Asp	Ala	Leu	Gln	Gln		
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Asn	Pro	Gly	Ala	Phe	Arg	Leu	Ala	Pro	Ala	Leu	Pro	Ala	Trp	Pro	His		
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cga	ggc	ctg	agc	acg	ttc	ccg	ggt	gcc	gag	cac	tgc	ctc	cgg	gcc	tcc	1253	
Arg	Gly	Leu	Ser	Thr	Phe	Pro	Gly	Ala	Glu	His	Cys	Leu	Arg	Ala	Ser		
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Pro	Glu	Thr	Thr	Leu	Ser	Ser	Gly	Phe	Phe	Val	Ala	Val	Ile	Glu	Arg		
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Val	Glu	Val	Pro	Ser	Ser	Ala	Ser	Gln	Ala	Lys	Ala	Ser	Ala	Pro	Glu		
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cgc	aca	ccc	agc	cca	gcc	cca	aag	aga	aag	aag	aga	cag	caa	aga	gcc	1397	
Arg	Thr	Pro	Ser	Pro	Ala	Pro	Lys	Arg	Lys	Lys	Arg	Gln	Gln	Arg	Ala		
425					430					435					440		
gca	gcc	ggt	gct	tgc	aca	ccg	cct	tgc	aca	tagcagaggc tccgggctga						1447	
Ala	Ala	Gly	Ala	Cys	Thr	Pro	Pro	Cys	Thr								
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seq YAAAAGVLAVGES/RQ
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Gly	Val	Leu	Ala	Gly	Val	Glu	Ser	Arg	Gln	Gly	Ser	Ile	Lys	Gly	Leu	
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Val	Tyr	Ser	Ser	Asn	Phe	Gln	Asn	Val	Lys	Gln	Leu	Tyr	Ala	Leu	Val	
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Cys	Glu	Thr	Gln	Arg	Tyr	Ser	Ala	Val	Leu	Asp	Ala	Val	Ile	Ala	Ser	
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Val	Leu	Val	Tyr	Glu	Leu	Leu	Leu	Gly	Lys	Gly	Phe	Arg	Gly	Gly	Gly	
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ggc	cga	tgg	aag	gct	ctg	ttg	ggc	cgg	cac	cag	gcg	agg	ctc	aag	gct	341
Gly	Arg	Trp	Lys	Ala	Leu	Leu	Gly	Arg	His	Gln	Ala	Arg	Leu	Lys	Ala	
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gag	ttg	gct	cgg	ctc	aag	gtt	cat	cgg	ggg	gtg	agc	cgg	aat	gag	gac	389
Glu	Leu	Ala	Arg	Leu	Lys	Val	His	Arg	Gly	Val	Ser	Arg	Asn	Glu	Asp	
	90					95						100				
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Leu	Leu	Glu	Val	Gly	Ser	Arg	Pro	Gly	Pro	Ala	Ser	Gln	Leu	Pro	Arg	
105					110					115				120		
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Phe	Val	Arg	Val	Asn	Thr	Leu	Lys	Thr	Cys	Ser	Asp	Asp	Val	Val	Asp	
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Tyr	Phe	Lys	Arg	Gln	Gly	Phe	Ser	Tyr	Gln	Gly	Arg	Ala	Ser	Ser	Leu	
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Asp	Asp	Leu	Arg	Ala	Leu	Lys	Gly	Lys	His	Phe	Leu	Leu	Asp	Pro	Leu	
	155						160					165				
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Met	Pro	Glu	Leu	Leu	Val	Phe	Pro	Ala	Gln	Thr	Asp	Leu	His	Glu	His	
	170					175						180				
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Pro	Leu	Tyr	Arg	Ala	Gly	His	Leu	Ile	Leu	Gln	Asp	Arg	Ala	Ser	Cys	
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Leu	Pro	Ala	Met	Leu	Leu	Asp	Pro	Pro	Pro	Gly	Ser	His	Val	Ile	Asp	
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Ala	Cys	Ala	Ala	Pro	Gly	Asn	Lys	Thr	Ser	His	Leu	Ala	Ala	Leu	Leu	
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Lys	Asn	Gln	Gly	Lys	Ile	Phe	Ala	Phe	Asp	Leu	Asp	Ala	Lys	Arg	Leu	
	235						240					245				
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Ala	Ser	Met	Ala	Thr	Leu	Leu	Ala	Arg	Ala	Gly	Val	Ser	Cys	Cys	Glu	
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Leu	Ala	Glu	Glu	Asp	Phe	Leu	Ala	Val	Ser	Pro	Ser	Asp	Pro	Arg	Tyr	
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His	Glu	Val	His	Tyr	Ile	Leu	Leu	Asp	Pro	Ser	Cys	Ser	Gly	Ser	Gly			
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Met	Pro	Ser	Arg	Gln	Leu	Glu	Glu	Pro	Gly	Ala	Gly	Thr	Pro	Ser	Pro			
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Arg	Ser	Leu	Ser	Leu	Pro	Cys	Ser	Gly	Ser	Ser	Thr	Pro	Arg	Ala	Pro			
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Ser	Ala	Arg	Arg	Arg	Met	Lys	Thr	Trp	Cys	Glu	Met	Arg	Cys	Ser	Arg			
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Thr	Arg	Ala	Pro	Ser	Gly													
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Phe	Thr	Gln	Ala	Ala	Arg	Thr	Ser	Leu	Leu	Leu	Leu	Arg	Leu	Asn	Asp			
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Val	Ile	Ala	Phe	Gln	Gly	His	Arg	Gly	Tyr	Leu	Arg	Leu	Pro	Gly	Pro			
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ggg	tgg	tcc	tgc	ctc	ttc	tcc	ttc	ata	gtg	tcc	cag	tgt	tgt	cag	gag	302		
Gly	Trp	Ser	Cys	Leu	Phe	Ser	Phe	Ile	Val	Ser	Gln	Cys	Cys	Gln	Glu			

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Gly Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser	
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Gly Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile	
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Ile Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly	
80 85 90	
cac aac ctg act gaa gat gcc aga cat cct gag agt tgg cag aac aca	494
His Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr	
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Gly Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu	
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Glu Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser	
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Leu Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser	
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cag acc cat gtt cca aac aga gaa cct gtt cag gca ctg cct tcc tct	686
Gln Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser	
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Ala Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr	
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gta gaa ctg gaa gaa aag agg ttc aga act ctg cct tta gtg ccc ccc	782
Val Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Pro	
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Pro Thr Arg Pro Asp Gln Ser Gly Phe Thr Arg Gly Arg Arg Leu Gly	
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Ala Arg Arg	
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 Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu
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 ccc gcg gcg tgg gtc ctg ctt ctg ttg cct ttc ctg ccg ctg ctg ctg 156
 Pro Ala Ala Trp Val Leu Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu
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 Leu Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val
 1 5 10
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 Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu
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 Tyr Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu
 35 40 45
 ttc gat ggg aga gag agc ttg cga ccc ctg tgg gaa cag gtg caa ggg 348
 Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly
 50 55 60
 ttc cga gag gct gtg gtc ccc atc atg gca aag gcc cct caa ggg gtg 396
 Phe Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val
 65 70 75
 cat ctc atc tgc tac tcg cag ggg ggc ctt gtg tgc cgg gct ctg ctt 444
 His Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu
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 Ser Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser
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 Pro Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe
 115 120 125
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 Pro Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro Leu
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 Ile Asn Gly Glu Arg Asp His Pro Asn Ala Thr Val Trp Arg Lys Asn
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 Phe Leu Arg Val Gly His Leu Val Leu Ile Gly Gly Pro Asp Asp Gly
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 Val Ile Thr Pro Trp Gln Ser Ser Phe Phe Gly Phe Tyr Asp Ala Asn
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 Glu Thr Val Leu Glu Met Glu Glu Gln Leu Val Tyr Leu Arg Asp Ser
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Met Ala Gly Ile Ser His Thr Ala Trp His Ser Asn Arg Thr Leu Tyr
      225                      230                      235
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Glu Thr Cys Ile Glu Pro Trp Leu Ser
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Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu
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ccc gcg gcg tgg gtc ctg ctt ctg ttg cct ttc ctg ccg ctg ctg ctg      156
Pro Ala Ala Trp Val Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu
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Leu Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val
      1                      5                      10
gtg cat ggg ctc ttc gac agc tcg tac agc ttc cgc cac ctg ctg gaa      252
Val His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu
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tac atc aat gag aca cac ccc ggg act gtg gtg aca gtg ctc gat ctc      300
Tyr Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu
      35                      40                      45
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Phe Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly

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His Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu			
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Ser Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser			
95	100	105	110
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Pro Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe			
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Pro Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro			
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Met Ala Phe Thr Phe Ala Ala		

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Phe	Cys	Tyr	Met	Leu	Ser	Leu	Val	Leu	Cys	Ala	Ala	Leu	Ile	Phe	Phe			
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Ser	Pro	Ile	Asp	Gln	Cys	Asn	Pro	Val	His	Ala	Arg	Glu	Arg	Leu	Arg			
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Asn	Ile	Glu	Arg	Ile	Cys	Phe	Leu	Leu	Arg	Lys	Leu	Val	Leu	Pro	Glu			
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Pro	Val	Val	Met	Asn	Pro	Asp	Thr	Leu	Ser	Tyr	Cys	Gln	Lys	Glu	Ala			
		105					110					115						
tgg	tgt	aag	ctg	gcc	ttc	tat	ctc	ctc	tcc	ttc	ttc	tac	tac	ctt	tac	726		
Trp	Cys	Lys	Leu	Ala	Phe	Tyr	Leu	Leu	Ser	Phe	Phe	Tyr	Tyr	Leu	Tyr			
	120				125						130							
tgc	atg	atc	tac	act	tta	gtg	agc	tct	taacgcaaag accatgcaca							773		
Cys	Met	Ile	Tyr	Thr	Leu	Val	Ser	Ser										
135					140													
tcatcagaga			ctgagatggg			agaggcctga			gacggagagg			tgcattttctg			ctggtgactg		833	
gaggagggac			cagaatgagg			atacgtgaga			aatagacccg			gcaggcagtc			agactgaatg		893	
ggagctggaa			tcacgcagca			gttggggagcc			gagttaaccc			tgcgtgtctg			tgtcacccctg		953	
tttgtcaatc			tttggcattc			gaattccaca			cacgggggtcc			tagagccctt			ctgagcatca		1013	
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<210> 76
<211> 1757
<212> DNA
<213> Homo sapiens
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<221> CDS
<222> 191..1468

<220>
<221> sig_peptide
<222> 191..274
<223> Von Heijne matrix
score 4.02941490119842
seq GXLLEPFVHQVGG/HS

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acagacagaa gacgtactgg ccgctggact ccgctgcctc ccccatctcc ccgccatctg 180
cgcccgagg atg agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc 229
Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg
-25 -20
gcc aaa ggc gtc ctt ctg gag ccc ttt gtc cac cag gtc ggg ggg cac 277
Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His
-15 -10 -5 1
tca tgc gtg ctc cgc ttc aat gag aca acc ctg tgc aag ccc ctg gtc 325
Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val
5 10 15
cca agg gaa cat cag ttc tac gag acc ctc cct tct gag atg cgc aaa 373
Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys
20 25 30
ttc act ccc cag tac aaa ggt gtg gta tct gtg cgc ttt gaa gaa gat 421
Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp
35 40 45
gaa gac agg aac ttg tgt cta ata gca tat cca ttg aaa ggg gac cat 469
Glu Asp Arg Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His
50 55 60 65
gga att gtg gac att gta gat aat tca gac tgt gaa cca aaa agt aag 517
Gly Ile Val Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys
70 75 80
ctc cta agg tgg aca aca aac aaa aaa cat cat gtc tta gaa aca gaa 565
Leu Leu Arg Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu
85 90 95
aag acc cct aag gac tgg gtg cgt cag cac cgt aaa gag gag aaa atg 613
Lys Thr Pro Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met
100 105 110
aag agc cat aag tta gaa gaa gaa ttt gag tgg cta aag aaa tct gaa 661
Lys Ser His Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu
115 120 125
gtc ttg tac tac act gta gag aag aag ggg aat ata agt tcc cag ctt 709
Val Leu Tyr Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu
130 135 140 145
aaa cac tat aac cct tgg agc atg aaa tgt cac cag caa cag tta cag 757
Lys His Tyr Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln
150 155 160
aga atg aag gag aat gca aag cat cgg aac cag tac aaa ttt atc tta 805
Arg Met Lys Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu
165 170 175
ctg gaa aac ctg act tcc cgc tat gag gtg cct tgt gtc ctt gac ctc 853
Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu
180 185 190
aag atg ggc aca cga caa cat ggt gat gat gct tca gag gag aag gca 901
Lys Met Gly Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala

195					200					205										
gcc	aac	cag	atc	cga	aaa	tgt	cag	cag	agc	aca	tct	gca	gtc	att	ggc		949			
Ala	Asn	Gln	Ile	Arg	Lys	Cys	Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly					
210					215					220					225					
gtg	cgt	gtg	tgt	ggc	atg	cag	gtg	tac	caa	gca	ggc	agt	ggg	cag	ctc		997			
Val	Arg	Val	Cys	Gly	Met	Gln	Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu					
230					235					240										
atg	ttc	atg	aac	aag	tac	cat	gga	cgg	aag	cta	tcg	gtg	cag	ggc	ttc		1045			
Met	Phe	Met	Asn	Lys	Tyr	His	Gly	Arg	Lys	Leu	Ser	Val	Gln	Gly	Phe					
245					250					255										
aag	gag	gca	ctt	ttc	cag	ttc	ttc	cac	aat	ggg	cgg	tac	ctg	cgc	cgt		1093			
Lys	Glu	Ala	Leu	Phe	Gln	Phe	Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg					
260					265					270										
gaa	ctc	ctg	ggc	cct	gtg	ctc	aag	ctg	act	gag	ctc	aag	gca	gtg		1141				
Glu	Leu	Leu	Gly	Pro	Val	Leu	Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val					
275					280					285										
ttg	gag	cga	cag	gag	tcc	tac	cgc	ttc	tac	tca	agc	tcc	ctg	ctg	gtc		1189			
Leu	Glu	Arg	Gln	Glu	Ser	Tyr	Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val					
290					295					300					305					
att	tat	gat	ggc	aag	gag	cgg	ccc	gaa	gtg	gtc	ctg	gac	tca	gat	gct		1237			
Ile	Tyr	Asp	Gly	Lys	Glu	Arg	Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala					
310					315					320										
gag	gat	ttg	gag	gac	ctg	tca	gag	gaa	tca	gct	gat	gag	tct	gct	ggc		1285			
Glu	Asp	Leu	Glu	Asp	Leu	Ser	Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly					
325					330					335										
gcc	tat	gcc	tac	aaa	ccc	atc	ggc	gcc	agc	tct	gta	gat	gtg	cgc	atg		1333			
Ala	Tyr	Ala	Tyr	Lys	Pro	Ile	Gly	Ala	Ser	Ser	Val	Asp	Val	Arg	Met					
340					345					350										
atc	gac	ttt	gca	cac	acc	acc	tgc	agg	ctg	tat	ggc	gag	gac	acc	gtg		1381			
Ile	Asp	Phe	Ala	His	Thr	Thr	Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val					
355					360					365										
gtg	cat	gag	ggc	cag	gat	gct	ggc	tat	atc	ttc	ggg	ctc	cag	agc	ctg		1429			
Val	His	Glu	Gly	Gln	Asp	Ala	Gly	Tyr	Ile	Phe	Gly	Leu	Gln	Ser	Leu					
370					375					380					385					
ata	gac	att	gtc	aca	gag	ata	agt	gag	gag	agt	ggg	gag	tgag	cttgct		1478				
Ile	Asp	Ile	Val	Thr	Glu	Ile	Ser	Glu	Glu	Ser	Gly	Glu								
390					395															
agctgctcca		gtacttgaga		gcgactctgt		gtcccaggca		cagctgtgct		gcgtcagggg							1538			
ggaagccagt		atggccaggt		ggtggctcct		gcagccttga		gctgatgtgc		agtggcctct							1598			
gtgagcccca		gcctgagcca		gtcccagctg		tgctttggagt		ctttattttat		tttaactatt							1658			
ctttcaacat		tccacatttg		atgatgatac		ctctttcttc		cctgagtgtg		tatgtttctaa							1718			
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<210> 77
<211> 2027
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> 48..950
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<220>
<221> sig_peptide
<222> 48..107
<223> Von Heijne matrix
score 6.64507667657896
seq LLPLLSLLVGAWL/KL
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<400> 77
atgcgcagcgc gggccgtggg tgtacgcggc gcagcgcggc agtcctg atg gcc cgg 56
Met Ala Arg
-20
cat ggg tta ccg ctg ctg ccc ctg ctg tcg ctc ctg gtc ggc gcg tgg 104
His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val Gly Ala Trp
-15 -10 -5
ctc aag cta gga aat gga cag gct act agc atg gtc caa ctg cag ggt 152
Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln Leu Gln Gly
1 5 10 15
ggg aga ttc ctg atg gga aca aat tct cca gac agc aga gat ggt gaa 200
Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg Asp Gly Glu
20 25 30
ggg cct gtg cgg gag gcg aca gtg aaa ccc ttt gcc atc gac ata ttt 248
Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile Asp Ile Phe
35 40 45
cct gtc acc aac aaa gat ttc agg gat ttt gtc agg gag aaa aag tat 296
Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu Lys Lys Tyr
50 55 60
cgg aca gaa gct gag atg ttt gga ttg agc ttt gtc ttt gag gac ttt 344
Arg Thr Glu Ala Glu Met Phe Gly Leu Ser Phe Val Phe Glu Asp Phe
65 70 75
gtc tct gat gag ctg aga aac aaa gcc acc cag cca atg aag tct gta 392
Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met Lys Ser Val
80 85 90 95
ctc tgg tgg ctt cca gtg gaa aag gca ttt tgg agg cag cct gca ggt 440
Leu Trp Trp Leu Pro Val Glu Lys Ala Phe Trp Arg Gln Pro Ala Gly
100 105 110
cct ggc tct ggc atc cga gag aga ctg gag cac cca gtg tta cac gtg 488
Pro Gly Ser Gly Ile Arg Glu Arg Leu Glu His Pro Val Leu His Val
115 120 125
agc tgg aat gac gcc cgt gcc tac tgt gct tgg cgg gga aaa cga ctg 536
Ser Trp Asn Asp Ala Arg Ala Tyr Cys Ala Trp Arg Gly Lys Arg Leu
130 135 140
ccc acg gag gaa gag tgg gag ttt gcc gcc cga ggg ggc ttg aag ggt 584
Pro Thr Glu Glu Glu Trp Glu Phe Ala Ala Arg Gly Gly Leu Lys Gly
145 150 155
caa gtt tac cca tgg ggg aac tgg ttc cag cca aac cgc acc aac ctg 632
Gln Val Tyr Pro Trp Gly Asn Trp Phe Gln Pro Asn Arg Thr Asn Leu
160 165 170 175
tgg cag gga aag ttc ccc aag gga gac aaa gct gag gat ggc ttc cat 680
Trp Gln Gly Lys Phe Pro Lys Gly Asp Lys Ala Glu Asp Gly Phe His
180 185 190
gga gtc tcc cca gtg aat gct ttc ccc gcc cag aac aac tac ggg ctc 728
Gly Val Ser Pro Val Asn Ala Phe Pro Ala Gln Asn Asn Tyr Gly Leu
195 200 205
tat gac ctc ctg ggg aac gtg tgg gag tgg aca gca tca ccg tac cag 776
Tyr Asp Leu Leu Gly Asn Val Trp Glu Trp Thr Ala Ser Pro Tyr Gln
210 215 220
gct gct gag cag gac atg cgc gtc ctc cgg ggg gca tcc tgg atc gac 824
Ala Ala Glu Gln Asp Met Arg Val Leu Arg Gly Ala Ser Trp Ile Asp
225 230 235
aca gct gat ggc tct gcc aat cac cgg gcc cgg gtc acc acc agg atg 872
Thr Ala Asp Gly Ser Ala Asn His Arg Ala Arg Val Thr Thr Arg Met
240 245 250 255
ggc aac act cca gat tca gcc tca gac aac ctc ggt ttc cgc tgt gct 920
Gly Asn Thr Pro Asp Ser Ala Ser Asp Asn Leu Gly Phe Arg Cys Ala

	260	265	270	
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Ala Asp Ala Gly Arg Pro Pro Gly Glu Leu				
	275	280		
aggagaaaaag cctttctaggg tcaactgtcat tccctggcca tgttgcaaac agcgcaattc				1030
caagctcgag agcttcagcc tcaggaaaga acttcccctt ccctgtctcc catccctctg				1090
tggcaggcgc ctctcaccag ggcaggagag gactcagcct cctgtgtttt ggagaagggg				1150
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aaccagatga tgtactaggt gaagcattgc attgtgggaa tcacaaagca aatagtactc				1570
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cccagggtgg tctcgaaact ctggcctcaa gcgacccctc cacctcgacc tcccaaagtg				1870
ctgggattac aggtgtgagc cacctcgctt gggccccctt ctccatatgc ctccaaaaac				1930
atgtccctgg agagtagcct gctcccacac tgtcactgga tgtcatgggg ccaataaaat				1990
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<210> 78

<211> 1880

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 156..512

<220>

<221> sig_peptide

<222> 156..206

<223> Von Heijne matrix

score 3.55618791452243

seq WLTAVASLLPSPG/NS

<400> 78

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agcgctgcga cggcgctcgg gacctccctc gtccactgct tgagttccag aggtgggtgc	120
ttccctgtcc tgaacttcag agtgcgagat cataa atg ggt tcc ggc tgg ctt	173
Met Gly Ser Gly Trp Leu	

-15

act gca gta gcc tcg ctc ctc ccc agc ccc ggt aac tcc gag cta ccc	221
Thr Ala Val Ala Ser Leu Leu Pro Ser Pro Gly Asn Ser Glu Leu Pro	
-10 -5 1 5	

gtc cag gcc ctc ggg cgt cgc ggg ggc agg gac tgg gcg cgg aac gag	269
Val Gln Ala Leu Gly Arg Arg Gly Gly Arg Asp Trp Ala Arg Asn Glu	
10 15 20	

gca ggg agg gac ctg gaa aaa cca ccc aga ttg cat tgc agt ggg cga	317
Ala Gly Arg Asp Leu Glu Lys Pro Pro Arg Leu His Cys Ser Gly Arg	
25 30 35	

ggc cgc ctg gag gag ccg gtt ccc cct aac cac ctc ccc gtg ggg ctc	365
Gly Arg Leu Glu Glu Pro Val Pro Pro Asn His Leu Pro Val Gly Leu	
40 45 50	

tcg gtg cgc ggt tcc cag gtg ctc agc tct gct ggg ccc agg agg tgc	413
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Ser Val Arg Gly Ser Gln Val Leu Ser Ser Ala Gly Pro Arg Arg Cys
55                                60                                65
cgc ctc aca ggg acg cgg aac ccc gtg cgt ggc ccc cgc cgg gtg gaa      461
Arg Leu Thr Gly Thr Arg Asn Pro Val Arg Gly Pro Arg Arg Val Glu
70                                75                                80                                85
cag ata gcg cgg ggc ggt ccg gag gct cgt cgc caa gca ggt gac tct      509
Gln Ile Ala Arg Gly Gly Pro Glu Ala Arg Arg Gln Ala Gly Asp Ser
90                                95                                100
tgc tgaaaaagtg gttggaacac ttaaggaaac cgggccccgc ctgttctttc      562
Cys
taggtcctttg gagtttggat taatcatttg tgtagcccgt ttggataaac cgaagacttt      622
attaaatcag cgcgtttaac aggaattccg cagtagtata cacattagaa tcttgagtct      682
tggagttgaa catattcaca cagacttgcc ttcttcctgt ttagtttatg ccttggtgtc      742
cgttattgga acgctaagct tgtgggagtt gtttacatcc tactgctcaa ggtcatcgct      802
aaggtgtgat ttttcacaaa aagaatttgc aacctccggc atgaatgact taagggaagt      862
ctaatacccg tttctgattt tttttttttt ttaatttaaa agttaatctt tctgggccgg      922
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gaatcgcttg aacctgggag gcgggggggt gcagtgagcc gagatctggc cattgcactc      1162
cagcgtgggc aacagagtga gactccatct caaaaaaaaaa ggtaaatctt tccaactaga      1222
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aggggtgaga ttgtcaaaat gggagtctac aggttaattta agacttaaat gtttaaagag      1462
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accaccatct ataaatctaa ttcactaagg ataatctgtg taaggtggct ggaaagaacc      1642
ttgaggagag aggcttattt aagtattggc tcaggaccac acctaaaatt ctcaaaacgt      1702
tgagattctg ttgttttgtt ttttaagcgc agagaccaa gttgaggaac agcctataaa      1762
ataactggcc tgtactctta catacatgaa agccatcaaa gacaaagact gaagaagaac      1822
ttttgcagat taaaggactt taagagacat gatcctgaac caaaaaaaaaa aaaaaaaaaa      1880

<210> 79
<211> 584
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 67..351

<220>
<221> sig_peptide
<222> 67..183
<223> Von Heijne matrix
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      seq FLCALCSFCPISA/AS

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ctgattcttc gaaatgatata aagtcctgag ggcttcagtc ccattcgcgc actcatactt      60
gcaatc atg gac tac agc cgt gtc ttt cag ggt gtg ttc ttc acc ttc      108
      Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe
      -35                                -30
aag cat gct ttt gct gat ggt gct tgg gat ctt tca ttt ctc tgt gct      156
Lys His Ala Phe Ala Asp Gly Ala Trp Asp Leu Ser Phe Leu Cys Ala
-25                                -20                                -15                                -10
ctt tgc agt ttc tgc cca atc tca gct gcc tct ggc aga cct tac agg      204

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Leu Cys Ser Phe Cys Pro Ile Ser Ala Ala Ser Gly Arg Pro Tyr Arg
      -5      1      5
tac ttg gaa ttc tgg aga tta tac ctg tct cct agt tcc atg gaa aat      252
Tyr Leu Glu Phe Trp Arg Leu Tyr Leu Ser Pro Ser Ser Met Glu Asn
      10      15      20
gga gtt caa aaa ttc cac gaa act ttt ttc att gtc ttt ttg ctt ttg      300
Gly Val Gln Lys Phe His Glu Thr Phe Phe Ile Val Phe Leu Leu Leu
      25      30      35
ttt gat atc gag agg aaa gga aaa agt tct gtt tgt cca ttt tgt tac      348
Phe Asp Ile Glu Arg Lys Gly Lys Ser Ser Val Cys Pro Phe Cys Tyr
      40      45      50      55
aga taaggaaaagt gggtttcaciaa aggttaagca acttggttcag tgttaccag      401
Arg
caaagagcag aatgattttc aacattcagt ttaaaagtcg gcgggggggca gtgggtcaca      461
cctgtaatat cagcaacttg ggaggccaag gtggtacggc cgcttgaagc caaggagttc      521
aagaccagcc tggtaacat agcaaaacct tgtctttaca aaaagtaaaa aaaaaaaaaa      581
aaa
<210> 80
<211> 1351
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 259..831

<220>
<221> sig_peptide
<222> 259..375
<223> Von Heijne matrix
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      seq FCVCVIAIGVVQA/LI

<400> 80
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gccagcagct tcgacagaag tgtacagagg cttctggcaa cacggattgc cgtctacctg      120
atgacctttc tcatcgtgac agtggcctgg gcagcacaca caaggttggt ccaagttggt      180
gggaaaacag acgacacact tgcctgctc aacctggccg catcatggct gtgatgcct      240
ccctccctcc aggctgc atg atg acc atc acc ttc ctg cct tac acg ttt      291
      Met Met Thr Ile Thr Phe Leu Pro Tyr Thr Phe
      -35      -30
tcg tta atg gtg acc ttc cct gat gtg cct ctg ggc atc ttc ttg ttc      339
Ser Leu Met Val Thr Phe Pro Asp Val Pro Leu Gly Ile Phe Leu Phe
      -25      -20      -15
tgt gtg tgt gtg atc gcc atc ggg gtc gtg cag gca ctg att gtg ggg      387
Cys Val Cys Val Ile Ala Ile Gly Val Val Gln Ala Leu Ile Val Gly
      -10      -5      1
tac gca ttc cac ttc ccg cac ctg ctg agc ccg cag atc cag cgc tct      435
Tyr Ala Phe His Phe Pro His Leu Leu Ser Pro Gln Ile Gln Arg Ser
      5      10      15      20
gcc cac agg gct ctg tac cga cga cac gtc ctg ggc atc gtc ctc caa      483
Ala His Arg Ala Leu Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln
      25      30      35
ggc ccg gcc ctg tgc ttt gca gcg gcc atc ttc tct ctc ttc ttt gtc      531
Gly Pro Ala Leu Cys Phe Ala Ala Ala Ile Phe Ser Leu Phe Phe Val
      40      45      50
ccc ttg tct tac ctg ctg atg gtg act gtc atc ctc ctc ccc tat gtc      579

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Pro Leu Ser Tyr Leu Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val
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Ser Lys Val Thr Gly Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu
70 75 80
ccc tgc gct cac cca gtg gaa gtc ttc tgc ttt gac ctc cac gag cca 675
Pro Ser Ala His Pro Val Glu Val Phe Ser Phe Asp Leu His Glu Pro
85 90 95 100
ctc agc aag gag cgc gtg gaa gcc ttc agc gac gga gtc tac gcc atc 723
Leu Ser Lys Glu Arg Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile
105 110 115
gtg gcc acg ctt ctc atc ctg gac atc tgc ccc tcc tgc tcc ctt tgg 771
Val Ala Thr Leu Leu Ile Leu Asp Ile Cys Pro Ser Cys Ser Leu Trp
120 125 130
ctg gct gtt gct tcc ttc cag cgt ctg ctc ctc cgc ggc ctc atc tgc 819
Leu Ala Val Ala Ser Phe Gln Arg Leu Leu Leu Arg Gly Leu Ile Cys
135 140 145
ctc ttc gtc tgt tagagcgcgc gtctcgtctc agtcgtcacg tttttgggtt 871
Leu Phe Val Cys
150
ttgtgggggtt tttttttttt tttttttttg agacagtcct gctgtgtcgc ccaggctgga 931
gtatagtggc tcaagctcag ctactgcaa cctccgcctc ccagggttcaa gcaattctcc 991
tgccctcagc tccaagtag ttgggattac aagcaccac caccatgccc agctaacttt 1051
ttgcattttt aatagagatg aggtttcacc aagttggcca ggctggtctt gaactcctga 1111
cctcaggtga tctgcccacc tgcgcctccc aaagtgtctg gattacaggt gtaagccacc 1171
gtgcccggcc atcgtaatgt ttgaatttgc ttttttacat cttccatcct tttggagtgt 1231
cttgttccct cgtcatagtt cagcactgtg accaccttgg ggtagacac tatgggttta 1291
tatcctgtac ttgatattct cgagtccaag tctcctgatg ctctcaaaaa aaaaaaaaaa 1351

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<223> Von Heijne matrix
score 5.26415334394122
seq LWFLAQIPSRVAG/SL

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tgcggctgag cgggcctccc atccctctta aaagagttag gcatttagcc atg cct 116
Met Pro
-40
ccc acc cgg gac cct ttc cag cag cct aca tta gat aac gat gat tcc 164
Pro Thr Arg Asp Pro Phe Gln Gln Pro Thr Leu Asp Asn Asp Asp Ser
-35 -30 -25
tac tta gga gaa ctg cgg gct tcc aag gta ctg tgg ttt ctt gcg cag 212
Tyr Leu Gly Glu Leu Arg Ala Ser Lys Val Leu Trp Phe Leu Ala Gln
-20 -15 -10
att ccc agt agg gtc gcc ggt agt ctt ctt tct gtc tgt gtg atg agc 260
Ile Pro Ser Arg Val Ala Gly Ser Leu Leu Ser Val Cys Val Met Ser

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agg gaa gtc tgt ttt ctg cct gcc tcc cta tct cca tat tca agt cgg 356
Arg Glu Val Cys Phe Leu Pro Ala Ser Leu Ser Pro Tyr Ser Ser Arg
30      35      40
cta acg ttt cag agg cgt ttt tgagcagagg aaagtagagt tctagtctag 407
Leu Thr Phe Gln Arg Arg Phe
45
aggaacaagg ggctctggca gctcaaatca attaaccaag atccaattcc ctggagaatt 467
ttaaacccct cccactccac ccatcacttg cctggctaac atcagacact ggatcaaccc 527
taaaaaggag tccatccaca gcatccaagg atccatagtg tcccctcaca ctgcagccac 587
caatggaggg tactcccgaa agaaagatgg tggcttcttc tccacctagt gttgacagat 647
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ccatatccac tcttaggata caacaagagc aagcccaatt ctcttggtgg tgtgggcagt 180
cggcttgac cagctaccta tctcagctct ttttgaagc tt atg tcc tcc cca 234
Met Ser Ser Pro
-35
caa ctt cca gct ttc tta tgg gac aag ggt aca ctc acc act gcc ata 282
Gln Leu Pro Ala Phe Leu Trp Asp Lys Gly Thr Leu Thr Thr Ala Ile
-30 -25 -20
tct aat cct gct tgc ctg gta aat gtt ctc ttc ttc ttt aca ccc ctg 330
Ser Asn Pro Ala Cys Leu Val Asn Val Leu Phe Phe Phe Thr Pro Leu
-15 -10 -5
atg act ctg gtc act cta ctc atc ctg gtc tgg aaa gta acc aaa gac 378
Met Thr Leu Val Thr Leu Leu Ile Leu Val Trp Lys Val Thr Lys Asp
1 5 10
aaa agc aac aag aac aga gag aca cac cca aga aag gag gca aca tgg 426
Lys Ser Asn Lys Asn Arg Glu Thr His Pro Arg Lys Glu Ala Thr Trp
15 20 25 30
ctg cca taaagatctg gatctcttgg tggggactcc actgaggtga agacctgatt 482
Leu Pro
gtacaagaga ggcacggcca ctggagctgt ctcagagccc agagccaggg gagccagagc 542
tgcttttagcc accctgttcc tccattgcca gatgtccccc caggcctcat ttccttctc 602
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aattattggg	agctcacagc	atctcaagtt	atataatgaa	gctattctgg	aagctcattt	902
ccagaagatc	cttaaaaatga	aatggctcac	tctctgctga	attaatttgg	agcaagttaa	962
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gagccatgtc	gcttgccctt	tacgttgctg	tacccttttt	cttttttgtc	atctctcgtg	540
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tggcttccat	ctcgttcact	catgtagcct	tcgctttgca	aggtggag	atg agg ggt	777

Met Arg Gly

-25

ccc act gct ggt cct tca gtt ctt tct gct gca cac ttg ctg gtc gta	825
Pro Thr Ala Gly Pro Ser Val Leu Ser Ala Ala His Leu Leu Val Val	
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ata ctg cct gca aac gcc gca ctc aag ctg ctg tct tgg gag aga ctg	873
Ile Leu Pro Ala Asn Ala Ala Leu Lys Leu Leu Ser Trp Glu Arg Leu	
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gcg gcc ccc gcc atc gag gtg gaa gta cct tcc aag gag gtg ctt gca	921
Ala Ala Pro Ala Ile Glu Val Glu Val Pro Ser Lys Glu Val Leu Ala	
15 20 25	
gca ccc acc aag gcc aag cta ata ccc tct gag gat atg ttg gca gca	969
Ala Pro Thr Lys Ala Lys Leu Ile Pro Ser Glu Asp Met Leu Ala Ala	
30 35 40	
cct gcc atg gac ttg ctg gat tca ttt tct cct gga ttt ttg ata gct	1017
Pro Ala Met Asp Leu Leu Asp Ser Phe Ser Pro Gly Phe Leu Ile Ala	
45 50 55	
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Ala Pro Ala Ser Ala Val Ile Thr Trp Pro Gly Pro Ala Asp Leu Val	
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Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala Ala Pro Ala
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Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala Thr Ala Met
      95      100      105
cca cct gct gtc ctt gct gct cct cct tca gca gcc cct gga gtg ctc      1209
Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro Gly Val Leu
      110      115      120
gtg gat gga gaa gcc gca cta gcc gtt ccg tgg gag gca tgt tgg att      1257
Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala Cys Trp Ile
      125      130      135
ccc tct ccc cca gca taagcagaag aggtggctgc agatacatca caaggcttgt      1312
Pro Ser Pro Pro Ala
      140
agagcccagt ctcaactctga tcccccttctc tgtggagctc tgcagcctat accaagggga      1372
agagaaacag atgagattga gatgactgaa agggagatca gaactttcta ctccctctctt      1432
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caagaccagc cttgccaca tagcaaaacc ccgactctac taaaaatata aaaaattagc      1612
tggacaggat ggcgcagcc tgtaatccca gctactcagt aggtctgaggt aggagtatcg      1672
cttgaactcg gatggcggag gctgcagtga gccaagactg cgccactcca ctgcactcca      1732
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      Met Leu Pro Leu Leu Ile Ile Cys
      -15      -10
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Leu Leu Pro Ala Ile Glu Gly Lys Asn Cys Leu Arg Cys Trp Pro Glu
      -5      1      5
ctg tct gcc ttg ata gac tat gac ctg cag atc ctc tgg gtg acc cca      149
Leu Ser Ala Leu Ile Asp Tyr Asp Leu Gln Ile Leu Trp Val Thr Pro
      10      15      20      25
ggg cca ccc aca gaa ctt tct caa aat cgt gac cat ttg gaa gaa gaa      197
Gly Pro Pro Thr Glu Leu Ser Gln Asn Arg Asp His Leu Glu Glu Glu
      30      35      40
aca gcc aaa ttc ttc act caa gta cac caa gcc att aaa acg tta cga      245
Thr Ala Lys Phe Phe Thr Gln Val His Gln Ala Ile Lys Thr Leu Arg
      45      50      55
gat gat aaa aca gta ctt ctg gaa gag atc tac acg cac aag aat ctc      293
Asp Asp Lys Thr Val Leu Leu Glu Glu Ile Tyr Thr His Lys Asn Leu
      60      65      70

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ttt act gag agg ctg aat aag ata tct gat ggg ctg aag gag aag gac 341
Phe Thr Glu Arg Leu Asn Lys Ile Ser Asp Gly Leu Lys Glu Lys Asp
75 80 85
ata cag tcc aca ctg aag gtc acc agc tgt gct gac tgc agg act cac 389
Ile Gln Ser Thr Leu Lys Val Thr Ser Cys Ala Asp Cys Arg Thr His
90 95 100 105
ttc ctc tcc tgc aat gac ccc act ttc tgc cca gcc agg aac cgg cgg 437
Phe Leu Ser Cys Asn Asp Pro Thr Phe Cys Pro Ala Arg Asn Arg Arg
110 115 120
acc tcc ctg tgg gct gtg agt ctc agc agt gct cta ctc ctg gcc ata 485
Thr Ser Leu Trp Ala Val Ser Leu Ser Ser Ala Leu Leu Leu Ala Ile
125 130 135
gct gga gat gtt tct ttt act ggc aaa gga aga agg agg cag 527
Ala Gly Asp Val Ser Phe Thr Gly Lys Gly Arg Arg Arg Gln
140 145 150
taaagcagga acagggcagc ccgcatgtct tccagaagtg aacagaggcc gcagctacca 587
ccgtcacaaa gtctactcat ctctgggtcc cggtagcccc atccccccat accctccatc 647
ctgggtcctg gggcccaaaa gctctgaggc ctaggagact gcgctgtctc gtggtttgcc 707
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aaaaaaaaaa aaaaaaaaaa aataaaaaaa aaaaaaaa 805

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 <213> Homo sapiens

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Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg Val Thr Lys Gly Ser Phe
-5 1 5
gaa ccc caa aaa tgt tgg aag aat aat gta gga cat tgc aga aga cga 152
Glu Pro Gln Lys Cys Trp Lys Asn Asn Val Gly His Cys Arg Arg Arg
10 15 20
tgt tta gat act gaa agg tac ata ctt ctt tgt agg aac aag cta tca 200
Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu Cys Arg Asn Lys Leu Ser
25 30 35
tgc tgc att tct ata ata tca cat gaa tat act cga cga cca gca ttt 248
Cys Cys Ile Ser Ile Ile Ser His Glu Tyr Thr Arg Arg Pro Ala Phe
40 45 50 55
cct gtg att cac cta gag gat ata aca ttg gat tat agt gat gtg gac 296
Pro Val Ile His Leu Glu Asp Ile Thr Leu Asp Tyr Ser Asp Val Asp
60 65 70
tct ttt act ggt tcc cca gta tct atg ttg aat gat ctg ata aca ttt 344
Ser Phe Thr Gly Ser Pro Val Ser Met Leu Asn Asp Leu Ile Thr Phe

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	75		80		85	
gac aca act aaa ttt gga gaa acc atg aca cct gag acc aat act cct						392
Asp Thr Thr Lys Phe Gly Glu Thr Met Thr Pro Glu Thr Asn Thr Pro						
	90		95		100	
gag act act atg cca cca tcc gag gcc act act ccc gag act act atg						440
Glu Thr Thr Met Pro Pro Ser Glu Ala Thr Thr Pro Glu Thr Thr Met						
	105		110		115	
cca cca tct gag act gct act tcc gag act atg cca cca cct tct cag						488
Pro Pro Ser Glu Thr Ala Thr Ser Glu Thr Met Pro Pro Pro Ser Gln						
120		125		130	135	
aca gct ctt act cat aat taattaacat ttacttctgg tatggaacaa						536
Thr Ala Leu Thr His Asn						
	140					
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gaaaattcca tcagggattg gatgaccatg gggatggaca taattgctac taccaacaca						656
acagccaaga gagttgcctt acaattagaa atgtgtagac agaaatgtat agaagataca						716
aggattctct taattggact taaattcttt atctgtcttc ctccgatgta ctcaaatata						776
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					Met	
gca aag atg ttt gat ctc agg acg aag atc atg atc ggc atc gaa agc						165
Ala Lys Met Phe Asp Leu Arg Thr Lys Ile Met Ile Gly Ile Glu Ser						
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agc tta ctg gtt gcc gcg atg gtg ctc cta agt gtt gtg ttc tgt ctt						213
Ser Leu Leu Val Ala Ala Met Val Leu Leu Ser Val Val Phe Cys Leu						
-15		-10		-5		1
tac ttc aaa gta gct aag gca cta aaa gct gca aag gac cct gat gct						261
Tyr Phe Lys Val Ala Lys Ala Leu Lys Ala Ala Lys Asp Pro Asp Ala						
5		10		15		
gtg gct gta aaa aat cac aac cca gac aag gtg tgt tgg gcc acg aac						309
Val Ala Val Lys Asn His Asn Pro Asp Lys Val Cys Trp Ala Thr Asn						
20		25		30		
agc cag gcc aaa gcc acc acc atg gag tct tgt cca tct ctc cag tgc						357
Ser Gln Ala Lys Ala Thr Thr Met Glu Ser Cys Pro Ser Leu Gln Cys						
35		40		45		
tgt gaa ggt tgt aga atg cat gcc agt tct gat tcc ctg cca cct tgc						405
Cys Glu Gly Cys Arg Met His Ala Ser Ser Asp Ser Leu Pro Pro Cys						
50		55		60		65
tgt tgt gac ata aat gag ggc ctc tgacttggga aagctgggca caaaaatctt						459

Cys Cys Asp Ile Asn Glu Gly Leu

70

catgagcaat	atttctttct	taatagaatg	ttttattatt	caagtcaagt	tctagagtgt	519
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actttattcc	agagctcagg
	tgtttgaact
	g atg tct gat gag gat gaa tcc
	Met Ser Asp Glu Asp Glu Ser
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agc gac tac ctc tgc ctg tcc atc ctg ggc ctc ttc tgt tgc ctt ccc	400
Ser Asp Tyr Leu Cys Leu Ser Ile Leu Gly Leu Phe Cys Cys Leu Pro	
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cta gcc atc cca gcc gtg atc ttt tct tgc ctg aca aag aac tac aat	448
Leu Ala Ile Pro Ala Val Ile Phe Ser Cys Leu Thr Lys Asn Tyr Asn	
1 5 10	
aaa tcc agt gac tat gag ctg gca gcc aag acc tcc aaa caa gcc tac	496
Lys Ser Ser Asp Tyr Glu Leu Ala Ala Lys Thr Ser Lys Gln Ala Tyr	
15 20 25	
tac tgg gcc atc gcg agc atc act gtg gga atc tta ggt acc atc ttg	544
Tyr Trp Ala Ile Ala Ser Ile Thr Val Gly Ile Leu Gly Thr Ile Leu	
30 35 40	
tac acc tac ctg ata tac tta ctt aga ttg taaactgctt cccagctctt	594
Tyr Thr Tyr Leu Ile Tyr Leu Leu Arg Leu	
45 50	
gaacaaacca ccaaatatac accacagtgc aatttaaaaa aaaaaaaaaa aaaaaaaaaa	654
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gaaaaaaaaa aaaaaa	699

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 agatgctgac ta atg act gac cag gat cga atc atc aat tta gtt gtt ggc 171
 Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly
 -25 -20 -15
 agc tta aca tcc tta ttg att cta gta acg ctg ata agt gct ttt gtt 219
 Ser Leu Thr Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val
 -10 -5 1
 ttc cct caa cta cct cca aaa ccg ttg aat ata ttc ttt gct gtc tgc 267
 Phe Pro Gln Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys
 5 10 15
 atc tct ttg agt agt att act gcc tgc ata atc tac tgg tat cga caa 315
 Ile Ser Leu Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln
 20 25 30
 gga gac tta gaa ccg aaa ttt aga aag cta att tac tat atc ata ttt 363
 Gly Asp Leu Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe
 35 40 45 50
 tct atc atc atg ttg tgt ata tgt gca aac ctg tac ttc cat gat gtg 411
 Ser Ile Ile Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val
 55 60 65
 gga agg tgaggctgcc aaggagaagt acttaccagg actcttcaaa atgatacatt 467
 Gly Arg
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 atgattttca tgttaattgt aaatgttaat tccctcttgc aaggagagaca tatcctagat 587
 cactttgctt tttctttaag gagctgatgt tgcacctaata cattccaacc cttaaagcta 647
 aaacagcaca aaaaaatttc actttttgaaa tgaaattttt ataattgtat ggcaaaaaggc 707
 tatgtaaaaa caaatcttgc atcttaagac aaatattctt ttattttctgt taaactgaat 767
 atacaattgt tccctaggca accaactttt gcttataact acaatttaat ttcacgttga 827
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Met Ala
-20
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Ala Ala Ala Val Pro Ser Leu Leu Leu Ser Leu Pro Pro His Gln Gly
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ctc act ttc tcc aac aaa ata caa cct ttt gga gct caa gga gtc ttg      214
Leu Thr Phe Ser Asn Lys Ile Gln Pro Phe Gly Ala Gln Gly Val Leu
1 5 10
cat ccg gaa cca gga ctg cga gac tgg ctg ctg cca acg tgc tcc aga      262
His Pro Glu Pro Gly Leu Arg Asp Trp Leu Leu Pro Thr Cys Ser Arg
15 20 25 30
caa ttg cga gtc gca ctg ccg gag aag ggg tcc gag ggc agt ctg tgt      310
Gln Leu Arg Val Ala Leu Pro Glu Lys Gly Ser Glu Gly Ser Leu Cys
35 40 45
caa acg cag ctg cca gct act cca tgc ttc ctg cct tcg aat acg gtg      358
Gln Thr Gln Leu Pro Ala Thr Pro Cys Phe Leu Pro Ser Asn Thr Val
50 55 60
aga acg tgaagtcag agctgctgct aaggcatgtg gcaaccttga agagaaggtc      414
Arg Thr
aagagctacc agccacaaaa agaatgccag cacttcctgt gtctttgctt tggattcatg      474
agaaatatac gttcctatctt gcttcaaaaa aaaaaaaaaa      514

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seq AVFAVLFFVFFLFA/ML

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gtt cct tgg ctc tat gct gtg ttt gct gtg ctt ttt gta ttt ttt ctt      98
Val Pro Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Phe Leu
-15 -10 -5
ttt gcc atg tta tct ccc ttt tta ctt gag ata gac cag cac ata aag      146
Phe Ala Met Leu Ser Pro Phe Leu Leu Glu Ile Asp Gln His Ile Lys
1 5 10
aaa ttc ttg atc aga tgc agg tat tct ctg cat aac act gtg cat aag      194
Lys Phe Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys
15 20 25 30
gac aaa aaa aac agt gag ata aag atg gac cat cta gaa agg cca ggc      242
Asp Lys Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly
35 40 45
tgt cca ctg gag tca cca agg aga gga gtt ctg gga ggg aag aaa aat      290
Cys Pro Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Lys Asn
50 55 60
ggg atg gga aac gac cca tta cta ttt gtg aaa gtg aca aaa gaa ccc      338

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Gly Met Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro
65 70 75
agg gat tct gag gct gaa atc tat acc cct ggg cct tca gtt 380
Arg Asp Ser Glu Ala Glu Ile Tyr Thr Pro Gly Pro Ser Val
80 85 90
tgagagtcatt ttagcctata tggaattacc tgtgacatta cattccagag agatgagaaa 440
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<222> 155..292
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gacccagaac agctaccagc agaatcagat tctc atg gac caa ctg gta ttc aaa 175
Met Asp Gln Leu Val Phe Lys
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Glu Thr Ile Trp Asn Asp Ala Phe Trp Gln Asn Pro Trp Asp Gln Gly
-35 -30 -25
ggc ctg gca gtg att atc tta ttc atc acc gct gtc ctg ctt ctc atc 271
Gly Leu Ala Val Ile Ile Leu Phe Ile Thr Ala Val Leu Leu Leu Ile
-20 -15 -10
tta ttt gcc atc gtg ttt ggt tta ctc act tcc aca gaa aac act cag 319
Leu Phe Ala Ile Val Phe Gly Leu Leu Thr Ser Thr Glu Asn Thr Gln
-5 1 5
tgt gaa gcg ggt gaa gag gag tgacctgact tgctggggac tgagatggca 370
Cys Glu Ala Gly Glu Glu Glu
10 15
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cacaggccca gccagcaatt tcacaaatcc ttgacagaga aagacacaac caaatgaaat 730
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seq SLLFICFFGESFC/IC

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agctaattta gctatttttaa aatagctaaa ttttagctac ttttttttca attgacaaaag 180
aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc 229
Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile
-20 -15 -10
tgc ttc ttc ggg gag agt ttc tgc att tgt gat gga act gtc tgg aca 277
Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr
-5 1 5
aag gtt gga tgg gag att ctt cca gaa gaa gta cat tat tgg aaa ggt 325
Lys Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly
10 15 20
tgt tta tat ctc att tat aat tta tta caa gct gtc ttc ttc gtc tta 373
Cys Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu
25 30 35 40
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Phe Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln
45 50 55
aaa aag ctg aaa aag caa gcc tcc tta gaa aaa cct ggt aat gat cta 469
Lys Lys Leu Lys Lys Gln Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu
60 65 70
gaa agc cca ttg atc aac aac att gac caa aca ctc cac aga gtg gca 517
Glu Ser Pro Leu Ile Asn Asn Ile Asp Gln Thr Leu His Arg Val Ala
75 80 85
acc aca gca tca gtg ata tac aag atc tgg gag cac agg tct cac cat 565
Thr Thr Ala Ser Val Ile Tyr Lys Ile Trp Glu His Arg Ser His His
90 95 100
cct tcc tct aag aaa att aag cac tgc aaa tta aag aag aag agt aaa 613
Pro Ser Ser Lys Lys Ile Lys His Cys Lys Leu Lys Lys Lys Ser Lys
105 110 115 120
gaa gaa gga gcc aga aga tac taaataaatg catatgcaaa tgtagcttag 664
Glu Glu Gly Ala Arg Arg Tyr
125
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Leu Gly Arg Leu Thr Ser Gln Leu Leu Arg Ala Val Pro Trp Ala Gly
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Gly Arg Pro Pro Trp Pro Val Ser Gly Val Leu Gly Ser Arg Val Cys
10 15 20
ggg ccc ctt tac agc aca tcg ccg gcc ggc cca ggt agg gcg gcc tct 202
Gly Pro Leu Tyr Ser Thr Ser Pro Ala Gly Pro Gly Arg Ala Ala Ser
25 30 35
ctc cct cgc aag ggg gcc cag ctg gag ctg gag gag atg gtc ccc agg 250
Leu Pro Arg Lys Gly Ala Gln Leu Glu Leu Glu Glu Met Val Pro Arg
40 45 50
aag atg tcc gtc agc ccc ctg gag agc tgg ctc acg gcc cgc tgc ttc 298
Lys Met Ser Val Ser Pro Leu Glu Ser Trp Leu Thr Ala Arg Cys Phe
55 60 65
ctg ccc aga ctg gat acc ggg acc gca ggg act gtg gct cca ccg caa 346
Leu Pro Arg Leu Asp Thr Gly Thr Ala Gly Thr Val Ala Pro Pro Gln
70 75 80 85
tcc tac cag tgt ccg ccc agc cag ata ggg gaa ggg gcc gag cag ggg 394
Ser Tyr Gln Cys Pro Pro Ser Gln Ile Gly Glu Gly Ala Glu Gln Gly
90 95 100
gat gaa ggc gtc gcg gat gcg cct caa att cag tgc aaa aac gtg ctg 442
Asp Glu Gly Val Ala Asp Ala Pro Gln Ile Gln Cys Lys Asn Val Leu
105 110 115
aag atc cgc cgg cgg aag atg aac cac cac aag tac cgg aag ctg gtg 490
Lys Ile Arg Arg Arg Lys Met Asn His His Lys Tyr Arg Lys Leu Val
120 125 130
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Lys Lys Thr Arg Phe Leu Arg Arg Lys Val Gln Glu Gly Arg Leu Arg
135 140 145
cgc aag cag atc aag ttc gag aaa gac ctg agg cgc atc tgg ctg aag 586
Arg Lys Gln Ile Lys Phe Glu Lys Asp Leu Arg Arg Ile Trp Leu Lys
150 155 160 165
gcg ggg cta aag gaa gcc ccc gaa ggc tgg cag acc ccc aag atc tac 634
Ala Gly Leu Lys Glu Ala Pro Glu Gly Trp Gln Thr Pro Lys Ile Tyr
170 175 180
ctg cgg ggc aaa tgagtctggc gccgcccttc ccgccggttg ctgctgtgat 686
Leu Arg Gly Lys
185
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<210> 94

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<212> DNA

<213> Homo sapiens

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 <222> 247..318
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 Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala
 -20 -15
 tta gaa gtg gtg ttg cca tcc tgt gat tgc agg agt cct ggc att ggc 336
 Leu Glu Val Val Leu Pro Ser Cys Asp Cys Arg Ser Pro Gly Ile Gly
 -10 -5 1 5
 ttg gtg gag gag cct atg gat aag gtg gag gaa gga cca tta tca ttc 384
 Leu Val Glu Glu Pro Met Asp Lys Val Glu Glu Gly Pro Leu Ser Phe
 10 15 20
 ctt atg aaa agg aag aca gcc cag aag ctt gct att cag aag gct ttg 432
 Leu Met Lys Arg Lys Thr Ala Gln Lys Leu Ala Ile Gln Lys Ala Leu
 25 30 35
 tca gat gca ttc cag aaa ctg ttg att gtt gtt cta ggt aag act gtc 480
 Ser Asp Ala Phe Gln Lys Leu Ile Val Val Leu Gly Lys Thr Val
 40 45 50
 ttg atc atc ctt gaa gta ctt cag ttt cag taagcaaata aactcatttt 530
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 55 60
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 cagagacggc aggttcatca ag atg gtg ctc atg tgg acc agt ggt gac gcc 172
 Met Val Leu Met Trp Thr Ser Gly Asp Ala
 -45 -40
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 Phe Lys Thr Ala Tyr Phe Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser
 -35 -30 -25 -20
 gtg tgc ggc ctg ctg cag gtg ctg gtg gac ctg gcc atc ctg ggg cag 268

Val	Cys	Gly	Leu	Leu	Gln	Val	Leu	Val	Asp	Leu	Ala	Ile	Leu	Gly	Gln	
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gcc	tac	gcc	ttc	gcc	cca	ccc	cca	gaa	gcc	ggc	gcc	cca	cgc	cgt	gca	316
Ala	Tyr	Ala	Phe	Ala	Pro	Pro	Pro	Glu	Ala	Gly	Ala	Pro	Arg	Arg	Ala	
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ccc	cac	tgg	cac	caa	ggc	cct	ctg	aca	gtg	ggg	agg	acg	agg	atg	tgg	364
Pro	His	Trp	His	Gln	Gly	Pro	Leu	Thr	Val	Gly	Arg	Thr	Arg	Met	Trp	
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gac	cgc	cag	ccg	cgg	gca	ctg	gtg	ggc	cct	gac	ctc	ccc	gcg	ggg	agg	412
Asp	Arg	Gln	Pro	Arg	Ala	Leu	Val	Gly	Pro	Asp	Leu	Pro	Ala	Gly	Arg	
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Val	Gly	Ala	Val	Ala	Pro	Ala	Gly	Val	Ala	Glu	Met	Gly	His	Gly	His	
				50					55					60		
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Trp	Gly	Leu	His	Gln	Pro	Leu	Trp	Gly	Val	Ser	Gly	Trp	Ala	Val	Gly	
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Val	Gly	Leu	Gly	Arg	Cys	Leu	Cys	Ser	Ala	Gly	Thr	Ala	Arg	Val	Asp	
		80				85					90					
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Leu	Ala	Pro	Arg	Val	Leu	Asp	Val	Phe	Arg	Met	Thr					
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<400> 96

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Val Phe Leu Leu Met Val Asn Gly Gln Val Glu Ser Ala Gln Phe Pro
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gag tat gat gac ttc tac tgc aag tac tgc ttt gtg tac ggc cag gac      149
Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr Cys Phe Val Tyr Gly Gln Asp
5                               10                               15                               20
tgg gcc ccc aca gcg ggt ctg gag gag ggg atc tca cag atc aca tcc      197
Trp Ala Pro Thr Ala Gly Leu Glu Glu Gly Ile Ser Gln Ile Thr Ser
                               25                               30                               35
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Lys Ser Gln Asp Val Arg Gln Ala Leu Val Trp Asn Phe Pro Ile Asp
                               40                               45                               50
gtc acc ttt aaa agc acc aac ccc tac ggc tgg cca cag atc gtg ctc      293
Val Thr Phe Lys Ser Thr Asn Pro Tyr Gly Trp Pro Gln Ile Val Leu
                               55                               60                               65
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Ser Val Tyr Gly Pro Asp Val Phe Gly Asn Asp Val Val Arg Gly Tyr
70                               75                               80
ggg gcc gtg cac gtg ccc ttc tca cct ggc cgg cac aaa agg acc atc      389
Gly Ala Val His Val Pro Phe Ser Pro Gly Arg His Lys Arg Thr Ile
85                               90                               95                               100
ccc atg ttt gtc cca gaa tct acg tct aaa ctg cag aag ttt aca aga      437
Pro Met Phe Val Pro Glu Ser Thr Ser Lys Leu Gln Lys Phe Thr Arg
                               105                               110                               115
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Ser Ala Ser Cys Ser Thr His
                               120
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Leu Cys Ser Asp Ser Leu Pro Glu Ser Gln Gln Gln Asp Gly Asn His
      -10      -5      1      5
gca ccc aac ttc tcc agc cac ggc tca tgc cgc cgt cgc cag cgg scc      144
Ala Pro Asn Phe Ser Ser His Gly Ser Cys Arg Arg Arg Gln Arg Xaa
      10      15      20
gac atg aca agg cgc tgc atg ccc gct agg cca ggt ttc ccc tca tcc      192
Asp Met Thr Arg Cys Met Pro Ala Arg Pro Gly Phe Pro Ser Ser
      25      30      35
cca gcc ccg ggg tgc tgc ccc ccg cgc tgc cat ctg aga ccc ggt agt      240
Pro Ala Pro Gly Ser Ser Pro Pro Arg Cys His Leu Arg Pro Gly Ser
      40      45      50
acc gcc cat gct gca gcg gga aag aga aca gag agt cct ggg gac agg      288
Thr Ala His Ala Ala Ala Gly Lys Arg Thr Glu Ser Pro Gly Asp Arg
      55      60      65
tac cgt gca gag ggc ttg aga agg ggc cgg gtc gcg ggg gca agg gta      336
Tyr Arg Ala Glu Gly Leu Arg Arg Gly Arg Val Ala Gly Ala Arg Val
      70      75      80      85
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tggagtttgc ttctctgtag ttgggcagct gctcttggtc tagtgaccac cagcctggac      516
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aaa
939

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<212> DNA
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gcacccctac ctcagaccat cagttgggta ggccaacagc tcaccatcaa ttc atg      176
Met
ccc tgc cta gac caa cag ctc act gtt cat gcc cta ccc tgc cct gcc      224
Pro Cys Leu Asp Gln Gln Leu Thr Val His Ala Leu Pro Cys Pro Ala
      -30      -25      -20
cag ccc tcc tct ctg gcc ttc tgc caa gtg ggg ttc tta aca gca cag      272
Gln Pro Ser Ser Leu Ala Phe Cys Gln Val Gly Phe Leu Thr Ala Gln

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-15          -10          -5          1
cct tca cct ccg aga agg cgc aat ggg aaa gac aga tac acg ttg gtt      320
Pro Ser Pro Pro Arg Arg Arg Asn Gly Lys Asp Arg Tyr Thr Leu Val
      5          10          15
ctg caa cac cag gaa tgc cag gat gat tta gcc acc tcc tca ctt gtc      368
Leu Gln His Gln Glu Cys Gln Asp Asp Leu Ala Thr Ser Ser Leu Val
      20          25          30
tac ctt tcc ctc ccc tgc ttc aaa gac ttg ggt cga tgc aag cac caa      416
Tyr Leu Ser Leu Pro Cys Phe Lys Asp Leu Gly Arg Ser Lys His Gln
      35          40          45
agc atc act gtt gct gac act aac aag tagtgccaag ggattgcctt      463
Ser Ile Thr Val Ala Asp Thr Asn Lys
      50          55
taaggaagat caggagcggg acatctgggt gcaaagaaaa tcttttctaag agccccattc      523
tagtgaccac cttcaacctc ctcatagcag gagagtttgg gagtagggga cttaggatgt      583
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tgtgaaagaa tctcctgatg tcataatttc cgggtgtcac cggaacattt gatcatcatt      180
cctttggcaa ttccagcctt ctgtggaaag gccagtagaa agcattgatt tattcacctc      240
tacaggaatc agactcagcc tcttttgggt ttcagtgaag t atg cct ttt caa ttt      296
                                     Met Pro Phe Gln Phe
                                     -35
gga acc cag cca agg agg ttt cca gtg gaa gga gga gat tct tca att      344
Gly Thr Gln Pro Arg Arg Phe Pro Val Glu Gly Gly Asp Ser Ser Ile
-30          -25          -20          -15
gag ctg gaa cct ggg ctg agc tcc agt gct gcc tgt aat ggg aag gag      392
Glu Leu Glu Pro Gly Leu Ser Ser Ser Ala Ala Cys Asn Gly Lys Glu
      -10          -5          1
atg tca cca acc agg caa ctc cgg agg tgc cct gga agt cat tgc ctg      440
Met Ser Pro Thr Arg Gln Leu Arg Arg Cys Pro Gly Ser His Cys Leu
      5          10          15
aca ata act gat gtt ccc gtc act gtt tat gca aca acg aga aag cca      488
Thr Ile Thr Asp Val Pro Val Thr Val Tyr Ala Thr Thr Arg Lys Pro
      20          25          30
cct gca caa agc agc aag gaa atg cat cct aaa tagcaccatt aagtcttttg      541
Pro Ala Gln Ser Ser Lys Glu Met His Pro Lys
      35          40          45
tcaaggtctg actaggtcaa gggtaatgga ccagtatcat ctggtgatct ggtaaacaaa      601

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taaaagtgggt ggcaccttta gatgatgaca aaaaaaaaaa aaaaaa

647

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<222> 251..643

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<222> 251..295

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score 3.74215118492367

seq LLMFTQLLLCGFL/YV

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ttcttgactt taattagtat ctaggaaagt ctaaactttg gacctacctc tttttttgat 180
actcattttt gtacttttgc tctctgggat tggtttctta aagaatctgg atccttttta 240
atatgtcaaa atg agt ctg ctg atg ttt aca caa cta ctg ctc tgt gga 289

Met Ser Leu Leu Met Phe Thr Gln Leu Leu Leu Cys Gly

-15 -10 -5

ttt tta tat gtt cgg gtt gat gga tcg cgt ctt cgc cag gag gac ttt 337
Phe Leu Tyr Val Arg Val Asp Gly Ser Arg Leu Arg Gln Glu Asp Phe

1 5 10

ccc ccg cgg att gtg gag cat cct tcc gat gtc atc gtc tct aag ggc 385
Pro Pro Arg Ile Val Glu His Pro Ser Asp Val Ile Val Ser Lys Gly

15 20 25 30
gag ccc acg act ctg aac tgc aag gcg gag ggc cgg cca acg ccc acc 433
Glu Pro Thr Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr Pro Thr

35 40 45

att gag tgg tac aaa gat ggg gag cga gtg gag act gac aag gac gat 481
Ile Glu Trp Tyr Lys Asp Gly Glu Arg Val Glu Thr Asp Lys Asp Asp

50 55 60

ccc cgg tcc cac agg atg ctt ctg ccc agc gga tcc tta ttc ttc ttg 529
Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe Phe Leu

65 70 75

cgc atc gtg cac ggg cgc agg agt aaa cct gat gaa gga agc tac gtt 577
Arg Ile Val His Gly Arg Arg Ser Lys Pro Asp Glu Gly Ser Tyr Val

80 85 90

tgt gtt gcg agg aac tat ctt ggt gaa gca gtg agt cga aat gcg tct 625
Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser Arg Asn Ala Ser

95 100 105 110
ctg gaa gtg gca tgt aag tgaacataat gaacctcatg tgcacattta 673
Leu Glu Val Ala Cys Lys

115

cttttattta tttcaagtaa gttttgatgt gttcccatag acgctgaaac ctaaagaatc 733
aatcaacaca ctgcataatt ttacttggtc ttcttcagag aagtctgggc aagatagtat 793

caagccaggg tggtgtagta agtttggtta tatgaaatca agatgaccaa tatgttatta 853
taagaaagca ggccgggcgc ggtggctcac gcctgtaatc ccagcacttt gggagggcga 913

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 seq PSLIAGLFVGCLA/GY

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 gacttctgtc ttttcagctg cagtgaaggc tcggggctgc agaattgcaa ccttgcca 178
 atg gac ctg atc ggt ttt ggt tat gca gcc ctc gtg aca ttt gga agc 226
 Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
 -35 -30 -25
 att ttt gga tat aag cgg aga ggt ggt gtt ccg tct ttg att gct ggt 274
 Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
 -20 -15 -10
 ctt ttt gtt gga tgt ttg gcc ggc tat gga gct tac cgt gtc tcc aat 322
 Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn
 -5 1 5
 gac aaa cga gat gta aaa gtg tca ctg ttt aca gct ttc ttc ctg gct 370
 Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala
 10 15 20 25
 acc ata atg ggt gtg aga ttt aag agg tcc aag aaa ata atg cct gct 418
 Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala
 30 35 40
 ggt ttg gtt gca ggt tta agc ctc atg atg atc ctg aga ctt gtc ttg 466
 Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu
 45 50 55
 ttg ctg ctc tgagcatctg gaggaacaga aaactaagtt catgtcatcc 515
 Leu Leu Leu
 60
 tgctgtaatg ggcagagcat attttttttg tattttaaag ataaacttca atatggaatg 575
 ctagaaacac aaatagcact gtcacctcta atatgaacat tagtttgagg tagttttttt 635
 ctaaagcaaa aatttttaact gtttttcta tgtcaagcac tatttttcatt aaaagtgtct 695
 aatgaatcat gatatactct tccatttggt gtgtctatatt tttatatatt tggatatttt 755
 tgaaaattcc aaatactcat gtctcaagta agcttaaaact acaacttgct acataaagga 815
 agtcttaagt ggagttcaca gaatgataat gtatctatatt gtcatttggt ttatatattga 875
 aattattaga aattatgctt tttccatttt aattgtattg ctgccagtgc tatttttttc 935
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 <213> Homo sapiens

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<222> 34..327

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<221> sig_peptide

<222> 34..162

<223> Von Heijne matrix

score 5.69273078757386

seq LGDALLFLRPAGS/CA

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Met Cys Glu Thr Leu Leu Thr

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agt aaa tgg gct tca gta tcc ccc atc cct gca ctc ctg cag gaa ggt 102
Ser Lys Trp Ala Ser Val Ser Pro Ile Pro Ala Leu Leu Gln Glu Gly

-35

-30

-25

gag aat cgg gac agt cgc agg ctg gga gac gct ctg ctt ttc ctg cgt 150
Glu Asn Arg Asp Ser Arg Arg Leu Gly Asp Ala Leu Leu Phe Leu Arg

-20

-15

-10

-5

cct gct ggg agc tgc gcg ctc cag gta tcc tgg cct gcc gcc cta gcc 198
Pro Ala Gly Ser Cys Ala Leu Gln Val Ser Trp Pro Ala Ala Leu Ala

1

5

10

ggc cca agg agc cac aca gga cag ttg acc caa cac ttc tgc cac ctg 246
Gly Pro Arg Ser His Thr Gly Gln Leu Thr Gln His Phe Cys His Leu

15

20

25

aag aac gac acc tgc att cct cca tct ctg gga cca cca agg aac tca 294
Lys Asn Asp Thr Cys Ile Pro Pro Ser Leu Gly Pro Pro Arg Asn Ser

30

35

40

ggg agc ttg gaa tct ctc aga tca aaa aga tac tgactcatcg gatagccatg 347
Gly Ser Leu Glu Ser Leu Arg Ser Lys Arg Tyr

45

50

55

gcacccctgaa aacggccttc cttgtgtgta cattatttgc aacaagcaac aagtttataa 407
gcacttttggg aaaattgcat gtgagggtta aaatattaaa gtcagtgcgt caacttgaaa 467
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<222> 303..359

<223> Von Heijne matrix

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atcaggtttt taacttaagt cgtgaggaat acaacggtga acacaagatt cattttattt 180

tcatcaccat gggacgtatc ctgttggtga gttctctggg tcagacctct gaagacttct 240

cagatggatc ctagtctctg ggcttgccct gaaattactc gctgctcagg gagagagttg 300

aa atg gtt ggc atc ctc cca ctc tgt tgc tcc ggc tgt gtc ccc tcg 347

Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser																	395
-15 -10 -5																	
ctc	tgt	tgt	tcc	agc	tat	gtc	ccc	tct	gtt	gct	cca	act	gca	gct	cat		
Leu	Cys	Cys	Ser	Ser	Tyr	Val	Pro	Ser	Val	Ala	Pro	Thr	Ala	Ala	His		
1 5 10																	443
tct	gtt	aga	gtt	cct	cat	tca	gct	ggg	cac	tgt	ggc	cag	agg	gtg	ttg		
Ser	Val	Arg	Val	Pro	His	Ser	Ala	Gly	His	Cys	Gly	Gln	Arg	Val	Leu	491	
15 20 25																	
gcc	tgc	tcc	ctt	cct	caa	gta	ttc	tta	aag	cca	tgg	att	ttt	gtg	gag	539	
Ala	Cys	Ser	Leu	Pro	Gln	Val	Phe	Leu	Lys	Pro	Trp	Ile	Phe	Val	Glu		
30 35 40																	587
cat	ttt	tct	tcc	tgg	ctc	tcc	ctt	gag	tta	ttt	tcc	ttt	ctt	cgc	tat		
His	Phe	Ser	Ser	Trp	Leu	Ser	Leu	Glu	Leu	Phe	Ser	Phe	Leu	Arg	Tyr		
45 50 55 60																	635
ctt	ggg	act	ctt	ctt	tgt	gct	tgc	gga	cat	cgg	ttg	aga	gaa	gga	cga		
Leu	Gly	Thr	Leu	Leu	Cys	Ala	Cys	Gly	His	Arg	Leu	Arg	Glu	Gly	Arg		
65 70 75																	683
ctt	ctt	cct	tgt	ctc	ctt	ggg	gtt	ggc	tcg	tgg	ttg	ctc	ttc	aac	aac		
Leu	Leu	Pro	Cys	Leu	Leu	Gly	Val	Gly	Ser	Trp	Leu	Leu	Phe	Asn	Asn		
80 85 90																	731
tgg	act	gga	ggc	tct	tgg	ttt	tct	ctt	cat	ctt	caa	caa	gtc	agt	ctc		
Trp	Thr	Gly	Gly	Ser	Trp	Phe	Ser	Leu	His	Leu	Gln	Gln	Val	Ser	Leu		
95 100 105																	779
tct	caa	ggg	tct	cac	gtt	gca	gca	ttc	tta	cca	gag	gcc	att	ggg	cct		
Ser	Gln	Gly	Ser	His	Val	Ala	Ala	Phe	Leu	Pro	Glu	Ala	Ile	Gly	Pro		
110 115 120																	827
gga	gtt	cca	gtt	cca	gtg	tct	gga	gag	tcc	acc	tca	gct	cag	caa	tct		
Gly	Val	Pro	Val	Pro	Val	Ser	Gly	Glu	Ser	Thr	Ser	Ala	Gln	Gln	Ser		
125 130 135 140																	875
cat	gcc	ggg	tgg	caa	ttg	tca	gca	gaa	gcc	gat	gcc	tgc	cca	tca	gtt		
His	Ala	Gly	Trp	Gln	Leu	Ser	Ala	Glu	Ala	Asp	Ala	Cys	Pro	Ser	Val		
145 150 155																	923
ctt	tac	tct	gag	gtg	tta	gag	tgg	aat	aaa	aat	ata	aat	act	tat	act		
Leu	Tyr	Ser	Glu	Val	Leu	Glu	Trp	Asn	Lys	Asn	Ile	Asn	Thr	Tyr	Thr		
160 165 170																	973
agt	ttt	cat	gac	ttc	tgc	tta	ata	ttg	ggg	att	ttt	ktt	gtt	ttg	ttt		
Ser	Phe	His	Asp	Phe	Cys	Leu	Ile	Leu	Gly	Ile	Phe	Xaa	Val	Leu	Phe		
175 180 185																	1033
tgt	ttt	ggc	ggg	gat	agg	ctt	acc	tta	cat	taa	acc	aggc	cttagc	cttt			
Cys	Phe	Gly	Gly	Asp	Arg	Leu	Thr	Leu	His								
190 195																	1093
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1153																	1158
aggtccacac	ctggggctgt	ttgtttttcta	cgtttacctc	aacataaggt	accttatcat												
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<222> 97..156
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<223> Von Heijne matrix
 score 8.42885652997473
 seq AVVGCLLVPPAEA/NK

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<221> misc_feature

<222> 972

<223> n=a, g, c or t

<400> 104

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                                     Met Lys Leu Leu Ser Leu
                                     -20 -15
gtg gct gtg gtc ggg tgt ttg ctg gtg ccc cca gct gaa gcc aac aag 162
Val Ala Val Val Gly Cys Leu Leu Val Pro Pro Ala Glu Ala Asn Lys
                                     -10 -5 1
agt tct gaa gat atc cgg tgc aaa tgc atc tgt cca cct tat aga aac 210
Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile Cys Pro Pro Tyr Arg Asn
                                     5 10 15
atc agt ggg cac att tac aac cag aat gta tcc cag aag gac tgc aac 258
Ile Ser Gly His Ile Tyr Asn Gln Asn Val Ser Gln Lys Asp Cys Asn
                                     20 25 30
tgc ctg cac gtg gtg gag ccc atg cca gtg cct ggc cat gac gtg gag 306
Cys Leu His Val Val Glu Pro Met Pro Val Pro Gly His Asp Val Glu
35 40 45 50
gcc tac tgc ctg ctg tgc gag tgc agg tac gag gag cgc agc acc acc 354
Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr
                                     55 60 65
acc atc aag gtc atc att gtc atc tac ctg tcc gtg gtg ggt gcc ctg 402
Thr Ile Lys Val Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu
                                     70 75 80
ttg ctc tac atg gcc ttc ctg atg ctg gtg gac cct ctg atc cga aag 450
Leu Leu Tyr Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys
85 90 95
ccg gat gca tac act gag caa ctg cac aat gag gag gag aat gag gat 498
Pro Asp Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp
100 105 110
gct cgc tct atg gca gca gct gct gca tcc ctc ggg gga ccc cga gca 546
Ala Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
115 120 125 130
aac aca gtc ctg gag cgt gtg gaa ggt gcc cag cag cgg tgg aag ctg 594
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys Leu
135 140 145
cag gtg cag gag cag cgg aag aca gtc ttc gat cgg cac aag atg ctc 642
Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys Met Leu
150 155 160
agc tagatgggct ggtgtggttg ggtcaaggcc ccaacacccat ggctgccagc 695
Ser
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tgteccctgt gcacttctcg cactggggca tggagtcccc atgcatactc tgctgcccgt 1295
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tgagccagac ggtcggttgg aacatgagac tcgaggctga gcgtggatct gaacaccaca 1415
gcccctgtac ttgggttgcc tcttgccct gaacttcggt gtaccagtgc atggagagaa 1475
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 seq MLVLRSAI~~TR~~ALA/SR

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                               Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala
                               -10                               -5
ctg gcc tca cgg acg ctg gcg cct cag atg tgc tca tct ttt gct acg 160
Leu Ala Ser Arg Thr Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr
      1              5              10
gga ccc aga caa tac gat gga ata ttc tat gaa ttt cgt tct tat tac 208
Gly Pro Arg Gln Tyr Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr
15              20              25              30
ctt aag ccc tca aag atg aat gag ttc ctg gaa aat ttt gag aaa aac 256
Leu Lys Pro Ser Lys Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn
              35              40              45
gct cat ctt cgg aca gct cac tct gaa ttg gtt gga tac tgg agt gta 304
Ala His Leu Arg Thr Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val
      50              55              60
gaa ttt gga ggc aga atg aat aca gtg ttt cat att tgg aag tat gat 352
Glu Phe Gly Gly Arg Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp
      65              70              75
aat ttt gct cat cga act gaa gtt cag aaa gcc ttg gcc aaa gat aag 400
Asn Phe Ala His Arg Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys
      80              85              90
gaa tgg caa gaa caa ttc ctc att cca aat ttg gct ctc att gat aaa 448
Glu Trp Gln Glu Gln Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys
95              100              105              110
caa gag agt gag att act tat ctg gta cca tgg tgc aaa tta gaa aaa 496
Gln Glu Ser Glu Ile Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys
              115              120              125
cct cca aaa gaa gga gtc tat gaa ctg gcc act ttt cag atg aaa cct 544
Pro Pro Lys Glu Gly Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro
              130              135              140
ggg ggg cca gct ctg tgg ggt gat gca ttt aaa agg gca gtt cat gct 592
Gly Gly Pro Ala Leu Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala
145              150              155

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160 165 170	
tac gga gca ctc aac aga gtt cat gtt ctt tgg tgg aat gag agt gca	688
Tyr Gly Ala Leu Asn Arg Val His Val Leu Trp Trp Asn Glu Ser Ala	
175 180 185 190	
gat agt cgt gca gct ggg aga cat aag tcc cat gag gat ccc aga gtt	736
Asp Ser Arg Ala Ala Gly Arg His Lys Ser His Glu Asp Pro Arg Val	
195 200 205	
gtg gca gct gtt cgg gaa agt gtc aac tac cta gta tct cag cag aat	784
Val Ala Ala Val Arg Glu Ser Val Asn Tyr Leu Val Ser Gln Asn	
210 215 220	
atg ctt ctg att cct aca tcg ttt tca cca ctg aaa tagttttcta	830
Met Leu Leu Ile Pro Thr Ser Phe Ser Pro Leu Lys	
225 230	
ctgaaataca aaacatttca ttaactgcta taggatctct ctgctaattgg tgcttaaatt	890
ctcccaagag gttctcactt ttatttgaag gaggtggtaa gtttaatttgc tatgtttctt	950
gcattatgaa ggctacatct gtgctttgta agtaccactt caaaaaatag ttctgtttac	1010
tttctgcatg gtatttcagt gtctgtcata cattaaaaat acttgtcact gttttaagat	1070
cttgactctt catttgtttc agaatagctc ttctactgta ttctgacaac tctttgcttt	1130
atagcatttt gttgtattca aatgataatg gtagcatttc catgcttggtg acagcatttt	1190
taagttatta atatatttta tcaaccttcc catcatgtct gttttcctgg ttttttttgg	1250
ttgttttttg accagtaaaa tttattttgt aataccaaat aggatttaag aaaattaacg	1310
tatttcttta ctatggaaaa ccacattgtc atttgtgaca tcatctatat taaatatggt	1370
tttcacatta gttatttgc acttacttgg aaaatgatgc tggttaggtcc tgggtattaaa	1430
aatctagaaa agacttggtg gtttatgtgc tgaaatgtct ttatttataa ttaattttaa	1490
ctactattta ctttatttcg gatcctgttt aacaaagata cttgagacat ccatttggtt	1550
taatgaaatc tgtatggata tggaaatgct tgccttaata aaagcctaca tatacaaaaa	1610
aaaaaaaaa a	1621

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 <213> Homo sapiens

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 <222> 77..388

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 <222> 77..217
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 score 4.57105404339594
 seq FLYLTLNQSCIFA/NY

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cctcccaaac caaaag atg ttc tct ccg cgc caa gct ttg acg ccc gac ccc	112
Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro	
-45 -40	
ctg cac tct ccc gcc tac tca ccg gtc cta ggg ggt tgg tcc cgc ttt	160
Leu His Ser Pro Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe	
-35 -30 -25 -20	
cgt agt gtg gat ttt cgt ttc ctc tac ttg act cta aat caa tcc tgt	208
Arg Ser Val Asp Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys	
-15 -10 -5	
ata ttc gca aac tac aaa gag gcg cat gca aat aga tac tgt act gag	256

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Ile Phe Ala Asn Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu
      1           5           10
ggc aga tac acg cgc gag atc cag agg ctt aca tcc cca gcc gct tgg      304
Gly Arg Tyr Thr Arg Glu Ile Gln Arg Leu Thr Ser Pro Ala Ala Trp
      15           20           25
ccc acc aga gac aag aac agg atg ata agc aat gga atg gca ttg aac      352
Pro Thr Arg Asp Lys Asn Arg Met Ile Ser Asn Gly Met Ala Leu Asn
      30           35           40           45
tct cct gct gaa gga ctt gca ttt caa tgt aga ttc tgaggctggg      398
Ser Pro Ala Glu Gly Leu Ala Phe Gln Cys Arg Phe
      50           55
tgaaaacttc tctgtcacct ttactacagc attctcaccc atttatatatt ctttcccctt      458
ctacatctct attactgttg cactatgtta tgcattacac catggcaaaa ttaatcaatt      518
aatacaataa aagcttaatt ttaaaaaaaaa aaaaaaaaaa      557

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<222> 139..201
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ggaggcagag cggctgcc atg gcc aag tac ctg gcc cag atc att gtg atg      171
      Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met
      -20           -15
ggc gtg cag gtg gtg ggc agg gcc ttt gca cgg gcc ttg cgg cag gag      219
Gly Val Gln Val Val Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu
-10           -5           1           5
ttt gca gcc agc cgg gcc gca gct gat gcc cga gga cgc gct gga cac      267
Phe Ala Ala Ser Arg Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His
      10           15           20
cgg tct gca gcc gct tcc aac ctc tcc ggc ctc agc ctc cag gag gca      315
Arg Ser Ala Ala Ala Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala
      25           30           35
cag cag att ctc aac gtg tcc aag ctg agc cct gag gag gtc cag aag      363
Gln Gln Ile Leu Asn Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys
      40           45           50
aac tat gaa cac tta ttt aag gtg aat gat aaa tcc gtg ggt ggc tcc      411
Asn Tyr Glu His Leu Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser
      55           60           65           70
ttc tac ctg cag tca aag gtg gtc cgc gca aag gag cgc ctg gat gag      459
Phe Tyr Leu Gln Ser Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu
      75           80           85
gaa ctc aaa atc cag gcc cag gag gac aga gaa aaa ggg cag atg ccc      507
Glu Leu Lys Ile Gln Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro
      90           95           100

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cat acg tgactgctcg gctccccccg cccaccccg cgctctaatt ttatagcttg 563
His Thr

gtaataaaatt tcttttctac aaaaaaaaaa aaaaaaa 600

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<211> 1129

<212> DNA

<213> Homo sapiens

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<222> 81...986

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<222> 81...134

<223> Von Heijne matrix

score 5.03543461931947

seq ITLLGLAVNVVTT/LV

<400> 108

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Met Ala Pro Asn Ser Ile Thr Leu Leu Gly Leu

-15 -10

gcc gtc aac gtg gtc acc acg ctc gtg ctc atc tcc tac tgt ccc acg 161
Ala Val Asn Val Val Thr Thr Leu Val Leu Ile Ser Tyr Cys Pro Thr

-5 1 5

gcc acc gaa gag gca cca tac tgg aca tac ctt tta tgt gca ctg gga 209
Ala Thr Glu Glu Ala Pro Tyr Trp Thr Tyr Leu Leu Cys Ala Leu Gly

10 15 20 25

ctt ttt att tac cag tca ctg gat gct att gat ggg aaa caa gcc aga 257
Leu Phe Ile Tyr Gln Ser Leu Asp Ala Ile Asp Gly Lys Gln Ala Arg

30 35 40

aga aca aac tct tgt tcc cct tta ggg gag ctc ttt gac cat ggc tgt 305
Arg Thr Asn Ser Cys Ser Pro Leu Gly Glu Leu Phe Asp His Gly Cys

45 50 55

gac tct ctt tcc aca gta ttt atg gca gtg gga gct tca att gcc gct 353
Asp Ser Leu Ser Thr Val Phe Met Ala Val Gly Ala Ser Ile Ala Ala

60 65 70

cgc tta gga act tat cct gac tgg ttt ttt ttc tgc tct ttt att ggg 401
Arg Leu Gly Thr Tyr Pro Asp Trp Phe Phe Phe Cys Ser Phe Ile Gly

75 80 85

atg ttt gtg ttt tat tgc gct cat tgg cag act tat gtt tca ggc atg 449
Met Phe Val Phe Tyr Cys Ala His Trp Gln Thr Tyr Val Ser Gly Met

90 95 100 105

ttg aga ttt gga aaa gtg gat gta act gaa att cag ata gct tta gtg 497
Leu Arg Phe Gly Lys Val Asp Val Thr Glu Ile Gln Ile Ala Leu Val

110 115 120

att gtc ttt gtg ttg tct gca ttt gga gga gca aca atg tgg gac tat 545
Ile Val Phe Val Leu Ser Ala Phe Gly Gly Ala Thr Met Trp Asp Tyr

125 130 135

acg ggc acc agt gtc ttg tca cct gga ctc cac ata gga cta att att 593
Thr Gly Thr Ser Val Leu Ser Pro Gly Leu His Ile Gly Leu Ile Ile

140 145 150

ata ctg gca ata atg atc tat aaa aag tca gca act gat gtg ttt gaa 641
Ile Leu Ala Ile Met Ile Tyr Lys Lys Ser Ala Thr Asp Val Phe Glu

155 160 165

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aag cat cct tgt ctt tat atc cta atg ttt gga tgt gtc ttt gct aaa      689
Lys His Pro Cys Leu Tyr Ile Leu Met Phe Gly Cys Val Phe Ala Lys
170                               175                               180                               185
gtc tca caa aaa tta gtg gta gct cac atg acc aaa agt gaa cta tat      737
Val Ser Gln Lys Leu Val Val Ala His Met Thr Lys Ser Glu Leu Tyr
                               190                               195                               200
ctt caa gac act gtc ttt ttg ggg cca ggt ctt ttg ttt tta gac cag      785
Leu Gln Asp Thr Val Phe Leu Gly Pro Gly Leu Leu Phe Leu Asp Gln
                               205                               210                               215
tac ttt aat aac ttt ata gac gaa tat gtt gtt cta tgg atg gca atg      833
Tyr Phe Asn Asn Phe Ile Asp Glu Tyr Val Val Leu Trp Met Ala Met
                               220                               225                               230
gtg att tct tca ttt gat atg gtg ata tac ttt agt gct ttg tgc ctg      881
Val Ile Ser Ser Phe Asp Met Val Ile Tyr Phe Ser Ala Leu Cys Leu
                               235                               240                               245
caa att tca aga cac ctt cat cta aat ata ttc aag act gca tgt cat      929
Gln Ile Ser Arg His Leu His Leu Asn Ile Phe Lys Thr Ala Cys His
250                               255                               260                               265
caa gca cct gaa cag gtt caa gtt ctt tct tca aag agt cat cag aat      977
Gln Ala Pro Glu Gln Val Gln Val Leu Ser Ser Lys Ser His Gln Asn
                               270                               275                               280
aac atg gat tgaagagact tccgaacact tgctatctct tgctgctgct      1026
Asn Met Asp
gttttcatgga aggagatatt aaacatttgt ttaattttta tttaagtgtt atacctattt      1086
cagcaaataa aatattttcat tgcttgaaaa aaaaaaaaaa aaa      1129

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<211> 778

<212> DNA

<213> Homo sapiens

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<222> 266..586

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<221> sig_peptide

<222> 266..307

<223> Von Heijne matrix

score 4.534746808071

seq ILVTVPGVCPAQC/CW

<400> 109

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taaattaatg cctcttttta aatactaact tgttactact ttgtggctgt gaatggtatc      180
ttttattgaa ctgaggcagc ttttaaaaga ctgtcctgat catttagagc actcccattg      240
agggttaaatt agacttgaat ctgta atg att ctc gta act gtt cct ggt gtg      292
                               Met Ile Leu Val Thr Val Pro Gly Val
                               -10
tgt cca gca caa tgt tgc tgg gca gag cag agg ggc aga ggc tca ggt      340
Cys Pro Ala Gln Cys Cys Trp Ala Glu Gln Arg Gly Arg Gly Ser Gly
-5                               1                               5                               10
atg tac ttc att gac aag tgg gca agg cca tcc tgg gta cca cat tgg      388
Met Tyr Phe Ile Asp Lys Trp Ala Arg Pro Ser Trp Val Pro His Trp
                               15                               20                               25
ctt aat gat ctc ttc att gtg aag tcc ggc tac ctc gtt tgc ata aga      436
Leu Asn Asp Leu Phe Ile Val Lys Ser Gly Tyr Leu Val Cys Ile Arg

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<222> 59..745
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Met	Ser	Phe	Leu	Gln	Asp	Pro	Ser	Phe	Phe	Thr	Met	Gly	Met	Trp	Ser			
				-30							-25						-20	
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc																154		
Ile	Gly	Ala	Gly	Ala	Leu	Gly	Ala	Ala	Ala	Leu	Ala	Leu	Leu	Leu	Ala			
				-15							-10						-5	
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac																202		
Asn	Thr	Asp	Val	Phe	Leu	Ser	Lys	Pro	Gln	Lys	Ala	Ala	Leu	Glu	Tyr			
		1				5						10						
ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc																250		
Leu	Glu	Asp	Ile	Asp	Leu	Lys	Thr	Leu	Glu	Lys	Glu	Pro	Arg	Thr	Phe			
15					20								25		30			
aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg																298		
Lys	Ala	Lys	Glu	Leu	Trp	Glu	Lys	Asn	Gly	Ala	Val	Ile	Met	Ala	Val			
				35							40		45					
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc																346		
Arg	Arg	Pro	Gly	Cys	Phe	Leu	Cys	Arg	Glu	Glu	Ala	Ala	Asp	Leu	Ser			
			50								55		60					
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg																394		
Ser	Leu	Lys	Ser	Met	Leu	Asp	Gln	Leu	Gly	Val	Pro	Leu	Tyr	Ala	Val			
				65							70		75					
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc																442		
Val	Lys	Glu	His	Ile	Arg	Thr	Glu	Val	Lys	Asp	Phe	Gln	Pro	Tyr	Phe			
80					85							90						

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aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa      490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
95                               100                               105                               110
agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac      538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
                               115                               120                               125
aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga      586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
                               130                               135                               140
gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga aag cag      634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln
                               145                               150                               155
ggc att ctt ctt gag cac cga gaa aaa gaa ttt gga gac aaa gta aac      682
Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn
                               160                               165                               170
cta ctt tct gtt ctg gaa gct gct aag atg atc aaa cca cag act ttg      730
Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu
175                               180                               185                               190
gcc tca gag aaa aaa tgattgtgtg aaactgccca gctcagggat aaccagggac      785
Ala Ser Glu Lys Lys
                               195
attcacctgt gttcatggga tgtattgttt ccactcgtgt ccctaaggag tgagaaaccc      845
atttatactc tactctcagt atggattatt aatgtatttt aatattctgt ttaggccac      905
taaggcaaaa tagcccaaaa acaagactga caaaaatctg aaaaactaat gaggattatt      965
aagctaaaaac ctgggaaata ggaggtttta aattgactgc caggctgggt gcagtggctc     1025
acacctgtaa tcccagcact ttgggaggcc aaggtgagca agtcacttga ggtcgggagt     1085
tcgagaccag cctgagcaac atggcgaaac cccgtctcta ctaaaaatac aaaaatcacc     1145
cgggtgtggt ggcaggcacc tgtagtccca gctaccgggg aggctgaggc aggagaaatca     1205
cttgaacctg ggaggtggag gttgcggtga gctgagatca caccactgta ttccagcctg     1265
ggtgactgag actctaacta aaaaaaaaaa aaaaaa      1301

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<222> 59..160
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      seq LGAAALALLLANT/DV

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atg tct ttc ctc cag gac cca agt ttc ttc acc atg ggg atg tgg tcc      106
Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
                               -30                               -25                               -20
att ggt gca gga gcc ctg ggg gct gct gcc ttg gca ttg ctg ctt gcc      154
Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Ala
                               -15                               -10                               -5
aac aca gac gtg ttt ctg tcc aag ccc cag aaa gcg gcc ctg gag tac      202
Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
      1                               5                               10

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ctg gag gat ata gac ctg aaa aca ctg gag aag gaa cca agg act ttc      250
Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
15                20                25                30
aaa gca aag gag cta tgg gaa aaa aat gga gct gtg att atg gcc gtg      298
Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
35                40                45
cgg agg cca ggc tgt ttc ctc tgt cga gag gaa gct gcg gat ctg tcc      346
Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
50                55                60
tcc ctg aaa agc atg ttg gac cag ctg ggc gtc ccc ctc tat gca gtg      394
Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
65                70                75
gta aag gag cac atc agg act gaa gtg aag gat ttc cag cct tat ttc      442
Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
80                85                90
aaa gga gaa atc ttc ctg gat gaa aag aaa aag ttc tat ggt cca caa      490
Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
95                100                105                110
agg cgg aag atg atg ttt atg gga ttt atc cgt ctg gga gtg tgg tac      538
Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
115                120                125
aac ttc ttc cga gcc tgg aac gga ggc ttc tct gga aac ctg gaa gga      586
Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
130                135                140
gaa ggc ttc atc ctt ggg gga gtt ttc gtg gtg gga tca gga agc agg      634
Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Ser Arg
145                150                155
gca ttc ttc ttg agc acc gag aaa aag aat ttg gag aca aag      676
Ala Phe Phe Leu Ser Thr Glu Lys Lys Asn Leu Glu Thr Lys
160                165                170
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agaaaaaatg attgtgtgaa actgcccagc tcagggataa ccagggacat tcacctgtgt      796
tcatgggatg tattgtttcc actcgtgtcc ctaaggagtg agaaacccat ttatactcta      856
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caggcacctg tagtcccagc taccggggag gctgaggcag gagaatcact tgaacctggg     1216
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 <222> 15..146
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 score 12.2610572403264
 seq PLFLLLLLSVTA/DI

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Gly Arg Arg Cys Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly
                -30                                -25                                -20
ccc act aca cct ctc ttt ctt ctt ttg ttg ttg ggg tct gtg act gcg      146
Pro Thr Thr Pro Leu Phe Leu Leu Leu Leu Leu Gly Ser Val Thr Ala
                -15                                -10                                -5
gat ata act gac ggc aac att gaa cat ctc aag cgg gag cat tcg ctc      194
Asp Ile Thr Asp Gly Asn Ile Glu His Leu Lys Arg Glu His Ser Leu
1           5           10           15
att aag ccc tac caa ggg gtc ggt tcc agc tcc ccc tct ggg act tcc      242
Ile Lys Pro Tyr Gln Gly Val Gly Ser Ser Ser Pro Ser Gly Thr Ser
                20           25           30
agg gca gca cta tgc tca cga gcc agt acg tac gtc tgacccctga      288
Arg Ala Ala Leu Cys Ser Arg Ala Ser Thr Tyr Val
                35           40
cgagcgcagc aaagaggggt ctatctggaa ccaccagccg tgccttctca aagactggga      348
aatgcacgtc cacttcaaag tccacggcac agggaagaag aacctccatg gagacggcat      408
cgcccttggtg tacacccggg accgcctcgt gccagggcct gtgtttggaa gcaaagataa      468
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gaacactgga ggggtccccg gaccacactg ggggtgggtc ctgaggacgt ggggaagtga      1428
ttttgttttg tgggtgtggt cagctgtggc gacggataag gcctgaactg gaaacccagg      1488
ccttctctgt gccctgagc tgcctctga gacagatgct caagtgaggc tgcaggcgcg      1548
gtgtgggtggg gccgagtggt accgtttgct aaataaagtg aaatacccaa caaaaaaaaa      1608
aaaaaaaaa

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<210> 113
<211> 1634
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 167..619
<220>
<221> sig_peptide
<222> 167..262
<223> Von Heijne matrix
score 6.8501239662158
seq LLSSCGLPPSTAS/AV

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<400> 113
gtactttccga gagagattaa agattcaatg gaactctgcg tctctcatct ggaacccagg      60
acacagaaca agggagggaa gaaaagctca gccttaaaaca tagcaagggtg aaacctttgt      120
cctggggaat agtctggccc gctccttgga accacactca gactca atg gac tct      175
                                   Met Asp Ser
                                   -30
gcc tca aat ccc acc aac ctt gtc agc acc tcc caa agg cac cgg ccc      223
Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg His Arg Pro
                                   -25
                                   -20
                                   -15
ttg ctt tca tcc tgt ggc ctc cca cca agc act gcc tca gct gtg cgc      271
Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser Ala Val Arg
                                   -10
                                   -5
                                   1
agg cta tgc tcc agg gga gtg tta aaa gga tca aat gaa aga agg gat      319
Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu Arg Arg Asp
                                   5
                                   10
                                   15
atg gaa tca ttt tgg aaa cta aat cgt tcc cca ggg tcg gac cga tac      367
Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser Asp Arg Tyr
                                   20
                                   25
                                   30
                                   35
ctg gag agc cgc gat gcc tct cga ctg agt ggc cgg gac ccc tcc tca      415
Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp Pro Ser Ser
                                   40
                                   45
                                   50
tgg aca gtc gag gat gtg atg cag ttt gtc cgg gaa gct gat cct cag      463
Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala Asp Pro Gln
                                   55
                                   60
                                   65
ctt gga ccc cac gct gac ctg ttt cgc aaa cac gag atc gat ggc aag      511
Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile Asp Gly Lys
                                   70
                                   75
                                   80
gcc ctg ctg ctg ctg cgc agt gac atg atg atg aag tac atg ggc ctg      559
Ala Leu Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr Met Gly Leu
                                   85
                                   90
                                   95
aag ctg ggg cct gca ctc aag ctc tcc tac cac att gac cgg ctg aag      607
Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp Arg Leu Lys
                                   100
                                   105
                                   110
                                   115
cag ggc aag ttc tgaaccagga gaggcagcct agacaaccaa gtggcagcag      659
Gln Gly Lys Phe
gtgggggcat tcttctagga atgaggggca tcagcccacc ccaggcacct cagtgggggtt      719
ccggggccacc tcaggactcc aagaggctgt gtggagccac cactcctagc cacagctgcc      779
atgataagtc cttccatgaa ggactgagga gggagagtgg ggggtccaggg ctggtgctgc      839
tcttccctca gctctgccgg ggctctaagg tccctctatt tatttctcaa ccttggtctg      899
cctctcacca ggagttagg ctgaatgcct tccacgtgat ggaggaaaag gccaactctg      959
tcctggtctt gctgtggcac cccatcgccc cacagctcgt accttctcac cagattcccc      1019
tgaatccaaa ctsgtgggtgc aaacctctac cttttttaca aaaagatctt attgttaatt      1079
tattgtttct ggcacttggg caaacctgtt agttaatact cctcccccac actagacact      1139
gggttttcagg aggagggaga ctgccttgcct ttggtcccca gagaggccct ctgcagatag      1199
gcggtggcccc tcttcagagg aactaccctt agggcacttt ctctttgagg tggagagacc      1259
cataaagcct tgaccacatc actccatatg gggaggagaa ggatccctgt caccttctcc      1319
tctcttcacg gggccctttt gcagccctag gcctcatctg tgggaaggga gtcctgtgct      1379
tatactgccc ccaccacagc tccttgccct ggccagaact gctgtcgaag aaaatcaggc      1439
cggaaggcca agaaggcgct aaggggggatg ggagggcagg ttttccaggc tggagtcggt      1499
tccacccact cgcctgtcca caggcttctt tgtaagcaag tcagcagcac agctactcac      1559
gctgccatct ggacttattt tatgtcaatc tgtttataaa taaaaaccaa tataggtaaa      1619
aaaaaaaaaa aaaaaa      1634

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<210> 114
 <211> 693
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 223..417

<220>
 <221> sig_peptide
 <222> 223..270
 <223> Von Heijne matrix
 score 4.19788230215007
 seq LACVRESTSVAWA/CK

<400> 114
 ttaggggggcc tgtcaccag cacgtgcatc gggggctgtc ccgggggtca ggggagggag 60
 gccagcgggc mgtgtcgggg tccgccccga ccccatccac gaccccgact cctatccgat 120
 cctatccccg gccccgctcg ggcctttccc cttgcgcctt ggctcggtcg gctcgacgag 180
 cagtaagttc gtacccgccc tccgaagccg ggcgtgcatg gg atg gca gag ttg 234
 Met Ala Glu Leu
 -15
 gcg tgc gtg cgt gag tcc acc agt gtg gca tgg gca tgt aag gtg cgc 282
 Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala Cys Lys Val Arg
 -10 -5 1
 gga ggg act gca cct tct cca tca ggt gca gaa ggc cac gtc atg ctg 330
 Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly His Val Met Leu
 5 10 15 20
 aac aag agc cga gaa gta gaa tcg cca gtg tca agc cgt cca cgt tgt 378
 Asn Lys Ser Arg Glu Val Glu Ser Pro Val Ser Ser Arg Pro Arg Cys
 25 30 35
 ggg atg ccc act gtt ccc cca gga tca ctc aag acc ctg tgacttgtgg 427
 Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr Leu
 40 45
 tcaactgatga gtggaccaag tgaagtccac aagatggctg ctgtggctcc aggcacacg 487
 tccacatgca aatccatcca gaggcaggaa ctgggaatag gcttggaggt ggccaggaca 547
 gcaagtgggc tgtctgtata aacctccccct ccacttgga aggaaaatca ccccccaagt 607
 cgattttctg tccatcttat tgatcagaga gcgttataaa ttcaccatt aaataatctg 667
 gacaaggga aaaaaaaaaa aaaaaa 693

<210> 115
 <211> 784
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 166..732

<220>
 <221> sig_peptide
 <222> 166..237
 <223> Von Heijne matrix
 score 6.60662787180923
 seq KMVHLLVLSGAWG/MQ

<400> 115
 attattggtt gggggaaacc cacgagggga cgcggccgag gagggctcgt gtccaccggg 60
 gggcgtagga gtgaggtacc agattcagcc catttgccc cgacgcctct gttctcgga 120
 tccgggtgct gcggattgag gtcccggttc ctaacggact gcaag atg gag gaa ggc 177
 Met Glu Glu Gly

```

ggg aac cta gga ggc ctg att aag atg gtc cat cta ctg gtc ttg tca 225
Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu Leu Val Leu Ser
-20 -15 -10 -5
ggg gcc tgg ggc atg caa atg tgg gtg acc ttc gtc tca ggc ttc ctg 273
Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val Ser Gly Phe Leu
1 5 10
ctt ttc cga agc ctt ccc cga cat acc ttc gga cta gtg cag agc aaa 321
Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys
15 20 25
ctc ttc ccc ttc tac ttc cac atc tcc atg ggc tgt gsc ttc atc aac 369
Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys Xaa Phe Ile Asn
30 35 40
ctc tgc atc ttg gct tca cag cat gct tgg gct cag ctc aca ttc tgg 417
Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp
45 50 55 60
gag gcc agc cag ctt tac ctg ctg ttc ctg agc ctt acg ctg gcc act 465
Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr
65 70 75
gtc aac gcc cgc tgg ctg gaa ccc cgc acc aca gct gcc atg tgg gcc 513
Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala
80 85 90
ctg caa acc gtg gag aag gag cga ggc ctg ggt ggg gag gta cca ggc 561
Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly
95 100 105
agc cac cag ggt ccc gat ccc tac cgc cag ctg cga gag aag gac ccc 609
Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro
110 115 120
aag tac agt gct ctc cgc cag aat ttc ttc cgc tac cat ggg ctg tcc 657
Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser
125 130 135 140
tct ctt tgc aat ctg ggc tgc gtc ctg agc aat ggg ctc tgt ctc gct 705
Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala
145 150 155
ggc ctt gcc ctg gaa ata agg agc ctc tagcatgggc cctgcatgct 752
Gly Leu Ala Leu Glu Ile Arg Ser Leu
160 165
aataaatgct tctccaaaaa aaaaaaaaaa aa 784

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<210> 116
 <211> 804
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 75..623

<220>
 <221> sig_peptide
 <222> 75..215
 <223> Von Heijne matrix
 score 8.34104221735598
 seq RLLLPCLVRMALC/AP

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<400> 116
agtacggtgg ccgacgggag tcagacgctg gggatgaatg aaggtgctgg gtgcaggatc 60
aacaaacagt aata atg act gaa tgt aca agt ctt cag ttt gtc agc cct 110
Met Thr Glu Cys Thr Ser Leu Gln Phe Val Ser Pro

```

```

-45 -40
ttt gct ttt gag gca atg cag aag gtg gat gtt gtt tgc ctg gca tct 158
Phe Ala Phe Glu Ala Met Gln Lys Val Asp Val Val Cys Leu Ala Ser
-35 -30 -25 -20
tta agt gat cca gaa tta aga ctt ctt ctg ccc tgt ttg gta cgg atg 206
Leu Ser Asp Pro Glu Leu Arg Leu Leu Leu Pro Cys Leu Val Arg Met
-15 -10 -5
gca ctt tgt gca cct gct gac cag agc caa agc tgg gct cag gat aag 254
Ala Leu Cys Ala Pro Ala Asp Gln Ser Gln Ser Trp Ala Gln Asp Lys
1 5 10
aaa ctc atc ctt cgc ctt ctt tct gga gtg gaa gct gtc aac tcc att 302
Lys Leu Ile Leu Arg Leu Leu Ser Gly Val Glu Ala Val Asn Ser Ile
15 20 25
gtt gca ttg ttg tcc gtg gac ttt cat gct tta gaa caa gat gcc agc 350
Val Ala Leu Leu Ser Val Asp Phe His Ala Leu Glu Gln Asp Ala Ser
30 35 40 45
aaa gaa cag cag ctt aga ccg agt ctt gcc ctg ttg ccc agg ctg gag 398
Lys Glu Gln Gln Leu Arg Pro Ser Leu Ala Leu Leu Pro Arg Leu Glu
50 55 60
tgc ggt ggc gtg atc tcg gct cac tgc aac ctc cac ctc ctg ggt tca 446
Cys Gly Gly Val Ile Ser Ala His Cys Asn Leu His Leu Leu Gly Ser
65 70 75
agt gat tct tct gcc tca gtc tcc cga gta gat ggg act aca ggc acg 494
Ser Asp Ser Ser Ala Ser Val Ser Arg Val Asp Gly Thr Thr Gly Thr
80 85 90
cgc cac cat gcc cgg ctt ttt tgt att att agt aga gac gag gtt tca 542
Arg His His Ala Arg Leu Phe Cys Ile Ile Ser Arg Asp Glu Val Ser
95 100 105
cca tat tgg cca ggc tgg tct cga act ccc aac ctt gtg atc cac ctg 590
Pro Tyr Trp Pro Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu
110 115 120 125
cct cag cct ccc aaa gta ctg gga tta ccg gcg tgagccactg tgccctggcct 643
Pro Gln Pro Pro Lys Val Leu Gly Leu Pro Ala
130 135
atgtggtgga gtattttatta tacgtaggat gtgaatccct gaaatacaca ggcaaactaa 703
atagcatttc agaagtaaca gaacatttta gaacacttta tacatccttt tatagcttat 763
ttcaataaaaa gataattttt atacaaaaaa aaaaaaaaaa a 804

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<210> 117
 <211> 484
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..335

<220>
 <221> sig_peptide
 <222> 30..71
 <223> Von Heijne matrix
 score 4.49063834776683
 seq FLTALLWRGRIPG/RQ

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<400> 117
gcagagtctt gagcagcgcg gcaggcacc atg ttc ctg act gcg ctc ctc tgg 53
Met Phe Leu Thr Ala Leu Leu Trp
-10

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cgc ggc cgc att ccc ggc cgt cag tgg atc ggg aag cac cgg cgg ccg      101
Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg Arg Pro
-5      1      5      10
cgg ttc gtg tgc ttg cgc gcc aag cag aac atg atc cgc cgc ctg gag      149
Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg Leu Glu
15      20      25
atc gag gcg gag aac cat tac tgg ctg agc atg ccc tac atg acc cgg      197
Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met Thr Arg
30      35      40
gag cag gag cgc ggc cac gcc gcg gtg cgc agg agg gag gcc ttc gag      245
Glu Gln Glu Arg Gly His Ala Ala Val Arg Arg Arg Glu Ala Phe Glu
45      50      55
gcc ata aag gcg gcc gcc act tcc aag ttc ccc ccg cat aga ttc att      293
Ala Ile Lys Ala Ala Ala Thr Ser Lys Phe Pro Pro His Arg Phe Ile
60      65      70
gcg gac cag ctc gac cat ctc aat gtc acc aag aaa tgg tcc      335
Ala Asp Gln Leu Asp His Leu Asn Val Thr Lys Lys Trp Ser
75      80      85
taatcctgag tcgtcaccct tggattttat ggatcacgga gctgaccatc tttacctggt      395
cctggaaactg aaaaaactgta gcttgtgtga aaatgagcct ttggaccagt ctttattaaa      455
acaaacaaac acaaaaaaaaa aaaaaaaaaa      484

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<210> 118
 <211> 985
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 21...752

<220>
 <221> sig_peptide
 <222> 21...107
 <223> Von Heijne matrix
 score 3.61056351168286
 seq FPLYLLNFLGLWS/WI

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<400> 118
gtttttttcc cttctgagca atg gag ctt acc atc ttt atc ctg aga ctg gcc      53
Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala
-25      -20
att tac atc ctg aca ttt ccc ttg tac ctg ctg aac ttt ctg ggc ttg      101
Ile Tyr Ile Leu Thr Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu
-15      -10      -5
tgg agc tgg ata tgc aaa aaa tgg ttc ccc tac ttc ttg gtg agg ttc      149
Trp Ser Trp Ile Cys Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe
1      5      10
act gtg ata tac aac gaa cag atg gca agc aag aag cgg gag ctc ttc      197
Thr Val Ile Tyr Asn Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe
15      20      25      30
agt aac ctg cag gag ttt gcg gcc ccc tcc ggg aaa ctc tcc ctg ctg      245
Ser Asn Leu Gln Glu Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu
35      40      45
gaa gtg ggc tgt ggc acg ggg gcc aac ttc aag ttc tac cca cct ggg      293
Glu Val Gly Cys Gly Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly
50      55      60
tgc agg gtg acc tgt att gac ccc aac ccc aac ttt gag aag ttt ttg      341

```

Cys	Arg	Val 65	Thr	Cys	Ile	Asp 70	Pro	Asn	Pro	Asn	Phe	Glu 75	Lys	Phe	Leu	
atc	aag	agc	att	gca	gag	aac	cga	cac	ctg	cag	ttt	gag	cgc	ttt	gtg	389
Ile	Lys	Ser	Ile	Ala	Glu	Asn	Arg	His	Leu	Gln	Phe	Glu	Arg	Phe	Val	
	80					85					90					
gta	gct	gcc	ggg	gag	aac	atg	cac	cag	gtg	gct	gat	ggc	tct	gtg	gat	437
Val	Ala	Ala	Gly	Glu	Asn	Met	His	Gln	Val	Ala	Asp	Gly	Ser	Val	Asp	
95					100						105				110	
gtg	gtg	gtc	tgc	acc	ctg	gtg	ctg	tgc	tct	gtg	aag	aac	cag	gag	cgg	485
Val	Val	Val	Cys	Thr	Leu	Val	Leu	Cys	Ser	Val	Lys	Asn	Gln	Glu	Arg	
				115					120					125		
att	ctc	cgc	gag	gtg	tgc	aga	gtg	ctg	aga	ccg	gga	ggg	gct	ttc	tat	533
Ile	Leu	Arg	Glu	Val	Cys	Arg	Val	Leu	Arg	Pro	Gly	Gly	Ala	Phe	Tyr	
			130					135					140			
ttc	atg	gag	cat	gtg	gca	gct	gag	tgt	tcg	act	tgg	aat	tac	ttc	tgg	581
Phe	Met	Glu	His	Val	Ala	Ala	Glu	Cys	Ser	Thr	Trp	Asn	Tyr	Phe	Trp	
		145					150					155				
caa	caa	gtc	ctg	gat	cct	gcc	tgg	cac	ctt	ctg	ttt	gat	ggg	tgc	aac	629
Gln	Gln	Val	Leu	Asp	Pro	Ala	Trp	His	Leu	Leu	Phe	Asp	Gly	Cys	Asn	
		160				165					170					
ctg	acc	aga	gag	agc	tgg	aag	gcc	ctg	gag	cgg	gcc	agc	ttc	tct	aag	677
Leu	Thr	Arg	Glu	Ser	Trp	Lys	Ala	Leu	Glu	Arg	Ala	Ser	Phe	Ser	Lys	
175					180					185					190	
ctg	aag	ctg	cag	cac	atc	cag	gcc	cca	ctg	tcc	tgg	gag	ttg	gtg	cgc	725
Leu	Lys	Leu	Gln	His	Ile	Gln	Ala	Pro	Leu	Ser	Trp	Glu	Leu	Val	Arg	
				195				200						205		
cct	cat	atc	tat	gga	tat	gct	gtg	aaa	tagt	gtgagc	tggcagttaa					772
Pro	His	Ile	Tyr	Gly	Tyr	Ala	Val	Lys								
		210					215									
gagctgaatg	gctcaaagaa		tttaaagctt		cagttttaca		tttaaaatgc		taggtgggtg							832
cctgtaatcc	caggtagctt		gaaggctgag		gcaggagaat		ctcttgaaacc		cagaaggcga							892
aggttgcagt	gaaccgagat		catggcattg		tactctagcc		tgggtgacaa		gagcaagact							952
ccgtctcaaa	aaaaaataaa		aaaaaaaaaa		aaa											981

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<210> 119
<211> 839
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 185..715
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<220>
<221> sig_peptide
<222> 185..253
<223> Von Heijne matrix
score 9.49395175807817
seq SLLFICFFGESFC/IC
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<400> 119
atatttttgc t gactggcaag gttatatgaa gtgctttttat tgaagcacca ttttaactaa      60
cagctcctgg tattttctgc ttcccttcgt agggaattta gttattttat tttattattt      120
agctaattta gctattttaa aatagctaaa ttttagctac ttttttttca attgacaaaag      180
aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc      229
      Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile
              -20                      -15                      -10
tgc ttc ttc ggg gag agt ttc tqc att tqt qat qqa act qtc tqg aca      277

```


Cys	Phe	Phe	Gly	Glu	Ser	Phe	Cys	Ile	Cys	Asp	Gly	Thr	Val	Trp	Thr		
			-5					1				5					
aag	ggt	gga	tgg	gag	att	ctt	cca	gaa	gaa	gta	cat	tat	tgg	aaa	ggt	325	
Lys	Val	Gly	Trp	Glu	Ile	Leu	Pro	Glu	Glu	Val	His	Tyr	Trp	Lys	Val		
	10					15					20						
aag	ggt	tct	cca	tct	cac	tgc	ctg	cct	tat	ctt	ctg	gat	aaa	cta	tgc	373	
Lys	Gly	Ser	Pro	Ser	His	Cys	Leu	Pro	Tyr	Leu	Leu	Asp	Lys	Leu	Cys		
25					30					35				40			
tgc	gac	ttt	gct	aac	atg	gat	ata	ttt	cag	ggg	tgt	tta	tat	ctc	att	421	
Cys	Asp	Phe	Ala	Asn	Met	Asp	Ile	Phe	Gln	Gly	Cys	Leu	Tyr	Leu	Ile		
				45					50					55			
tat	aat	tta	tta	caa	gct	gtc	ttc	ttc	gtc	tta	ttt	ggt	ttg	tct	gtg	469	
Tyr	Asn	Leu	Leu	Gln	Ala	Val	Phe	Phe	Val	Leu	Phe	Val	Leu	Ser	Val		
			60				65						70				
cat	tac	ctg	tgg	aag	aaa	tgg	aag	aaa	cac	caa	aaa	aag	ctg	aaa	aag	517	
His	Tyr	Leu	Trp	Lys	Lys	Trp	Lys	Lys	His	Gln	Lys	Lys	Leu	Lys	Lys		
		75					80					85					
caa	gcc	tcc	tta	gaa	aaa	cct	ggg	aag	gat	cta	gaa	agc	cca	ttg	atc	565	
Gln	Ala	Ser	Leu	Glu	Lys	Pro	Gly	Asn	Asp	Leu	Glu	Ser	Pro	Leu	Ile		
	90					95					100						
aac	aac	att	gac	caa	aca	ctc	cac	aga	gtg	gca	acc	aca	gca	tca	gtg	613	
Asn	Asn	Ile	Asp	Gln	Thr	Leu	His	Arg	Val	Ala	Thr	Thr	Ala	Ser	Val		
105					110					115					120		
ata	tac	aag	atc	tgg	gag	cac	agg	tct	cac	cat	cct	tcc	tct	aag	aaa	661	
Ile	Tyr	Lys	Ile	Trp	Glu	His	Arg	Ser	His	His	Pro	Ser	Ser	Lys	Lys		
				125					130					135			
att	aag	cac	tgc	aaa	tta	aag	aag	aag	agt	aaa	gaa	gaa	gga	gcc	aga	709	
Ile	Lys	His	Cys	Lys	Leu	Lys	Lys	Lys	Ser	Lys	Glu	Glu	Gly	Ala	Arg		
			140				145						150				
aga	tac	taaataaatg	catatgcaaa	tgtagcttac	tcaattatag	atatcacaaa										765	
Arg	Tyr																
agaaatctat	catctaagga	ttaaaaaattg	ttctttggaa	acctttataa	aaaaaaaaaga											825	
aaaaaaaaaaaa	aaaa															839	

<210> 120
 <211> 583
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 54..527

<220>
 <221> sig_peptide
 <222> 54..116
 <223> Von Heijne matrix
 score 6.80928714315144
 seq ALXSLNLAPPTVA/AP

<400> 120
 aacgtcatct aggagcaccg agcagcttgg ctaaaagtaa ggggtgctgtg ctg atg
 Met
 gcc ctg tgc gca ctg acc cgc gct ctg ccs tct ctg aac ctg gcg ccc
 Ala Leu Cys Ala Leu Thr Arg Ala Leu Pro Ser Leu Asn Leu Ala Pro
 -20 -15 -10 -5
 ccg acc gtc gcc gcc cct gcc ccg agt ctg ttc ccc gcc gcc cag atg
 Pro Thr Val Ala Ala Pro Ala Pro Ser Leu Phe Pro Ala Ala Gln Met
 152

				1				5				10				
atg	aac	aat	ggc	ctc	ctc	caa	cag	ccc	tct	gcc	ttg	atg	ttg	ctc	ccc	200
Met	Asn	Asn	Gly	Leu	Leu	Gln	Gln	Pro	Ser	Ala	Leu	Met	Leu	Leu	Pro	
				15		20				25						
tgc	cgc	cca	gtt	ctt	act	tct	gtg	gcc	ctt	aat	gcc	aac	ttt	gtg	tcc	248
Cys	Arg	Pro	Val	Leu	Thr	Ser	Val	Ala	Leu	Asn	Ala	Asn	Phe	Val	Ser	
				30		35				40						
tgg	aag	agt	cgt	acc	aag	tac	acc	att	aca	cca	gtg	aag	atg	agg	aag	296
Trp	Lys	Ser	Arg	Thr	Lys	Tyr	Thr	Ile	Thr	Pro	Val	Lys	Met	Arg	Lys	
				45		50				55				60		
tct	ggg	ggc	cga	gac	cac	aca	ggg	gct	gga	aac	gtg	cgt	aga	aca	gta	344
Ser	Gly	Gly	Arg	Asp	His	Thr	Gly	Ala	Gly	Asn	Val	Arg	Arg	Thr	Val	
				65		70				75						
ggc	cga	gta	tcc	aac	gtt	gat	cat	aac	aaa	cgg	gtc	att	ggc	aag	gca	392
Gly	Arg	Val	Ser	Asn	Val	Asp	His	Asn	Lys	Arg	Val	Ile	Gly	Lys	Ala	
				80		85				90						
ggg	cgc	aac	cgc	tgg	ctg	ggc	aag	agg	cct	aac	agt	ggg	cgg	tgg	cac	440
Gly	Arg	Asn	Arg	Trp	Leu	Gly	Lys	Arg	Pro	Asn	Ser	Gly	Arg	Trp	His	
				95		100				105						
cgc	aag	ggg	ggc	tgg	gct	ggc	cga	aag	att	cgg	cca	cta	ccc	ccc	atg	488
Arg	Lys	Gly	Gly	Trp	Ala	Gly	Arg	Lys	Ile	Arg	Pro	Leu	Pro	Pro	Met	
				110		115				120						
aag	agt	tac	gtg	aag	ctg	cct	tct	gct	tct	gcc	caa	agc	tgat	atc	cct	537
Lys	Ser	Tyr	Val	Lys	Leu	Pro	Ser	Ala	Ser	Ala	Gln	Ser				
				125		130				135						
gtactctaataaaaatgcccc cccccctca aaaaaaaaaa aaaaaa																583

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<210> 121
<211> 1024
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 129..686
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<220>
<221> sig_peptide
<222> 129..185
<223> Von Heijne matrix
      score 6.45239823575329
      seq  SVFLLMVNGQVES/AQ
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gcaacgccgg cgtctcttag caaccgcgcg cggcctaggt ggggtccccc ggcaccccca																	120
gacctgcc atg gcg acc gcg agt cct agc gtc ttt cta ctc atg gtc aac																	170
Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn																	
-15 -10																	
ggg cag gtg gag agc gcc cag ttt cca gag tat gat gac ctc tac tgc																	218
Gly Gln Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Leu Tyr Cys																	
-5 1 5 10																	
aag tac tgc ttt gtg tac ggc cag gac tgg gcc ccc aca gcg ggt ctg																	266
Lys Tyr Cys Phe Val Tyr Gly Gln Asp Trp Ala Pro Thr Ala Gly Leu																	
15 20 25																	
gag gag ggg atc tca cag atc aca tcc aag agc caa gat gtg cgg caa																	314
Glu Glu Gly Ile Ser Gln Ile Thr Ser Lys Ser Gln Asp Val Arg Gln																	
30 35 40																	

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gca ctg gtg tgg aac ttc ccc att gat gtc acc ttt aaa agc acc aac 362
Ala Leu Val Trp Asn Phe Pro Ile Asp Val Thr Phe Lys Ser Thr Asn
45 50 55
ccc tac ggc tgg cca cag atc gtg ctc agc gtg tat gga cca gat gtg 410
Pro Tyr Gly Trp Pro Gln Ile Val Leu Ser Val Tyr Gly Pro Asp Val
60 65 70 75
ttc ggg aac gat gtg gtt cga ggc tat ggg gcc gtg cac gtg ccc ttc 458
Phe Gly Asn Asp Val Val Arg Gly Tyr Gly Ala Val His Val Pro Phe
80 85 90
tca cct ggc cgg cac aaa agg acc atc ccc atg ttt gtc cca gaa tct 506
Ser Pro Gly Arg His Lys Arg Thr Ile Pro Met Phe Val Pro Glu Ser
95 100 105
acg tct aaa ctg cag aag ttt aca agc tgg ttc atg ggg cgg cgg ccc 554
Thr Ser Lys Leu Gln Lys Phe Thr Ser Trp Phe Met Gly Arg Arg Pro
110 115 120
gag tac aca gac ccc aag gtg gtg gct cag ggt gaa ggc cgg gaa gct 602
Glu Tyr Thr Asp Pro Lys Val Val Ala Gln Gly Glu Gly Arg Glu Ala
125 130 135
atc aca gct ccc cgg aaa gct gtc ttc tct gtc cat ggc ctc acc tca 650
Ile Thr Ala Pro Arg Lys Ala Val Phe Ser Val His Gly Leu Thr Ser
140 145 150 155
ccc agg gca ctg gcc ttg gtc cac atc aag ggg acc tgaagcttcc 696
Pro Arg Ala Leu Ala Leu Val His Ile Lys Gly Thr
160 165
ctgaagcctc tagcctgtgg tgtgcacgta caagcctcag gccccatttg tccagcctgt 756
cagcagctgg gaaataactaa gtcaccctct tctggttatg ttttaatttc caatttttct 816
caacattact gaaatgtcta aatgtggaaa agttgacatc attttacagt gaacaccaca 876
taccaccac ctagatttta ccattaccaa tttcctgttc cgtacttgta tattcacata 936
tatccaacta ttcattccctg cttcaatcca tcctattttt attgcatttc aaaataaact 996
gtgaaatcag gaaaaaaaaa aaaaaaaaaa 1024

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<210> 122
 <211> 760
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 165..614

<220>
 <221> sig_peptide
 <222> 165..305
 <223> Von Heijne matrix
 score 5.10820788278539
 seq ALGLALCSTKALS/VG

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<400> 122
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gcctctccag gcctcgaagg cttctcctgg gctgatgcga gctggggaac gggagggacg 120
gacgtgggag cgagaacgtc aactggagg cagctgggtg cacg atg ggg gac aga 176
Met Gly Asp Arg
-45
gtg aaa ggt agc aag tca aga gcc ttc gtg tca cca tgg cca cac acc 224
Val Lys Gly Ser Lys Ser Arg Ala Phe Val Ser Pro Trp Pro His Thr
-40 -35 -30
ccg atg gct tcc ggc ttg agg gac ccc tgg ctg cag ccc aca gcc ctg 272
Pro Met Ala Ser Gly Leu Arg Asp Pro Trp Leu Gln Pro Thr Ala Leu

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-25          -20          -15
ggc ctt gca ctg tgc tct acg aag gcc ctg tcc gtg ggc tct gcc cct 320
Gly Leu Ala Leu Cys Ser Thr Lys Ala Leu Ser Val Gly Ser Ala Pro
-10          -5          1          5
ttg ccc ccg cga aat tcc aac acc atg gcg gcg gct gcc ctg gct gcc 368
Leu Pro Pro Arg Asn Ser Asn Thr Met Ala Ala Ala Ala Leu Ala Ala
10          15          20
ccc agc ctg ggc ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc 416
Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr
25          30          35
agc ctc acg gac atg cac gtg gtg gat gta gag ctg agc gga ccc cgg 464
Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg
40          45          50
ggc ccc acg ggc cga agc ttt gct gtg cac acc cgc aga gag aac cct 512
Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro
55          60          65
gcc gag cca ggc gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg 560
Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp
70          75          80          85
cgg agc ctc ctg gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat 608
Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His
90          95          100
ctc tgc tgagaagcct cctccctccc gagacaagat catctgcctg gcctctcacc 664
Leu Cys
accaccatcc caccctgcc ctgccccact tccccagggt ctccttctg actcagtaaa 724
gatcaccgct gcctccctca aaaaaaaaaa aaaaaa 760

<210> 123
<211> 594
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 192..476

<220>
<221> sig_peptide
<222> 192..326
<223> Von Heijne matrix
      score 6.60884760057354
      seq FILLLLLSGPAEM/SA

<400> 123
actttttattg aaaaagacta cagcaaatca tactgaggtg aatgaagaca gtgaaatgaa 60
ggagaaggca ggctcctcttt atgttttcgc agctgggttca aggggttttg ggttttctat 120
ctaggttaaa gattgcgtaa tacacagctg gagccataga cattaatgca tgtttatcac 180
acgcaacaac g atg ctg cat cat gtg att aca gct ggg cct gtg ctg ctt 230
      Met Leu His His Val Ile Thr Ala Gly Pro Val Leu Leu
-45          -40          -35
cta cac ctc cct cgc cct gac act tcc acc agg ttg ctc ctc acc tcc 278
Leu His Leu Pro Arg Pro Asp Thr Ser Thr Arg Leu Leu Leu Thr Ser
-30          -25          -20
gtc tct gct ttt atc ctc tta ctg ctc ctt tca gga cca gca gaa atg 326
Val Ser Ala Phe Ile Leu Leu Leu Leu Ser Gly Pro Ala Glu Met
-15          -10          -5
tca gct tcc cag gaa tcc ttc cct gga tct ctg cag caa gaa ata gct 374
Ser Ala Ser Gln Glu Ser Phe Pro Gly Ser Leu Gln Gln Glu Ile Ala

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1           5           10           15
tct ctg atc act gta gca ctt ggt tct tta ata tct tta tct tgc tct 422
Ser Leu Ile Thr Val Ala Leu Gly Ser Leu Ile Ser Leu Ser Cys Ser
          20          25          30
acc ttg tta tat ttt tct tgt gaa ctt aaa att ccc tgt gag gac gta 470
Thr Leu Leu Tyr Phe Ser Cys Glu Leu Lys Ile Pro Cys Glu Asp Val
          35          40          45
aac ctt tgaaggtatg tctcatatct ctgaacctct ttaaaatgcc tagcatccct 526
Asn Leu
          50
gtgtgggtgc caattgcttg tgtattgaat taaattgtga ttgttaactt gaaaaaaaaa 586
aaaaaaaaa 594

<210> 124
<211> 559
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..297

<220>
<221> sig_peptide
<222> 16..93
<223> Von Heijne matrix
      score 6.65836819891491
      seq FCGSACLLAVIRA/FF

<400> 124
ttacacaggg gataa atg gca gca atc gag att gaa gtc aag cct aac cag 51
      Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln
          -25          -20          -15
ggc ttt tgc ggg agc gca tgc ctt ttg gct gta att cgt gca ttt ttt 99
Gly Phe Cys Gly Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe
          -10          -5          1
ttt aag aaa aac gcc tgc ctt ctg cgt gag att ctc cag agc aaa ctg 147
Phe Lys Lys Asn Ala Cys Leu Leu Arg Glu Ile Leu Gln Ser Lys Leu
          5          10          15
ggc ggc atg ggc cct gtg gtc ttt tcg tac aga ggg ctt cct ctt tgg 195
Gly Gly Met Gly Pro Val Val Phe Ser Tyr Arg Gly Leu Pro Leu Trp
          20          25          30
ctc ttt gcc tgg ttg ttt cca aga tgt act gtg cct ctt act ttc ggt 243
Leu Phe Ala Trp Leu Phe Pro Arg Cys Thr Val Pro Leu Thr Phe Gly
          35          40          45          50
ttt gaa aac atg agg ggg ttg ggc gtg gta gct tac gcc tgt aat ccc 291
Phe Glu Asn Met Arg Gly Leu Gly Val Ala Tyr Ala Cys Asn Pro
          55          60          65
agc act tagggaggcc gaggcgggag gatggccttga ggtccgtagt tgagaccagc 347
Ser Thr
ctggccaaca tgggtgaagcc tgggtctctac aaaaaaataa taacaaaaat tagccgggtg 407
tgggtggctcg tgcctgtggt ccagctgct cccgtggctg aggcgggagg atctcttgag 467
cttaggcttt tgagctatca tggcgccagt gcactccagc gtgggcaaca gagcgagacc 527
ctgtctctca aaaacaaaaa aaaaaaaaaa aa 559

<210> 125
<211> 744
<212> DNA

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<213> Homo sapiens

<220>

<221> CDS

<222> 216..635

<220>

<221> sig_peptide

<222> 216..335

<223> Von Heijne matrix

score 4.38054120608596

seq ITLVSAAPGKVIC/EM

<400> 125

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gctcgccctga ctcccgccct cttgcgctcc taggggcgga gaaggggtgcg ggctcttcgc 120
cctttgtgtc ctctctcttt cactaacttc tggactttcc agctcttcgc aagttcgttc 180
ttgcgcaaag cccaaaggct ggaaaaccgt ccacg atg acc agc atg act cag 233
Met Thr Ser Met Thr Gln
-40 -35
tct ctg cgg gag gtg ata aag gcc atg acc aag gct cgc aat ttt gag 281
Ser Leu Arg Glu Val Ile Lys Ala Met Thr Lys Ala Arg Asn Phe Glu
-30 -25 -20
aga gtt ttg gga aag att act ctt gtc tct gct gct cct ggg aaa gtg 329
Arg Val Leu Gly Lys Ile Thr Leu Val Ser Ala Ala Pro Gly Lys Val
-15 -10 -5
att tgt gaa atg aaa gta gaa gaa gag cat acc aat gca ata ggc act 377
Ile Cys Glu Met Lys Val Glu Glu Glu His Thr Asn Ala Ile Gly Thr
1 5 10
ctc cac ggc ggt ttg aca gcc acg tta gta gat aac ata tca aca atg 425
Leu His Gly Gly Leu Thr Ala Thr Leu Val Asp Asn Ile Ser Thr Met
15 20 25 30
gct ctg cta tgc acg gaa agg gga gca ccc gga gtc agt gtc gat atg 473
Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro Gly Val Ser Val Asp Met
35 40 45
aac ata acg tac atg tca cct gca aaa tta gga gaa gat ata gtg att 521
Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu Gly Glu Asp Ile Val Ile
50 55 60
aca gca cat gtt ctg aag caa gga aaa aca ctt gca ttt acc tct gtg 569
Thr Ala His Val Leu Lys Gln Gly Lys Thr Leu Ala Phe Thr Ser Val
65 70 75
gat ctg acc aac aag gcc aca gga aaa tta ata gca caa gga aga cac 617
Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu Ile Ala Gln Gly Arg His
80 85 90
aca aaa cac ctg gga aac tgagagaaca gcagaatgac ctaaagaaac 665
Thr Lys His Leu Gly Asn
95 100
ccaacaatga atatcaagta tagatttgac tcaacaatt gtaatttttg aaataaacta 725
gcaaaaaaaaa aaaaaaaaaa 744

<210> 126

<211> 824

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 164..280

<220>
 <221> sig_peptide
 <222> 164..268
 <223> Von Heijne matrix
 score 5.73290676305402
 seq TLPLCPVTSPVWG/WS

<400> 126
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 ccaggagacc tacacagtgg cccacgagga gaatgtccgc tttgtgtccg aaggtagcga 120
 gcggggccag aggggtgcggc ataggctgct gggtcgcaaa acc atg gac ccg gga 175
 Met Asp Pro Gly
 -35
 tgg ccc cac ttc aag ctg acc cac agc cgc tgc atg gct gtg ctt ttc 223
 Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met Ala Val Leu Phe
 -30 -25 -20
 ctt ggc act ctg ccc ttg tgt cct gtg acc agc cct gtg tgg ggc tgg 271
 Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro Val Trp Gly Trp
 -15 -10 -5 1
 agt cca ggg tgaccatcag gccctgggtg ggcgatgggg tgccctgggac 320
 Ser Pro Gly
 ctggctcagc ccgactgccc tcctcccaca gcctggcagc aggtgcaaca gcagctggat 380
 ggtggcccg cccgtgaggg cgggccaagg cctgtgcagt acgtggagag gacccccaat 440
 ccccggtgc agaactttgt gccattttac cttagacgagt ggtgggcgca gcagttcctg 500
 gcgagaatca ccagctgttc ctagtggctg ctgggagggg gcgctgctac acggccgacc 560
 tgctgccagg agagaagcat ggcgccctgc ccacccactg cgcctggctg ggtgccggcc 620
 acacctgaag tgccagcatt tggacttttg cacctttttt tcccttggcc cggctgtccc 680
 aaccaagctg ccattggccaa gggccgaacc cgtctgacct cagccctgct cactgtgccc 740
 agggaccagc gaccagcccc tggggctggc agggaggagc tccaggctaa taaagtggag 800
 aaactgtcaa aaaaaaaaaa aaaa 824

<210> 127
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 68..301

<220>
 <221> sig_peptide
 <222> 68..190
 <223> Von Heijne matrix
 score 4.68908216483476
 seq AYLLYILLTGALQ/FG

<400> 127
 acatccggtg tggtcgacgg gtccctccaag agtttggggc gcggaccgga gtaccttgcg 60
 tgcagtt atg tcg gcg tcg gta gtg tct gtc att tcg cgg ttc tta gaa 109
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu
 -40 -35 -30
 gag tac ttg agc tcc act ccg cag cgt ctg aag ttg ctg gac gcg tac 157
 Glu Tyr Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr
 -25 -20 -15
 ctg ctg tat ata ctg ctg acc ggg gcg ctg cag ttc ggt tac tgt ctc 205
 Leu Leu Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu

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      -10      -5      1      5
ctc gtg ggg acc ttc ccc ttc aac tct ttt ctc tcg ggc ttc atc tct 253
Leu Val Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser
      10      15      20
tgt gtg ggg agt ttc atc cta gcg ggt tca ctc ttt gaa ttt cct gga 301
Cys Val Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly
      25      30      35
taagagttct ggagatggca gcttattgga cacatggatt ttcttcagat ttgcacttac 361
tgctagctct gctttttatg caggagaaaa gccagagatt cactgtgtgt cagaacaact 421
ttctaacaaa catttattaa tccagcctct gcctttcatt aaatgtaacc ttttgccttc 481
caaattaaag aactccatgc cactcctcaa aaaaaaaaaa aaaaa 526

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<210> 128
 <211> 618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 179..427

<220>
 <221> sig_peptide
 <222> 179..298
 <223> Von Heijne matrix
 score 7.72883276007822
 seq CLVVVTMATLSLA/RP

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<400> 128
aagcgaagag atgggtctgc actttggagg agccggacac tgttgacttt cctgatgtga 60
aatctaccca ggaacaaaac accagtgact gcagcagcag cggcagcgcc tcggttcctg 120
agccaccgcg aggtgaagg cattgcgcgt agtccatgcc cgtagaggaa gtgtgcag 178
atg gga tta acg tcc aca tgg aga tat gga aga gga ccg ggg att ggt 226
Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly
-40      -35      -30      -25
acc gta acc atg gtc agc tgg ggt cgt ttc atc tgc ctg gtc gtg gtc 274
Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val
      -20      -15      -10
acc atg gca acc ttg tcc ctg gcc cgg ccc tcc ttc agt tta gtt gag 322
Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu
      -5      1      5
gat acc aca tta gag cca gaa gat gcc atc tca tcc gga gat gat gag 370
Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu
      10      15      20
gat gac acc gat ggt gcg gaa gat ttt gtc agt gag aac agt aac aac 418
Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn
      25      30      35      40
aag agt aag taactgccc gctccgatgg tccccgagag aggagcatgg 467
Lys Ser Lys
agggaaagttc tgccgtgtcac ctgtcttctt gtgcactctt ctgcgccatg ctgtgtcccg 527
cggcccttgc ctttccccgc tgtgtctact ttcttgactt tcaaacctga gaataaacca 587
gtgttgctgc acataaaaaa aaaaaaaaaa a 618

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<210> 129
 <211> 776
 <212> DNA
 <213> Homo sapiens

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Met Ala Ala Pro Val Arg Arg Thr Leu Leu Gly Val Ala Gly	
-40 -35 -30	
ggt tgg cgg cgg ttc gag agg ctc tgg gcc ggc agt cta agc tct cgc	98
Gly Trp Arg Arg Phe Glu Arg Leu Trp Ala Gly Ser Leu Ser Ser Arg	
-25 -20 -15	
agc ctg gct ctt gca gcc gca ccc tca agc aac gga tcc cca tgg cgc	146
Ser Leu Ala Leu Ala Ala Ala Pro Ser Ser Asn Gly Ser Pro Trp Arg	
-10 -5 1	
ttg ttg ggc gcg ttg tgc ctg cag cgg cca cct gta gtc tcc aag ccg	194
Leu Leu Gly Ala Leu Cys Leu Gln Arg Pro Val Val Ser Lys Pro	
5 10 15 20	
ttg acc cca ttg cag gaa gag atg gcg tct cta ctg cag cag att gag	242
Leu Thr Pro Leu Gln Glu Glu Met Ala Ser Leu Leu Gln Gln Ile Glu	
25 30 35	
ata gag aga agc ctg tat tca gac cac gag ctt cgt gct ctg gat gaa	290
Ile Glu Arg Ser Leu Tyr Ser Asp His Glu Leu Arg Ala Leu Asp Glu	
40 45 50	
aac cag cga ctg gca aag aag aaa gct gac ctt cat gat gaa gaa gat	338
Asn Gln Arg Leu Ala Lys Lys Lys Ala Asp Leu His Asp Glu Glu Asp	
55 60 65	
gaa cag gat ata ttg ctg gcg caa gat ttg gaa gat atg tgg gag cag	386
Glu Gln Asp Ile Leu Leu Ala Gln Asp Leu Glu Asp Met Trp Glu Gln	
70 75 80	
aaa ttt cta cag ttc aaa ctt gga gct cgc ata aca gaa gct gat gaa	434
Lys Phe Leu Gln Phe Lys Leu Gly Ala Arg Ile Thr Glu Ala Asp Glu	
85 90 95 100	
aag aat gac cga aca tcc ctg aac agg aac cta gac agg aac ctt gtc	482
Lys Asn Asp Arg Thr Ser Leu Asn Arg Asn Leu Asp Arg Asn Leu Val	
105 110 115	
ctg tta gtc aga gag aag ttt gga gac cag gat gtt tgg ata ctg ccc	530
Leu Leu Val Arg Glu Lys Phe Gly Asp Gln Asp Val Trp Ile Leu Pro	
120 125 130	
cag gca gag tgg cag cct ggg gag acc ctt cga gga aca gct gaa cga	578
Gln Ala Glu Trp Gln Pro Gly Glu Thr Leu Arg Gly Thr Ala Glu Arg	
135 140 145	
acc ctg gcc aca ctc tca gaa aac aac atg gaa gcc aag ttc cta gga	626
Thr Leu Ala Thr Leu Ser Glu Asn Asn Met Glu Ala Lys Phe Leu Gly	
150 155 160	
aat gca ccc tgt ggg cac tac aca ttc aag ttc ccc cag gca atg cgg	674
Asn Ala Pro Cys Gly His Tyr Thr Phe Lys Phe Pro Gln Ala Met Arg	
165 170 175 180	
aca gag agt aac ctc gga gcc aag gtg ttc ttc ttc aaa gca ctg cta	722
Thr Glu Ser Asn Leu Gly Ala Lys Val Phe Phe Phe Lys Ala Leu Leu	
185 190 195	
tta act gga gac ttt tcc cag gct ggg aat aag ggc cat cat gtg tgg	770
Leu Thr Gly Asp Phe Ser Gln Ala Gly Asn Lys Gly His His Val Trp	
200 205 210	
gtc att aag gat gag ctg ggt gac tat ttg aaa cca aaa tac ctg gcc	818
Val Ile Lys Asp Glu Leu Gly Asp Tyr Leu Lys Pro Lys Tyr Leu Ala	
215 220 225	
caa gtt agg agg ttt gtt tca gac ctc tgatgggccg agctgcctgt	865
Gln Val Arg Arg Phe Val Ser Asp Leu	
230 235	
ggacgggtgct cagacaagtc tgggattaga gcctcaagga cattgtgtga ttgcctcaca	925
tttgaggta atatcaagca gcaactaaa ttctgagaaa taaacgagtc tattacaaa	985
aaaaaaaaaaa aaa	998

<210> 131
 <211> 779
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 27..578

<220>
 <221> sig_peptide
 <222> 27..119
 <223> Von Heijne matrix
 score 4.50637135496675
 seq TALMVGAASLLEG/RP

<400> 131
 atctttctg actggccctg cagagg atg gca tgc acc act act gcc ccc gcc 53
 Met Ala Cys Thr Thr Thr Ala Pro Ala
 -30 -25
 cag gaa cac atg ctt ctc acc cct ctc act gct ctg atg gtg ggg gct 101
 Gln Glu His Met Leu Leu Thr Pro Leu Thr Ala Leu Met Val Gly Ala
 -20 -15 -10
 gct tct ctg ctt gag ggc cgg cca cag atc tca gct cca tac tcc cga 149
 Ala Ser Leu Leu Glu Gly Arg Pro Gln Ile Ser Ala Pro Tyr Ser Arg
 -5 1 5 10
 gct gca tgt tgc agc cct ggg gca ctg gga tgt cct gca gct cgg gtt 197
 Ala Ala Cys Cys Ser Pro Gly Ala Leu Gly Cys Pro Ala Ala Arg Val
 15 20 25
 ggg att ctg gat ctg atg tat tcc tgg gtt gcc agg aaa gtg ctc agg 245
 Gly Ile Leu Asp Leu Met Tyr Ser Trp Val Ala Arg Lys Val Leu Arg
 30 35 40
 tgc agc aat act ggg ctg cag ggg ctg cac tgt gca cca gct tat gca 293
 Cys Ser Asn Thr Gly Leu Gln Gly Leu His Cys Ala Pro Ala Tyr Ala
 45 50 55
 gca cag ctt ggt atg gac cct ggg agg ggc caa cga gca gga ggg cct 341
 Ala Gln Leu Gly Met Asp Pro Gly Arg Gly Gln Arg Ala Gly Gly Pro
 60 65 70
 gta gag cag aca tac ttc agt ccc atg ggg aag ctg ccc act ctt tcg 389
 Val Glu Gln Thr Tyr Phe Ser Pro Met Gly Lys Leu Pro Thr Leu Ser
 75 80 85 90
 tgg ctg gaa ggc tgt aca gca gtc atg acg ctg gca tct gct tgg ctt 437
 Trp Leu Glu Gly Cys Thr Ala Val Met Thr Leu Ala Ser Ala Trp Leu
 95 100 105
 ctg ggg agc cct cgg gaa act tac aat cat gag aag gtg aag gag aag 485
 Leu Gly Ser Pro Arg Glu Thr Tyr Asn His Glu Lys Val Lys Glu Lys
 110 115 120
 cag tgt cca ttc tcc agt atg gtt ttg ggg gag tat ggc ttc cta cct 533
 Gln Cys Pro Phe Ser Ser Met Val Leu Gly Glu Tyr Gly Phe Leu Pro
 125 130 135
 act gtg gac cac ctg tca act ctg ggc tgt aac atg aga gaa ttg 578
 Thr Val Asp His Leu Ser Thr Leu Gly Cys Asn Met Arg Glu Leu
 140 145 150
 tgaacttctg tcttggttga gccatgggtt cattctcttt ttcagccatg tagcctgtgc 638
 tgtaactcag taccacatta gcaactagt aaagtcaatg tgggttaaatt tgtcattctt 698
 cagggttagaa catttcttcc ttttattctt gtgtttttgg ctaaataaac tgggaaatta 758
 tagtaaaaaa aaaaaaaaaa a 779

<210> 132
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 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> 408..710

<220>
 <221> sig_peptide
 <222> 408..533
 <223> Von Heijne matrix
 score 5.66440183652506
 seq QLCFHLISWLYSWA/SQ

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 cacatgatta atccagtctg ggtcatgacc ttttcttcat ccaaaacaag gtgatgggaa 120
 gacaaaaaca atagctacta caaacaatag gagtttataa ttatgtgctg atgtattcga 180
 agatgtgttg acagtcgtga gtgtgtatcc taggaaaggc gagctggact ctgtctccat 240
 ggtggctctc accccaggga cctaggaaca gcctgtcacc acacaattac ttttataacc 300
 ctggagatga aaatctcctt gtcctcaaaa tacttccaga agaacaacca gatgggaagg 360
 accttggttg ggactctttc cagttcactt ggggcagagg gaattta atg gct cac 416
 Met Ala His
 -40
 gta gct gaa aag gat ggg cta gat tgg gct tca ggc tgc atc cca gga 464
 Val Ala Glu Lys Asp Gly Leu Asp Trp Ala Ser Gly Cys Ile Pro Gly
 -35 -30 -25
 ctc caa aca ggg atc tgt ctc ttt ggc tct cag ctc tgc ttt cat ttg 512
 Leu Gln Thr Gly Ile Cys Leu Phe Gly Ser Gln Leu Cys Phe His Leu
 -20 -15 -10
 agt tgg ctt tat tct tgg gct tca cag tgt ggc ccc aca gca cca gtt 560
 Ser Trp Leu Tyr Ser Trp Ala Ser Gln Cys Gly Pro Thr Ala Pro Val
 -5 1 5
 att gat aaa aag agc tcc cct ttg ctg aca gaa ctg ctg gat ttg gtt 608
 Ile Asp Lys Lys Ser Ser Pro Leu Leu Thr Glu Leu Leu Asp Leu Val
 10 15 20 25
 ctc att ggt cca gag gag gaa ggt atc cag cct caa gtc atc att gtg 656
 Leu Ile Gly Pro Asp Glu Glu Gly Ile Gln Pro Gln Val Ile Ile Val
 30 35 40
 gcc agg aag atg gaa tac acc aaa tgg aca ggc ctg gca tgt acc cac 704
 Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala Cys Thr His
 45 50 55
 aga gac tgagagtttg tgctggtggt tgtggtggca gatgatatta cctgaagaag 760
 Arg Asp
 ggacgaatgg gtgctgggca ggacaaagca tcagctgtcc agttcaggcc tctcctcttt 820
 ccctggtgtc ttcattttcc tccgtctccc tgctgtccct taccctctgc ccaatctcat 880
 tactcctggt cttgggagtt gccttctgag gatactccac tgggggtacc tgagcctgga 940
 ttagagggca gggggaggat attgcctagc caaagtgggt gttcaataaa gaaccatttg 1000
 gagatggcaa aaaaaaaaaa aaaaa 1025

<210> 133
 <211> 607
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 247..501

<220>
<221> sig_peptide
<222> 247..306
<223> Von Heijne matrix
score 6.43040298500966
seq LLLVTLVASTVPG/NS

<400> 133
tgttacaaat attccctatg atctctcctt taaatattct tatcaggata ttggaaattc 60
ttgattttca caactctgct tcagtggcat atgttttagct ttttgtcttc tgaattaatt 120
gggcttctga tgggtccctag aggtatcagc tactcagtca gaaaacatac atggggaaga 180
aactgaagtt catgccacaa actgtagcag ctttgggaaca gaagggaacca gacaacctca 240
aggaga atg ggc cca aat acc aaa aat tta ctc ttg gtg acc ctt gtt 288
Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val
-20 -15 -10
gct tct act gta cca ggc aac tct ctt ggg cag gat ttt act ttt gca 336
Ala Ser Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala
-5 1 5 10
cac tta gaa aga tcc tgc acc agg gaa aat cgg tct cct ggg gag gta 384
His Leu Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val
15 20 25
ttc cag caa cca tgc aag tct gga ggc ggg ggg gtt gga gaa cca aat 432
Phe Gln Gln Pro Cys Lys Ser Gly Gly Gly Val Gly Glu Pro Asn
30 35 40
gcc caa ggg cag cta ctt agc cag cac cca cta cct gcc ttc att aat 480
Ala Gln Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn
45 50 55
tgt tct cac ggg cag gcc ttt tgaaccaccc tggtagagaa caccaaccct 531
Cys Ser His Gly Gln Ala Phe
60 65
ggtgcttttag gctgtctgtg ccatttctag gcaatgaacg agtagttact gtaccaaccc 591
aaaaaaaaaa aaaaaa 607

<210> 134
<211> 774
<212> DNA
<213> Homo sapiens

<220>
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<222> 333..602

<220>
<221> sig_peptide
<222> 333..416
<223> Von Heijne matrix
score 4.79986448293481
seq VPALPLLSSLCA/MV

<400> 134
ctcttcagtc cggggcttgg ttgaacggac tcaccaggaa acgtgacttt cgtgtccgac 60
ctctgctgta tcaggattcg attcttggtg ttaaacaaga caacgctgaa ggctcggtgc 120
agcagccctg caaaggtttt tccagcgctc ttgggaggtg ggctgtgccc tgcctggccc 180
acctggccca cctggcccac cattacctga agggaagcat gaacagcctt tgacgtggga 240
gtggcgactg ctgagaggga actgtctgta cacaagcaat gtagccttat gggacctgag 300

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tggagcccca acccacgcag ggcgtgktct tc atg gct ttt cct ggc caa tct 353
                                Met Ala Phe Pro Gly Gln Ser
                                -25
gat acc aag atg cag tgg cca gaa gta cct gca ctt cca ctg tca 401
Asp Thr Lys Met Gln Trp Pro Glu Val Pro Ala Leu Pro Leu Leu Ser
-20 -15 -10
agt ctc tgc atg gct atg gtg agg aag agc tct gca ctg ggc aag gaa 449
Ser Leu Cys Met Ala Met Val Arg Lys Ser Ser Ala Leu Gly Lys Glu
-5 1 5 10
gtt ggc cgt cga gtg aag gaa atg gtg atg ctg gtg gcc cct ttc cgg 497
Val Gly Arg Arg Val Lys Glu Met Val Met Leu Val Ala Pro Phe Arg
15 20 25
cag tca agt tcc cta tca agg aca ttc agt tct cgg aaa gtg gtg aag 545
Gln Ser Ser Ser Leu Ser Arg Thr Phe Ser Ser Arg Lys Val Val Lys
30 35 40
gca cat gct tcc ctg cat ggt gcc cgc ctc tct cca ctc tct aga aat 593
Ala His Ala Ser Leu His Gly Ala Arg Leu Ser Pro Leu Ser Arg Asn
45 50 55
att aga ggc taggctgctg ctgtatgtca gggctagtcc ctcttctatg 642
Ile Arg Gly
60
aatccagaat aactctgaag aagccgagta acaggcatga agtgaagaga aatcgctgta 702
acaggaagac agcaaagcag atgctaataa ccacactatt taacgaactg gaaccaacaa 762
aaaaaaaaaa aa 774

<210> 135
<211> 611
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 110..376

<220>
<221> sig_peptide
<222> 110..208
<223> Von Heijne matrix
score 3.64796206065748
seq LVPHSPLPGALSS/AP

<220>
<221> misc_feature
<222> 347
<223> n=a, g, c or t

<400> 135
tcttgtcaac actgcccact cagcgaggaa gcagccgcga cgccacact tctgtttgga 60
gcctgcgcag agccagaggc ctcagaagcc acaggaacat ggcctaggc atg gct cag 118
                                Met Ala Gln
cca gca gcc ccc tcc ctg acg cgg ccc ttc ctg gca gag gcc ccg aca 166
Pro Ala Ala Pro Ser Leu Thr Arg Pro Phe Leu Ala Glu Ala Pro Thr
-30 -25 -20 -15
gca ctg gtc cca cac agc ccc ctg cct ggg gcc ctg tca agc gcc cct 214
Ala Leu Val Pro His Ser Pro Leu Pro Gly Ala Leu Ser Ser Ala Pro
-10 -5 1
ggc ccg aag cag ccc ccg acg gca agc aca ggc ccg gag ctg ctg ctg 262
Gly Pro Lys Gln Pro Pro Thr Ala Ser Thr Gly Pro Glu Leu Leu Leu

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      5              10              15
ctg cct ctt tcc tcc ttc atg ccc tgc ggg gcg gct gca cca gcc agg 310
Leu Pro Leu Ser Ser Phe Met Pro Cys Gly Ala Ala Pro Ala Arg
      20              25              30
gtg tca tca cag cgg gct act cct agg gat aag ccc ncc ggt ccc ctc 358
Val Ser Ser Gln Arg Ala Thr Pro Arg Asp Lys Pro Xaa Gly Pro Leu
      35              40              45              50
atc cct ggc cag tgt ccc tgacccccat ctactccttc ctgggggactt 406
Ile Pro Gly Gln Cys Pro
      55
ctcagcgcca gccattggc gcctgcgttg cccgcattcca ggccctgcgg caggccctgt 466
gctagcgtgt tcgcaccagg aacgcagggtg ctgggctgtc ggggaggcct caggccacct 526
ccaggaacag aacacagttt taagtttgat tttttttatt tcaaaatgct ttgcaattaa 586
atgaattact gttcaaaaaa aaaaa 611

<210> 136
<211> 925
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 22..417

<220>
<221> sig_peptide
<222> 22..66
<223> Von Heijne matrix
      score 5.47092708754574
      seq RVLCAPAAGAVRA/LR

<400> 136
agtcgaggag tcaaggcagc a atg aat cgt gtc ttg tgt gcc ccg gcg gcc 51
                        Met Asn Arg Val Leu Cys Ala Pro Ala Ala
                        -15              -10
ggg gcc gtc cgg gcg ctg agg ctc ata ggc tgg gct tcc cga agc ctt 99
Gly Ala Val Arg Ala Leu Arg Leu Ile Gly Trp Ala Ser Arg Ser Leu
-5              1              5              10
cat ccg ttg ccc ggt tcc cgg gat cgg gcc cac cct gcc gcc gag gaa 147
His Pro Leu Pro Gly Ser Arg Asp Arg Ala His Pro Ala Ala Glu Glu
      15              20              25
gag gac gac cct gac cgc ccc att gag ttt tcc tcc agc aaa gcc aac 195
Glu Asp Asp Pro Asp Arg Pro Ile Glu Phe Ser Ser Ser Lys Ala Asn
      30              35              40
cct cac cgc tgg tcg gtg ggc cat acc atg gga aag gga cat cag cgg 243
Pro His Arg Trp Ser Val Gly His Thr Met Gly Lys Gly His Gln Arg
      45              50              55
ccc tgg tgg aag gtg ctg ccc ctc agc tgc ttc ctc gtg gcg ctg atc 291
Pro Trp Trp Lys Val Leu Pro Leu Ser Cys Phe Leu Val Ala Leu Ile
      60              65              70              75
atc tgg tgc tac ctg agg gag gag agc gag gcg gac cag tgg ttg aga 339
Ile Trp Cys Tyr Leu Arg Glu Glu Ser Glu Ala Asp Gln Trp Leu Arg
      80              85              90
cag gtg tgg gga gag gtg cca gag ccc agt gat cgt tct gag gag cct 387
Gln Val Trp Gly Glu Val Pro Glu Pro Ser Asp Arg Ser Glu Glu Pro
      95              100              105
gag act cca gct gcc tac aga gcg aga act tgacgggggtg cccgctgggg 437
Glu Thr Pro Ala Ala Tyr Arg Ala Arg Thr

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110      115
ctggcaggaa gggagccgac agccgcccctt cggatttgat gtcacgtttg cccgtgactg 497
tcctggctat gcgtgcgtcc tcagcactga aggacttggc tggatggatgg ggcacttggc 557
tatgctgatt cgcgtgaagg cggagcagaa tctcagcaga tcggaaactg ctccctgcct 617
ggctcttgat gtccaaggat tccatcgga agactttctca gatccttggg gaagggtttca 677
gttgactgt atgctgttgg atttgccaag tctttgtata acataatcat gtttccaaag 737
cacttctggt gacacttgtc atccagtgtt agtttgcagg taatttgctt tctgagatag 797
aatatctggc agaagtgtga aactgtattg catgctgcgg cctgtgcaag gaacacttcc 857
acatgtgagt tttacacaac aacaaatgaa aataaatttt aattttataa taaaaaaaaa 917
aaaaaaaaa 925

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<210> 137
<211> 674
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 62..367

<220>
<221> sig_peptide
<222> 62..103
<223> Von Heijne matrix
      score 4.49063834776683
      seq FLTALLWRGRIPG/RQ

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<400> 137
acgccacggc gtctgctggc ggccgcggag acgcagagtc ttgagcagcg cggcaggcac 60
c atg ttc ctg act gcg ctc ctc tgg cgc ggc cgc att ccc ggc cgt cag 109
  Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
      -10      -5      1
tgg atc ggg aag cac cgg cgg ccg cgg ttc gtg tgg ttg cgc gcc aag 157
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
      5      10      15
cag aac atg atc cgc cgc ctg gag atc gat gcg gag aac cat tac tgg 205
Gln Asn Met Ile Arg Arg Leu Glu Ile Asp Ala Glu Asn His Tyr Trp
      20      25      30
ctg agc atg ccc tac atg acc cgg gag cag gag cgc ggc cac gcc gsg 253
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Arg Gly His Ala Xaa
      35      40      45      50
dtg cgc agg agg gag gcc ttc gag gcc ata aag gcg gcc gcc act tcc 301
Xaa Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
      55      60      65
aag ttc ccc ccg cat aga ttc att gcg gac cag ctc gac cat ctc aat 349
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
      70      75      80
gtc acc aag aaa tgg tcc taatcctgag tagtcaccct tggattttat 397
Val Thr Lys Lys Trp Ser
      85
ggatcacgga gctgaccatc tttacctggt cctggaactg aaaaactgta gcttgtgtga 457
aaatgagcct ttggaccagt ctttattaaa acaaacaaac atgagtagtc tgcatatcga 517
atatctagag ctctaaaccc cccaatactt aaaagtctaa ttgctgtcct gtgggtttcat 577
tagtctgata ggaagatagg gatttcctca gtcacagatg atattttgaa ggaaagctgc 637
aataaagcca caatgattcg aaaaaaaaaa aaaaaaaa 674

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<210> 138
<211> 1725

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 107..1618

<220>
<221> sig_peptide
<222> 107..178
<223> Von Heijne matrix
score 6.19650168602189
seq LGLYSLVLSGALA/YA

<400> 138
agagctcagc cggtcgcacg gacggacagt tggaagccgg accccagagc ctgaggtggg 60
cagtgtgccca gggtccttg cggcctctc aagccctgtc caggct atg ggc atc 115
Met Gly Ile
aag aca gca ttg ccg gcg gct gag ctg ggc ctc tac tct ctg gtg ctg 163
Lys Thr Ala Leu Pro Ala Ala Glu Leu Gly Leu Tyr Ser Leu Val Leu
-20 -15 -10
agt ggg gcc ctg gcc tat gct ggc cgg ggc ctc ctt gag gct tca caa 211
Ser Gly Ala Leu Ala Tyr Ala Gly Arg Gly Leu Leu Glu Ala Ser Gln
-5 1 5 10
gat ggg gcc cac agg aag gcc ttc cgg gag tct gtg cga cct ggc tgg 259
Asp Gly Ala His Arg Lys Ala Phe Arg Glu Ser Val Arg Pro Gly Trp
15 20 25
gag tac att ggc cgg aag atg gat gtg gct gac ttc gag tgg gtg atg 307
Glu Tyr Ile Gly Arg Lys Met Asp Val Ala Asp Phe Glu Trp Val Met
30 35 40
tgg ttc acc tcc ttt cgc aac gtc atc atc ttt gcc ctc tcc gga cat 355
Trp Phe Thr Ser Phe Arg Asn Val Ile Ile Phe Ala Leu Ser Gly His
45 50 55
gtg ctg ttt gct aaa ctc tgc acg atg gtt gcc cca aag ctc cgc tcc 403
Val Leu Phe Ala Lys Leu Cys Thr Met Val Ala Pro Lys Leu Arg Ser
60 65 70 75
tgg atg tat gct gtg tac ggg gcc ttg gct gtg atg ggc aca atg ggc 451
Trp Met Tyr Ala Val Tyr Gly Ala Leu Ala Val Met Gly Thr Met Gly
80 85 90
cct tgg tac ctg ctg ctg ctt ggt cac tgt gtg ggc ctc tat gtg 499
Pro Trp Tyr Leu Leu Leu Leu Leu Gly His Cys Val Gly Leu Tyr Val
95 100 105
gcc tcg ctt ttg ggc cag ccc tgg ctc tgt ctt ggc ctt ggc ttg gcc 547
Ala Ser Leu Leu Gly Gln Pro Trp Leu Cys Leu Gly Leu Gly Leu Ala
110 115 120
agc ctg gcc tcc ttc aag atg gac ccc cta atc tct tgg cag agc ggg 595
Ser Leu Ala Ser Phe Lys Met Asp Pro Leu Ile Ser Trp Gln Ser Gly
125 130 135
ttt gta aca ggc act ttt gat ctt caa gag gtg ctg ttt cat ggg ggc 643
Phe Val Thr Gly Thr Phe Asp Leu Gln Glu Val Leu Phe His Gly Gly
140 145 150 155
agc agc ttc aca gtg ctg cgt tgc acc agc ttt gca ctg gag agc tgt 691
Ser Ser Phe Thr Val Leu Arg Cys Thr Ser Phe Ala Leu Glu Ser Cys
160 165 170
gcc cac cct gac cgc cac tac tcc tta gct gac ctg ctc aag tac agc 739
Ala His Pro Asp Arg His Tyr Ser Leu Ala Asp Leu Leu Lys Tyr Ser
175 180 185
ttc tac ctg ccc ttc ttc ttc ttc ggg ccc atc atg acc ttt gat cgc 787

Phe	Tyr	Leu	Pro	Phe	Phe	Phe	Phe	Gly	Pro	Ile	Met	Thr	Phe	Asp	Arg	
190							195					200				
ttc	cat	gct	cag	gtg	agc	cag	gtg	gag	cca	gtg	aga	cgc	gag	ggt	gag	835
Phe	His	Ala	Gln	Val	Ser	Gln	Val	Glu	Pro	Val	Arg	Arg	Glu	Gly	Glu	
205						210					215					
ctg	tgg	cac	atc	cga	gcc	cag	gca	ggc	cta	agc	gtg	gtg	gcc	atc	atg	883
Leu	Trp	His	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Ser	Val	Val	Ala	Ile	Met	
220					225					230					235	
gcc	gtc	gac	atc	ttc	ttt	cac	ttc	ttc	tac	atc	ctc	act	atc	ccc	agc	931
Ala	Val	Asp	Ile	Phe	Phe	His	Phe	Phe	Tyr	Ile	Leu	Thr	Ile	Pro	Ser	
				240					245					250		
gac	ctc	aag	ttc	gcc	aac	cgc	ctc	cca	gac	att	gcc	ctc	gct	ggc	cta	979
Asp	Leu	Lys	Phe	Ala	Asn	Arg	Leu	Pro	Asp	Ile	Ala	Leu	Ala	Gly	Leu	
			255				260						265			
gcc	tat	tca	aac	ctg	gtg	tat	gac	tgg	gtg	aag	gcg	gcc	gtc	ctc	ttt	1027
Ala	Tyr	Ser	Asn	Leu	Val	Tyr	Asp	Trp	Val	Lys	Ala	Ala	Val	Leu	Phe	
		270					275				280					
ggg	gtt	gtc	aac	act	gtg	gca	tgc	ctc	gac	cac	ctg	gac	cca	ccc	cag	1075
Gly	Val	Val	Asn	Thr	Val	Ala	Cys	Leu	Asp	His	Leu	Asp	Pro	Pro	Gln	
	285					290					295					
cct	ccc	aag	tgc	atc	acc	gca	ctc	tac	gtc	ttt	gcg	gaa	acg	cac	ttt	1123
Pro	Pro	Lys	Cys	Ile	Thr	Ala	Leu	Tyr	Val	Phe	Ala	Glu	Thr	His	Phe	
300					305					310					315	
gac	cgt	ggc	atc	aac	gac	tgg	ctt	tgc	aaa	tat	gtg	tat	aac	cac	att	1171
Asp	Arg	Gly	Ile	Asn	Asp	Trp	Leu	Cys	Lys	Tyr	Val	Tyr	Asn	His	Ile	
				320					325					330		
ggg	ggg	gag	cat	tcc	gct	gtg	atc	cca	gag	ctg	gca	gcc	aca	gtg	gcc	1219
Gly	Gly	Glu	His	Ser	Ala	Val	Ile	Pro	Glu	Leu	Ala	Ala	Thr	Val	Ala	
			335					340					345			
aca	ttt	gcc	atc	acc	aca	ctg	tgg	ctt	ggg	cct	tgt	gac	att	gtc	tac	1267
Thr	Phe	Ala	Ile	Thr	Thr	Leu	Trp	Leu	Gly	Pro	Cys	Asp	Ile	Val	Tyr	
		350					355				360					
ctg	tgg	tca	ttc	ctt	aac	tgc	ttt	ggc	ctc	aac	ttt	gag	ctc	tgg	atg	1315
Leu	Trp	Ser	Phe	Leu	Asn	Cys	Phe	Gly	Leu	Asn	Phe	Glu	Leu	Trp	Met	
	365					370					375					
caa	aaa	ctg	gca	gag	tgg	ggg	ccc	cta	gca	cga	att	gag	gcc	tct	ctg	1363
Gln	Lys	Leu	Ala	Glu	Trp	Gly	Pro	Leu	Ala	Arg	Ile	Glu	Ala	Ser	Leu	
380					385					390					395	
tca	gtg	cag	atg	tcc	cgt	agg	gtc	cgg	gcc	ctg	ttt	gga	gcc	atg	aac	1411
Ser	Val	Gln	Met	Ser	Arg	Arg	Val	Arg	Ala	Leu	Phe	Gly	Ala	Met	Asn	
				400					405					410		
ttc	tgg	gcc	atc	atc	atg	tac	aac	ctt	gtg	agc	ctg	aac	agc	ctc	aaa	1459
Phe	Trp	Ala	Ile	Ile	Met	Tyr	Asn	Leu	Val	Ser	Leu	Asn	Ser	Leu	Lys	
			415				420						425			
ttc	aca	gag	ctg	gtt	gcc	cgg	cgc	ctg	cta	ctc	aca	ggg	ttc	ccc	cag	1507
Phe	Thr	Glu	Leu	Val	Ala	Arg	Arg	Leu	Leu	Leu	Thr	Gly	Phe	Pro	Gln	
		430					435					440				
acc	acg	ctg	tcc	atc	ctg	ttt	gtc	acc	tac	tgt	ggc	gtc	cag	ctg	gta	1555
Thr	Thr	Leu	Ser	Ile	Leu	Phe	Val	Thr	Tyr	Cys	Gly	Val	Gln	Leu	Val	
		445				450					455					
aag	gag	cgt	gag	cga	acc	ttg	gca	ctg	gag	gag	gag	cag	aag	cag	gac	1603
Lys	Glu	Arg	Glu	Arg	Thr	Leu	Ala	Leu	Glu	Glu	Glu	Gln	Lys	Gln	Asp	
460					465				470						475	
aaa	gag	aag	ccg	gag	taggagggag	cgggtagagg	gatgggctct	gctcagctat								1658
Lys	Glu	Lys	Pro	Glu												
				480												
tcttgggcca	gatggggcct	gaccgataga	ataaaagact	tttctacaac	aaaaaaaaaa											1718
aaaaaaa																1725

[illegible]

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<222> 16..93
<223> Von Heijne matrix
score 5.809301698725
seq FCVCVIAIGVVOA/LI
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159

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agcctcccaa gtagttggga ttacaagcac ccaccaccat gccagctaa ctttttgcat 1201
ttttaataga gatgaggttt caccaagttg gccaggctgg tcttgaactc ctgacctcag 1261
gtgatctgcc cacctcggcc tcccaaagtg ctgggattac aggtgtaagc caccgtgcc 1321
ggccatcgta atgtttgaat ttgctttttt acatcttcca tccttttgga gtgtcttggt 1381
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<210> 140
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<212> DNA
<213> Homo sapiens

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<222> 222..374

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<220>
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<222> 222..299
<223> Von Heijne matrix
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      seq ILFKFSLCPYAAA/LS

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taataatggt gttaaattat tgccttctca tctgcgtgtc tcttatgttc tgcttaaaga 60
gattgtcagt ttgttcaagc tcttttttagt tgttgctcct ccagtgccta gctttgagct 120
ttgtacacgg tagttattga gttgagtaac atagtttggt ctgagtcatt tgttccacat 180
gcttgaagac ttggcttaac ctagttagata ataggaaaga a atg gaa atg ctc ttt 236
                                         Met Glu Met Leu Phe
                                         -25

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gat gaa aga gcc cct ctc tta ttc atc ctt ttt aaa ttt tct ttg tgc 284
Asp Glu Arg Ala Pro Leu Leu Phe Ile Leu Phe Lys Phe Ser Leu Cys
-20 -15 -10

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cca tat gca gca gct ctc agc aaa cct ata ttt ggc agt gtg gcc tgt 332
Pro Tyr Ala Ala Ala Leu Ser Lys Pro Ile Phe Gly Ser Val Ala Cys
-5 1 5 10

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atg act aaa gaa atc ctg gcc agg cac ggt ggc tca cgc ctg 374
Met Thr Lys Glu Ile Leu Ala Arg His Gly Gly Ser Arg Leu
15 20 25

```

```

taatcccagc actttgggag gccgaggcgg gtggattacg aggtcaggag attgagacca 434
tcctggctaa catggcgaaa ccccatctct acgaaaaata caaaaaaaaaa aattagccgg 494
gcatcatggc gggcgctgt agtcttagct actcaggagg ctgaggcagg agaatggcgt 554
gaacccggga ggcggagctt gcagtgagcc gagattgcgc cactgcactc cagcctgggg 614
caacagagca agactccgtc tcaaaaaaaaaa aaaaaaaaaa 653

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<210> 141
<211> 1490
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 59..274

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<220>
<221> sig_peptide
<222> 59..127

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<223> Von Heijne matrix
score 7.37647149292058
seq LGLCSLLVGEAEA/PS

<400> 141
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atg ctg cgt cca gcg tta ccg tgg ctg tac ctt ggc ctc tgc agc ctc 106
Met Leu Arg Pro Ala Leu Pro Trp Leu Tyr Leu Gly Leu Cys Ser Leu
-20 -15 -10
ctg gtg ggg gag gca gag gcc ccg agc ccc gtg gat ccg ctg gag cgg 154
Leu Val Gly Glu Ala Glu Ala Pro Ser Pro Val Asp Pro Leu Glu Arg
-5 1 5
agc cgg ccg tac gcg gtg ctg cga ggg cag aac ctg gtg ttg atg gga 202
Ser Arg Pro Tyr Ala Val Leu Arg Gly Gln Asn Leu Val Leu Met Gly
10 15 20 25
acc att ttc agc atc ctg ctg gtg act gtc atc ctt atg gca ttt tgt 250
Thr Ile Phe Ser Ile Leu Leu Val Thr Val Ile Leu Met Ala Phe Cys
30 35 40
gtc tac aag ccc att cgg cgt cgg tgacagccag acaagttctt caatgagtat 304
Val Tyr Lys Pro Ile Arg Arg Arg
45
ttgggaatag gataagttgt gttgcacaca ggccagtggg gaagttggaa ccaaaacttt 364
cctacttgga aatgaccttt ggtctggaca gttggtaaat gctaaatgaa ttagaagaaa 424
acatgtacta gacattatct tttcctaaca ctgtagcgca aataattggc ccctgagtcc 484
gcttctcagt gtttctgact gtacttgta aaagtaagac ctgaaagctc caaaggctcag 544
tgtaaagatg gagtgttcat gagaaagaaa acatggtaac cttgtgagtg cctgtaagaa 604
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tgacagacatt ccctatttaa gaaccatttg gttacagtgg gttagaatc acagattttt 724
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<211> 661
<212> DNA
<213> Homo sapiens

<220>
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<222> 158..442

<220>
<221> sig_peptide
<222> 158..301
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seq FVILLLFIFTVVS/LV

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ccaaaaagat tcaaaagagc aagtggaatc tctaaga atg gct tcc agc cac tgg      175
                               Met Ala Ser Ser His Trp
                               -45
aat gaa acc act acc tct gtt tat cag tac ctt ggt ttt caa gtt caa      223
Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr Leu Gly Phe Gln Val Gln
-40                               -35                               -30
aaa att tac cct ttc cat gac aac tgg aac act gcc tgc ttt gtc atc      271
Lys Ile Tyr Pro Phe His Asp Asn Trp Asn Thr Ala Cys Phe Val Ile
-25                               -20                               -15
ctg ctt tta ttt ata ttt aca gtg gta tct tta gtg gtg ctg gct ttc      319
Leu Leu Leu Phe Ile Phe Thr Val Val Ser Leu Val Val Leu Ala Phe
-10                               -5                               1                               5
ctt tat gaa gtg ctt gac tgc tgc tgc tgt gta aaa aac aaa acc gtg      367
Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys Val Lys Asn Lys Thr Val
10                               15                               20
aaa gac ttg aaa agt gaa ccc aac cct ctt aga agt atg atg gac aac      415
Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu Arg Ser Met Met Asp Asn
25                               30                               35
atc aga aaa cgt gaa act gaa gtg gtc taacactcta tagaagatga      462
Ile Arg Lys Arg Glu Thr Glu Val Val
40                               45
acaaaatctc tgaaagcagc tcaacctctt ctgagaaaaa aaatatattc tgaggccaac      522
tgttgctaca aaacaaattc tgactgaatg tttaaaacat ttctagtaga aggggaaaaa      582
aaagttaaac atgcactgtt tgtgtgtata gccatttcat taaatataca gtaaaacttc      642
ataaaaaaaaa aaaaaaaaaa      661

<210> 143
<211> 1789
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 5..454

<220>
<221> sig_peptide
<222> 5..64
<223> Von Heijne matrix
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      seq LLPLLSLLVGAWL/KL

<400> 143
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      Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu
      -20                               -15                               -10
gtc ggc gcg tgg ctc aag cta gga aat gga cag gct act agc atg gtc      97
Val Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val
-5                               1                               5                               10
caa ctg cag ggt ggg aga ttc ctg atg gga aca aat tct cca gac agc      145
Gln Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser
15                               20                               25
aga gat ggt gaa ggg cct gtg cgg gag gcg aca gtg aaa ccc ttt gcc      193
Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala
30                               35                               40

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atc gac ata ttt cct gtc acc aac aaa gat ttc agg gat ttt gtc agg	241
Ile Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg	
45 50 55	
gag aaa aag tat cgg aca gaa gct gag atg ttt gga tgg agc ttt gtc	289
Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val	
60 65 70 75	
ttt gag gac ttt gtc tct gat gag ctg aga aac aaa gcc acc cag cca	337
Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro	
80 85 90	
atg aag gtc aag ttt acc cat ggg gga act ggt tcc agc caa acc gca	385
Met Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala	
95 100 105	
cca acc tgt ggc agg gaa agt tcc cca agg gag aca aag ctg agg atg	433
Pro Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met	
110 115 120	
gct tcc atg gag tct ccc cag tgaatgcttt ccccgcccag aacaactacg	484
Ala Ser Met Glu Ser Pro Gln	
125 130	
ggctctatga cctcctgagg aacgtgtggg agtggacagc atcacctgtac caggctgctg	544
agcaggacat gcgcgtcctc cggggggcat cctggatcga cacagctgat ggctctgcca	604
atcacctggc cggggtcacc accaggatgg gcaacactcc agattcagcc tcagacaacc	664
tcggtttccg ctgtgctgca gacgcaggcc ggccgcccagg ggagctgtaa gcagccgggt	724
ggtgacaagg agaaaagcct tctagggtca ctgtcattcc ctggccatgt tgcaaacagc	784
gcaattccaa gctcgagagc ttcagcctca ggaaagaact tccccctccc tgtctcccat	844
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gaaggggccc aatgtgtgtt gacgatggct gggggccagg tgtttctgtt agaggccaag	964
tattattgac acaggattgc aaacacacaa acaattggaa cagagcactc tgaaaggcca	1024
ttttttaagc attttaaaat ctattctctc cccctttctc cctggatgat tcaggaagct	1084
gacattgttt cctcaaggca gaattttcct ggttctgttt tctcagccag ttgctgtgga	1144
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 <212> DNA
 <213> Homo sapiens

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 <222> 241..1302

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cctggactgg tcatatacct cttgtggccc tggcagaatc aagatgaggc cctgtcatgc	180
ctccccagtg aggcctacag tctgagcaga cagcatggcc tgccactggc agtgaacacc	240
atg tct gca gga ggt ggc cgg gcc ttt gct tgg caa gtg ttc ccc ccc	288
Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro	
1 5 10 15	

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Met	Pro	Thr	Cys	Arg	Val	Tyr	Gly	Thr	Val	Ala	His	Gln	Asp	Gly	His	
			20					25					30			
ctg	ctg	gtg	ttg	ggg	ggg	tgt	ggc	cgg	gct	gga	ctg	ccc	ctg	gac	act	384
Leu	Leu	Val	Leu	Gly	Gly	Cys	Gly	Arg	Ala	Gly	Leu	Pro	Leu	Asp	Thr	
		35					40					45				
gct	gag	aca	ctg	gac	atg	gcc	tcg	cac	aca	tgg	ctg	gca	ctg	gca	ccc	432
Ala	Glu	Thr	Leu	Asp	Met	Ala	Ser	His	Thr	Trp	Leu	Ala	Leu	Ala	Pro	
		50				55					60					
ctg	ccc	act	gcc	cgg	gct	ggg	gca	gct	gcg	gta	gtt	ctg	ggc	aag	cag	480
Leu	Pro	Thr	Ala	Arg	Ala	Gly	Ala	Ala	Ala	Val	Val	Leu	Gly	Lys	Gln	
	65				70					75					80	
gtg	cta	gtg	gtg	tgt	ggg	gtg	gat	gag	gtc	cag	agc	ccg	gta	gct	gct	528
Val	Leu	Val	Val	Cys	Gly	Val	Asp	Glu	Val	Gln	Ser	Pro	Val	Ala	Ala	
				85				90						95		
gta	gag	gcc	ttc	ctg	atg	gat	gag	ggc	cgc	tgg	gag	cgt	cgg	gcc	acc	576
Val	Glu	Ala	Phe	Leu	Met	Asp	Glu	Gly	Arg	Trp	Glu	Arg	Arg	Ala	Thr	
			100					105					110			
ctc	cct	caa	gca	gcc	atg	ggg	gtt	gca	act	gtg	gag	aga	gat	ggg	atg	624
Leu	Pro	Gln	Ala	Ala	Met	Gly	Val	Ala	Thr	Val	Glu	Arg	Asp	Gly	Met	
		115					120						125			
gtg	tat	gct	ctg	ggg	gga	atg	ggc	cct	gac	acg	gcc	ccc	cag	gcc	cag	672
Val	Tyr	Ala	Leu	Gly	Gly	Met	Gly	Pro	Asp	Thr	Ala	Pro	Gln	Ala	Gln	
		130				135					140					
gta	cgt	gtg	tat	gac	ccc	cgt	cgg	gac	tgc	tgg	ctt	tcg	cta	ccc	tcc	720
Val	Arg	Val	Tyr	Asp	Pro	Arg	Arg	Asp	Cys	Trp	Leu	Ser	Leu	Pro	Ser	
				150						155					160	
atg	ccc	aca	ccc	tgc	tat	ggg	gcc	tcc	acc	ttc	ctg	cac	ggg	aac	aag	768
Met	Pro	Thr	Pro	Cys	Tyr	Gly	Ala	Ser	Thr	Phe	Leu	His	Gly	Asn	Lys	
				165				170						175		
atc	tat	gtc	ctg	ggg	ggc	cgc	cag	ggc	aag	ctc	ccg	gtg	act	gct	ttt	816
Ile	Tyr	Val	Leu	Gly	Gly	Arg	Gln	Gly	Lys	Leu	Pro	Val	Thr	Ala	Phe	
			180					185					190			
gaa	gcc	ttt	gat	ctg	gag	gcc	cgt	aca	tgg	acc	cgg	cat	cca	agc	cta	864
Glu	Ala	Phe	Asp	Leu	Glu	Ala	Arg	Thr	Trp	Thr	Arg	His	Pro	Ser	Leu	
		195					200					205				
ccc	agc	cgt	cgg	gcc	ttt	gct	ggc	tgc	gcc	atg	gct	gaa	ggc	agc	gtc	912
Pro	Ser	Arg	Arg	Ala	Phe	Ala	Gly	Cys	Ala	Met	Ala	Glu	Gly	Ser	Val	
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ttt	agc	ctg	ggg	ggc	ctg	cag	cct	ggg	ccc	cac	aac	ttc	tac	tct		960
Phe	Ser	Leu	Gly	Gly	Leu	Gln	Gln	Pro	Gly	Pro	His	Asn	Phe	Tyr	Ser	
		225			230				235					240		
cgc	cca	cac	ttt	gtc	aac	act	gtg	gag	atg	ttt	gac	ctg	gag	cat	ggg	1008
Arg	Pro	His	Phe	Val	Asn	Thr	Val	Glu	Met	Phe	Asp	Leu	Glu	His	Gly	
			245					250						255		
tcc	tgg	acc	aaa	ttg	ccc	cgc	agc	ctg	cgc	atg	agg	gat	aag	agg	gca	1056
Ser	Trp	Thr	Lys	Leu	Pro	Arg	Ser	Leu	Arg	Met	Arg	Asp	Lys	Arg	Ala	
			260					265					270			
gac	ttt	gtg	gtt	ggg	tcc	ctt	ggg	ggc	cac	att	gtg	gcc	att	ggg	ggc	1104
Asp	Phe	Val	Val	Gly	Ser	Leu	Gly	Gly	His	Ile	Val	Ala	Ile	Gly	Gly	
		275					280					285				
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Leu	Gly	Asn	Gln	Pro	Cys	Pro	Leu	Gly	Ser	Val	Glu	Ser	Phe	Ser	Leu	
		290				295					300					
gca	cgg	cgg	cgc	tgg	gag	gca	ttg	cct	gcc	atg	ccc	act	gcc	cgc	tgc	1200
Ala	Arg	Arg	Arg	Trp	Glu	Ala	Leu	Pro	Ala	Met	Pro	Thr	Ala	Arg	Cys	
		305			310				315						320	
tcc	tgc	tct	agt	ctg	cag	gct	ggg	ccc	cgg	ctg	ttt	gtt	att	ggg	ggg	1248

Ser Cys Ser Ser Leu Gln Ala Gly Pro Arg Leu Phe Val Ile Gly Gly
325 330 335
gtg gcc cag ggc ccc agt caa gcc gtg gag gca ctg tgt ctg cgt gat 1296
Val Ala Gln Gly Pro Ser Gln Ala Val Glu Ala Leu Cys Leu Arg Asp
340 345 350
ggg gtc tgaaggcttg gtgggagctg tccactggag cagctcattg ccagaggcag 1352
Gly Val
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<220>
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1 5 10
cgc tgg gga gcc aaa cga ttg gga gtt gcc tcc aca gag gcc cag aga 98
Arg Trp Gly Ala Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg
15 20 25
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Gly Val Ser Phe Lys Leu Glu Glu Lys Thr Ala His Ser Ser Leu Ala
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Leu Phe Arg Asp Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu
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Pro Thr Lys Val Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val
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gtg ctg gca gac aca gcg gtc acc agt ggc aga cac tac tgg gaa gtg 290
Val Leu Ala Asp Thr Ala Val Thr Ser Gly Arg His Tyr Trp Glu Val
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Thr Val Lys Arg Ser Gln Gln Phe Arg Ile Gly Val Ala Asp Val Asp
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Met Ser Arg Asp Ser Cys Ile Gly Val Asp Asp Arg Ser Trp Val Phe
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acc tat gcc cag cgc aag tgg tac acc atg ttg gcc aac gag aaa gcc 434
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125 130 135 140
cca gtt gag ggt att ggg cag cca gag aag gtg ggg ctg ttg ctg gag 482
Pro Val Glu Gly Ile Gly Gln Pro Glu Lys Val Gly Leu Leu Leu Glu

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Val	Pro	Val	Ala	Pro	Ile	Cys	Thr	Asp	Lys	Ile	Asn	Ala	Ala	Asn	Tyr	
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Ala	Ser	Val	Lys	Thr	Pro	Ala	Leu	Ile	Val	Tyr	Gly	Asp	Gln	Asp	Pro	
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<222> 21..1145

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Cys	Pro	Leu	Leu	Leu	Pro	Gln	Asn	Arg	Ser	Lys	Thr	Val	Tyr	Glu	Gly	
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Phe	Ile	Ser	Ala	Gln	Gly	Arg	Asp	Phe	His	Leu	Arg	Ile	Val	Leu	Pro	
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gaa	gat	tta	caa	ctg	aag	aat	gca	aga	tta	tta	tgt	att	tgg	cag	ctg	197
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	gaa	gtt	gcc	tta	aag	aat	aga	caa	gag	ctg	tat	gca	cta	cct	cct	cct	341
	Glu	Val	Ala	Leu	Lys	Asn	Arg	Gln	Glu	Leu	Tyr	Ala	Leu	Pro	Pro	Pro	
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	Pro	Gln	Phe	Tyr	Ser	Ser	Leu	Ile	Glu	Glu	Ile	Gly	Thr	Leu	Gly	Trp	
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	Asp	Lys	Leu	Val	Tyr	Ala	Asp	Thr	Cys	Phe	Ser	Thr	Ile	Lys	Leu	Lys	
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	140					145				150						155	
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	Ala	Lys	Tyr	Pro	Ala	Glu	Ser	Pro	Asp	Tyr	Phe	Val	Asp	Phe	Pro	Val	
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	Pro	Phe	Cys	Ala	Ser	Trp	Thr	Pro	Gln	Ser	Ser	Leu	Ile	Ser	Ile	Tyr	
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	Ser	Gln	Phe	Leu	Ala	Ala	Ile	Glu	Ser	Leu	Lys	Ala	Phe	Trp	Asp	Val	
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	Met	Asp	Glu	Ile	Asp	Glu	Lys	Thr	Trp	Val	Leu	Glu	Pro	Glu	Lys	Pro	
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	Pro	Arg	Ser	Ala	Thr	Ala	Arg	Arg	Ile	Ala	Leu	Gly	Asn	Asn	Val	Ser	
	220					225				230						235	
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	Ile	Asn	Ile	Glu	Val	Asp	Pro	Arg	His	Pro	Thr	Met	Leu	Pro	Glu	Cys	
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	Lys	Ser	Asp	Phe	Thr	Met	Asp	Cys	Gly	Ile	Cys	Tyr	Ala	Tyr	Gln	Leu	
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	Pro	Phe	His	Gln	Ile	Cys	Leu	Tyr	Glu	Trp	Leu	Arg	Gly	Leu	Leu	Thr	
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	Ser	Arg	Gln	Ser	Phe	Asn	Ile	Ile	Phe	Gly	Glu	Cys	Pro	Tyr	Cys	Ser	
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	Lys	Pro	Ile	Thr	Leu	Lys	Met	Ser	Gly	Arg	Lys	His					
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Met Ala Ala Ile Gly Val His Leu Gly Cys Thr Ser Ala Cys						
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gtg gcc gtc tat aag gat ggc cgg gct ggt gtg gtt gca aat gat gcc						159
Val Ala Val Tyr Lys Asp Gly Arg Ala Gly Val Val Ala Asn Asp Ala						
15 20 25 30						
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Gly Asp Arg Val Thr Pro Ala Val Val Ala Tyr Ser Glu Asn Glu Glu						
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Ile Val Gly Leu Ala Ala Lys Gln Ser Arg Ile Arg Asn Ile Ser Asn						
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Thr Val Met Lys Val Lys Gln Ile Leu Gly Arg Ser Ser Ser Asp Pro						
65 70 75						
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Gln Ala Gln Lys Tyr Ile Ala Glu Ser Lys Cys Leu Val Ile Glu Lys						
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Asn Gly Lys Leu Arg Tyr Glu Ile Asp Thr Gly Glu Glu Thr Lys Phe						
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Val Asn Pro Glu Asp Val Ala Arg Leu Ile Phe Ser Lys Met Lys Glu						
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Thr Ala His Ser Val Leu Gly Ser Asp Ala Asn Asp Val Val Ile Thr						
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Ala Arg Ala Ala Gly Phe Asn Val Leu Arg Leu Ile His Glu Pro Ser						
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Cys	Gly	Gly	Ser	Ser	Arg	Ile	Pro	Lys	Leu	Gln	Gln	Leu	Ile	Lys	Asp		
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Asn	Leu	Leu	Val	Glu	Asp	Ser	Leu	Met	Ile	Glu	Cys	Ser	Ala	Arg	Asp		
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Gln	Ala	Pro	Gly	Ser	Ile	Ser	Ser	Val	Cys	Leu	Glu	Leu	Tyr	Glu	Ser		
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Val	Leu	Thr	Met	Lys	Arg	Asp	Gly	Ser	Leu	His	Val	Thr	Cys	Thr	Asp		
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Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys
1 5 10
gag cac ttg gtc aac ata tct gga ggg ccc atg aca tac agc cac cgg 218
Glu His Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg
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ctg gag gag atc cga cta cac ttt ggg agt gag gac agc caa ggg tcg 266
Leu Glu Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser
35 40 45
gag cac ctc ctc aat gga cag gcc ttc tct ggg gag ctt caa gag agg 314
Glu His Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg
50 55 60
gat ttg ttc atc ttg ttg act tct gta tca gga cat ctg ccc gat aca 362
Asp Leu Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr
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Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val Ser Ala Phe
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Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly	
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	Met Ala 1
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Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	Arg	Met	Gln	Cys	Lys	Ile		
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Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	Asp	Leu	Gln	Ala	Ala	Arg	Gly		
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Leu	Met	Cys	Ala	Ala	Ser	Val	Met	Ser	Phe	Leu	Ala	Phe	Met	Met	Ala		
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Tyr	Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His		
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 Met Arg Leu Gln Asp
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 Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met Met Leu Thr Thr Ala
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 Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile Phe Ile Arg Asp Val
 25 30 35
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 His Asn Phe Cys Ile Thr Tyr His Tyr Asp His Met Ser Phe His Tyr
 40 45 50
 acg gtc gtc ctg atg ttc tcc cag gtg atc agc atc tgc tgg gct gcc 306
 Thr Val Val Leu Met Phe Ser Gln Val Ile Ser Ile Cys Trp Ala Ala
 55 60 65
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 Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn Asn Ala Gln Arg Ser
 70 75 80 85
 cat gtt ctt caa ccg cct gtc ctt gga gtt tct ggc cat cga gta ccg 402
 His Val Leu Gln Pro Pro Val Leu Gly Val Ser Gly His Arg Val Pro
 90 95 100
 gga gga gca cca ctg agg cct ggg gag tcg gaa cag ggc taaggagggg 451
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 Thr Pro Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp
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 Ala Ala Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro
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 gcc cat tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc 196

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Cys	Glu	Glu	Arg	Asp	Val	Ser	Leu	Pro	Gln	Ser	Glu	His	Lys	Glu	Pro	
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Arg	Thr	Phe	Thr	Gly	Glu	His	Val	Val	Ala	Leu	Met	Pro	Glu	Val	Gly	
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Val	Tyr														
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Glu	Glu	Met	Lys	Ser	Leu	Ile	Arg	Leu	Pro	Asp	Ile	Ile	Ala	Cys	Ala		
				130					135					140			
aag	cag	aac	atc	acc	acg	gca	gaa	atc	agc	gcc	cgt	gaa	ggc	act	ggc		481
Lys	Gln	Asn	Ile	Thr	Thr	Ala	Glu	Ile	Ser	Ala	Arg	Glu	Gly	Thr	Gly		
				145					150					155			
tta	gca	ggg	gtg	ctg	gcc	tgg	ctc	cag	gcc	acc	cac	aga	gcc	aac	gat		529
Leu	Ala	Gly	Val	Leu	Ala	Trp	Leu	Gln	Ala	Thr	His	Arg	Ala	Asn	Asp		
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gctttgctgc	caatagtttc	ttctcacagg	ggcagaataa	cccaaagtaa	ccctacatga												649
tggggctctg	tgctgggatg	caatgatgtg	taaaactgagg	catgtggaga	tggaagtga												709
catctggcct	ctgaaaaaag	tgtccccagg	ggctaggcat	ggtggctcac	acctgtaatc												769
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gcaccttccg	gaaa	atg	gcg	gct	gcc	agg	ccc	agc	ctg	ggc	mga	gtc	ctc				170
		Met	Ala	Ala	Ala	Arg	Pro	Ser	Leu	Gly	Arg	Val	Leu				
		1				5					10						
cca	gga	tcc	tct	gtc	ctg	ttc	ctg	tgt	gac	atg	cag	gag	aag	ttc	cgc		218
Pro	Gly	Ser	Ser	Val	Leu	Phe	Leu	Cys	Asp	Met	Gln	Glu	Lys	Phe	Arg		
		15				20					25						
cac	aac	atc	gcc	tac	ttc	cca	cag	atc	gtc	tca	gtg	gct	gcc	cgc	atg		266
His	Asn	Ile	Ala	Tyr	Phe	Pro	Gln	Ile	Val	Ser	Val	Ala	Ala	Arg	Met		
	30				35				40								
ctc	aag	gtg	gcc	cgg	ctg	ctt	gag	gtg	cca	gtc	atg	ctg	acg	gag	cag		314
Leu	Lys	Val	Ala	Arg	Leu	Leu	Glu	Val	Pro	Val	Met	Leu	Thr	Glu	Gln		
	45			50			55				60						
tac	cca	caa	ggc	ctg	ggc	ccc	acg	gtg	ccc	gag	ctg	ggg	act	gag	ggc		362
Tyr	Pro	Gln	Gly	Leu	Gly	Pro	Thr	Val	Pro	Glu	Leu	Gly	Thr	Glu	Gly		
			65				70				75						
ctt	cgg	ccg	ctg	gcc	aag	acc	tgc	ttc	agc	atg	gtg	cct	gcc	ctg	cag		410
Leu	Arg	Pro	Leu	Ala	Lys	Thr	Cys	Phe	Ser	Met	Val	Pro	Ala	Leu	Gln		
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cag	gag	ctg	gac	agt	cgg	ccc	cag	ctg	cgc	tct	gtg	ctg	ctc	tgt	ggc		458
Gln	Glu	Leu	Asp	Ser	Arg	Pro	Gln	Leu	Arg	Ser	Val	Leu	Leu	Cys	Gly		
		95				100					105						
att	gag	gca	cag	gcc	tgc	atc	ttg	aac	acg	acc	ctg	gac	ctc	cta	gac		506
Ile	Glu	Ala	Gln	Ala	Cys	Ile	Leu	Asn	Thr	Thr	Leu	Asp	Leu	Leu	Asp		
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Arg Gly Leu Gln Val His Val Val Val Asp Ala Cys Ser Ser Arg Ser
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cag gtg gac cgt ctg gtg gct ctg gcc cgc atg aga cag agt ggt gcc      602
Gln Val Asp Arg Leu Val Ala Leu Ala Arg Met Arg Gln Ser Gly Ala
          145          150          155
ttc ctc tcc acc agc gaa ggg ctc att ctg cag ctt gtg ggc gat gcc      650
Phe Leu Ser Thr Ser Glu Gly Leu Ile Leu Gln Leu Val Gly Asp Ala
          160          165          170
gtc cac ccc cag ttc aag gag atc cag aaa ctc atc aag gag ccc gcc      698
Val His Pro Gln Phe Lys Glu Ile Gln Lys Leu Ile Lys Glu Pro Ala
          175          180          185
cca gac agc gga ctg ctg ggc ctc ttc caa ggc cag aac tcc ctc ctc      746
Pro Asp Ser Gly Leu Leu Gly Leu Phe Gln Gly Gln Asn Ser Leu Leu
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cac tgaactccaa cctgccttg agggaagacc accctcctgt caccgagacc      799
His
205
tcagtggaag cccgttcccc ccattccctgg atcccaagag tgggtgcgac caccaggagt      859
gccgccccct tgtggggggg ggcagggtgc tgccttccca ttggacagct gctcccgaa      919
atgcaaataa gactcctgga aactgggtgg gaattggctg agccaagatg gagggcgggc      979
tcggcccccg gccacttcac ggggcgggaa ggggagggga agaagagtct cagactgtgg      1039
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                               Met Trp Leu Tyr Arg Asn
                               1           5
ccc tac gtg gag gcg gag tat ttc ccc acc aag ccg atg ttt gtt att      163
Pro Tyr Val Glu Ala Glu Tyr Phe Pro Thr Lys Pro Met Phe Val Ile
          10          15          20
gca ttt ctc tct cca ctg tct ctg atc ttc ctg gcc aaa ttt ctc aag      211
Ala Phe Leu Ser Pro Leu Ser Leu Ile Phe Leu Ala Lys Phe Leu Lys
          25          30          35
aag gca gac aca aga gac agc aga caa gcc tgc ctg gct gcc agc ctt      259
Lys Ala Asp Thr Arg Asp Ser Arg Gln Ala Cys Leu Ala Ala Ser Leu
          40          45          50
gcc ctg gct ctg aat ggc gtc ttt acc aac aca ata aaa ctg atc gta      307
Ala Leu Ala Leu Asn Gly Val Phe Thr Asn Thr Ile Lys Leu Ile Val
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ggg agg cca cgc cca gat ttc ttc tac cgc tgc ttc cct gat ggg cta      355
Gly Arg Pro Arg Pro Asp Phe Phe Tyr Arg Cys Phe Pro Asp Gly Leu
          75          80          85
gcc cat tct gac ttg atg tgt aca ggg gat aag gac gtg gtg aat gag      403
Ala His Ser Asp Leu Met Cys Thr Gly Asp Lys Asp Val Val Asn Glu
          90          95          100
ggc cga aag agc ttc ccc agt gga cat tct tcc ttt gca ttt gct ggt      451
Gly Arg Lys Ser Phe Pro Ser Gly His Ser Ser Phe Ala Phe Ala Gly
          105          110          115

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Leu Ala Phe Ala Ser Phe Tyr Leu Ala Gly Lys Leu His Cys Phe Thr	
120 125 130	
cca caa ggc cgt ggg aaa tct tgg agg ttc tgt gcc ttt ctg tca cct	547
Pro Gln Gly Arg Gly Lys Ser Trp Arg Phe Cys Ala Phe Leu Ser Pro	
135 140 145 150	
cta ctt ttt gca gct gtg att gca ctg tcc cgc aca tgt gac tac aag	595
Leu Leu Phe Ala Ala Val Ile Ala Leu Ser Arg Thr Cys Asp Tyr Lys	
155 160 165	
cat cac tgg caa gat ctg ctc aaa tgc acc aac act gcc aag	637
His His Trp Gln Asp Leu Leu Lys Cys Thr Asn Thr Ala Lys	
170 175 180	
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tctgcccctt cttcacaatg gaatataagg aacaattatg ggatgtcatc agaatggatg	757
ccataggacc tacagctccc tttctcttta ttgtgattat actttaaata tgacattgtc	817
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atctgcttag ttctacaaag tggagtttct gggcatcatt cttcatttct gtacacaaag	180
tgctgtgaag ctcaagaaga aatagctctg cacaggaacg atg tgc act gcc cta	235
Met Cys Thr Ala Leu	
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ctg ctt ctt tat cta aga tgg tgt ttc aac tta aaa ctt gtg aat gtg	283
Leu Leu Leu Tyr Leu Arg Trp Cys Phe Asn Leu Lys Leu Val Asn Val	
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aaa tat gag cca aaa gac tct ctc ggc cct gaa atg acc ttt gta gca	331
Lys Tyr Glu Pro Lys Asp Ser Leu Gly Pro Glu Met Thr Phe Val Ala	
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gat gct gcc aga ggc ccc ctg tta tcc tcc ctg gac tct cca gct aac	379
Asp Ala Ala Arg Gly Pro Leu Leu Ser Ser Leu Asp Ser Pro Ala Asn	
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Leu Met Ser Thr Ala Ser Val Cys Ile Ser Leu Pro Glu Gly Cys Ser	
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ggg ggc agg agt cct tgc tac tca cag aaa tgg cca cca gaa gtg cca	475
Gly Gly Arg Ser Pro Cys Tyr Ser Gln Lys Trp Pro Pro Glu Val Pro	
70 75 80 85	
gaa aaa tta acc tcc ctt ggc cag cag tcc tca acc agc tcc ctc act	523
Glu Lys Leu Thr Ser Leu Gly Gln Gln Ser Ser Thr Ser Ser Leu Thr	
90 95 100	
gac act gat gtg cag gtg tct cct atg ctg gtt gct gga gtc aac cac	571
Asp Thr Asp Val Gln Val Ser Pro Met Leu Val Ala Gly Val Asn His	
105 110 115	
agc agc agc ctt ctt gac aac ata ccc ttc act ggc tgc ctt cct ttc	619
Ser Ser Ser Leu Leu Asp Asn Ile Pro Phe Thr Gly Cys Leu Pro Phe	
120 125 130	

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Lys
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atgtttcccg ggaagaactg ggataaagga aggggtcccag cacc atg gag gac ccg      176
                                Met Glu Asp Pro
                                1
aac cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt      224
Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser
5              10              15              20
ccc cag agc cca gga ggc aac atc tgc cac ctg ggg gcc ccg aag tgc      272
Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly Ala Pro Lys Cys
              25              30              35
acc cgc tgc ctc atc acc ttc gca gat tcc aag ttc cag gag cgt cac      320
Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe Gln Glu Arg His
              40              45              50
atg aag cgg gag cac cca gcg gac ttc gtg gcc cag aag ctg cag ggg      368
Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln Lys Leu Gln Gly
              55              60              65
gtc ctc ttc atc tgc ttc acc tgc gcc cgc tcc ttc ccc tcc tcc aaa      416
Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe Pro Ser Ser Lys
              70              75              80
gcc cta atc acc cac cag cgc agc cac ggt cca gcc gcc aag ccc acc      464
Ala Leu Ile Thr His Gln Arg Ser His Gly Pro Ala Ala Lys Pro Thr
85              90              95              100
ctg ccg gtt gca acc act act gcc cag ccc acc ttc cct tgt cct gac      512
Leu Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp
              105              110              115
tgt ggc aag acc ttt ggg cag gct gtt tct ctg agg cgg cac cgc cag      560
Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg His Arg Gln
              120              125              130
atg cat gag gtc cgt gcc cct cct gcc acc ttc gcc tgc aca gag tgc      608
Met His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Glu Cys
              135              140              145
ggg cag gac ttt gct cag gaa gca ggg ctg cat caa cac tac att cgg      656
Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His Tyr Ile Arg
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cat gcc cgg ggg gag ctc tgagtgcagc ttaagcctct ccacggtgac      704
His Ala Arg Gly Glu Leu
165              170
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 Met Glu Asp Pro
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 aac cct gaa gag aac atg aag cag cag gat tca ccc aag gag aga agt 224
 Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro Lys Glu Arg Ser
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 Pro Gln Pro Arg Arg Gln His Leu Pro Pro Gly Gly Pro Glu Val His
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 ccg ctg cct cat cac ctt cgc aga ttc caa gtt cca gga gcg tca cat 320
 Pro Leu Pro His His Leu Arg Arg Phe Gln Val Pro Gly Ala Ser His
 40 45 50
 gaa gcg gga gca ccc agc gga ctt cgt ggc cca gaa gct gca ggg ggt 368
 Glu Ala Gly Ala Pro Ser Gly Leu Arg Gly Pro Glu Ala Ala Gly Gly
 55 60 65
 cct ctt cat ctg ctt cac ctg cgc ccg ctc ctt ccc ctc ctc caa agc 416
 Pro Leu His Leu Leu His Leu Arg Pro Leu Leu Pro Leu Leu Gln Ser
 70 75 80
 cct aat cac cca cca gcg cag cac ggt cca gcc gcc aag ccc acc ctg 464
 Pro Asn His Pro Pro Ala Gln His Gly Pro Ala Ala Lys Pro Thr Leu
 85 90 95 100
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 Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro Cys Pro Asp Cys
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 Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg His Arg Gln Met
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 cat gag gtc cgt gcc cct cct ggc acc ttc gcc tgc aca gag tgc ggt 608
 His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys Thr Glu Cys Gly
 135 140 145
 cag gac ttt gct cag gaa gca ggg ctg cat caa cac tac att cgg cat 656
 Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His Tyr Ile Arg His
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 Ala Arg Gly Glu Leu
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Thr Asn Cys Ser Trp Trp Pro Ile Ser Ala Leu Glu Ser Asp Ala Ala
10           15           20           25
aag cca gcg gag gcc ccc gac gct ccc gag gcg gcc agc ccc gcc cat      150
Lys Pro Ala Glu Ala Pro Asp Ala Pro Glu Ala Ala Ser Pro Ala His
           30           35           40
tgg ccc agg gag agc ctg gtt ctg tac cac tgg acc cag tcc ttc agc      198
Trp Pro Arg Glu Ser Leu Val Leu Tyr His Trp Thr Gln Ser Phe Ser
           45           50           55
tcg cag aag gtg cgg ctg gtg atc gcc gag aag ggc ctg gtg tgc gag      246
Ser Gln Lys Val Arg Leu Val Ile Ala Glu Lys Gly Leu Val Cys Glu
           60           65           70
gag cgg gac gtg agc ctg cca cag agc gag cac aag gag ccc tgg ttc      294
Glu Arg Asp Val Ser Leu Pro Gln Ser Glu His Lys Glu Pro Trp Phe
           75           80           85
atg cgg ctc aac ctg ggc gag gag gtg ccc gtc atc atc cac cgc gac      342
Met Arg Leu Asn Leu Gly Glu Glu Val Pro Val Ile Ile His Arg Asp
90           95           100           105
aac atc atc agt gac tat gac cag atc att gac tat gtg gag cgc acc      390
Asn Ile Ile Ser Asp Tyr Asp Gln Ile Ile Asp Tyr Val Glu Arg Thr
           110           115           120
ttc aca gga gag cac gtg gtg gcc ctg atg ccc gag gtg ggc agc ctg      438
Phe Thr Gly Glu His Val Val Ala Leu Met Pro Glu Val Gly Ser Leu
           125           130           135
cag cac gca cgg gtg ctg cag tac cgg gag ctg ctg gac gca ctg ccc      486
Gln His Ala Arg Val Leu Gln Tyr Arg Glu Leu Leu Asp Ala Leu Pro
           140           145           150
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Met Asp Ala Tyr Thr His Gly Cys Ile Leu His Leu Glu Leu Thr Thr
           155           160           165
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Asp Ser Met Ile Pro Lys Tyr Ala Thr Ala Glu Ile Arg Arg His Leu
170           175           180           185
gcc aat gcc acc acg gac ctc atg aaa ctg gac cat gaa gag gag ccc      630
Ala Asn Ala Thr Thr Asp Leu Met Lys Leu Asp His Glu Glu Glu Pro
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cag ctc tcc gag ccc tac ctt tct aaa caa aag aag ctc atg gcc aag      678
Gln Leu Ser Glu Pro Tyr Leu Ser Lys Gln Lys Lys Leu Met Ala Lys
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atc ttg gag cat gat gat gtg agc tac ctg aag aag atc ctc ggg gaa      726
Ile Leu Glu His Asp Asp Val Ser Tyr Leu Lys Lys Ile Leu Gly Glu
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Leu Ala Met Val Leu Asp Gln Ile Glu Ala Glu Leu Glu Lys Arg Lys
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ctg gag aac gag ggg cag aaa tgc gag ctg tgg ctc tgt ggc tgt gcc      822
Leu Glu Asn Glu Gly Gln Lys Cys Glu Leu Trp Leu Cys Gly Cys Ala
250           255           260           265
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270	275	280	
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Val Leu Gly Asp Ile His Thr Thr Leu Leu Ser Ala Val Ile Pro Asn			
315	320	325	
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gaattggctg agccaagatg gagggggggc tggggccgg gccacttcac gggggcgggaa			1004
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Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val Gly Met
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Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val Ser Ala
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ttc att gaa aac aac atc gtg gtt ttt gaa aac ttc tgg gaa gga ctg      322
Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu Gly Leu
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tgg atg aat tgc gtg agg cag gct aac atc agg atg cag tgc aaa atc      370
Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile
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tat gat tcc ctg ctg gct ctt tct ccg gac cta cag gca gcc aga gga      418
Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly
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Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met Ala
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Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu Lys Val
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Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly
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Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly
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Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly
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Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
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acc gga aag aag tca ccg agc gtc tac tcc aga agt cag tat gtg      847
Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
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attacaggaa ctgtgcatca gctatttatg attctataag ctatttcagc agaatgagat      1027
attaaaccca atgctttgat tgttctagaa agtattgtaa tttgttttct aagggtgggttc      1087
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Tyr	Gln	Asp	Phe	Tyr	Ala	Phe	Asp	Leu	Ser	Gly	Ala	Thr	Arg	Val	Leu
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aaa	aag	aat	gaa	att	ctt	cat	ctg	aaa	tta	cct	ctc	aga	ctt	tct	193
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Trp	Gln	Val	Ala	Glu	Asp	Ser	Asp	Val	Ile	Lys	Ala	Val	Ser	Thr	Ile
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Ala	Val	His	Glu	Lys	Glu	Glu	Ser	Leu	Trp	Pro	Arg	Val	Ala	Val	Phe
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Ser	Thr	Leu	Ala	Pro	Gly	Val	Leu	His	Gly	Ala	Arg	Leu	Arg	Ser	Leu
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Ser Asp Ser Glu Glu Leu Ser Ser Leu Gln Val Leu Asp Ala Asp Thr	
175 180 185 190	
ttt gcc ttc tgc tgt gct tcg ggc cgg ctg ggg ctt gtt gac acc cgg	625
Phe Ala Phe Cys Cys Ala Ser Gly Arg Leu Gly Leu Val Asp Thr Arg	
195 200 205	
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Gln Lys Trp Ala Pro Leu Glu Asn Arg Ser Pro Gly Pro Gly Ser Gly	
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Pro Ser Ile Ala Ser Leu Ser Ser Asp Gly Arg Leu Cys Leu Leu Asp	
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Pro Arg Asp Leu Cys His Pro Val Ser Ser Val Gln Cys Pro Val Ser	
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355 360 365	
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Leu Gly Gly Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro
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cag tgg aga gtg tcg gcc ttc att gaa aac aac atc gtg gtt ttt      264
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Ser	Ala	Leu	Ile	Pro	Pro	Val	Glu	Glu	Thr	Val	Phe	Tyr	Pro	Ser	Pro	
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Lys	Trp	Trp	Asn	Asn	Leu	Ser	Asp	Gly	Gln	Arg	Thr	Val	Thr	Gly	Ile	
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Leu	Cys	Ser	Pro	Met	Leu	Leu	Ser	Thr	Phe	Ser	His	Phe	Ser	Leu	Phe	
205					210					215					220	
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Met Lys Arg Ser Gly Asn Pro Gly Ala Glu Val Thr Asn Ser				
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Ser Val Ala Gly Pro Asp Cys Cys Gly Gly Leu Gly Asn Ile Asp Phe				
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Arg Gln Ala Asp Phe Cys Val Met Thr Arg Leu Leu Gly Tyr Val Asp				
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Pro Leu Tyr Trp Asn Val Val Ala Arg Trp Glu His Lys Thr Arg Lys				
65 70 75				
ctg agc agg gcc ttc gga tcc ccc tac ctg gcc tgc tac tct cta agc				351
Leu Ser Arg Ala Phe Gly Ser Pro Tyr Leu Ala Cys Tyr Ser Leu Ser				
80 85 90				
atc acc atc ctg ctc ctg aac ttc ctg cgc tgc cac tgc ttc acg cag				399
Ile Thr Ile Leu Leu Leu Asn Phe Leu Arg Ser His Cys Phe Thr Gln				
95 100 105 110				
gcc atg ctg agc cag ccc agg atg gag agc ctg gac acc ccc gcg gcc				447
Ala Met Leu Ser Gln Pro Arg Met Glu Ser Leu Asp Thr Pro Ala Ala				
115 120 125				
tac agc ctg gtc ctc gca ctc ctg gga ctg ggc gtc gtg ctc gtg ctc				495
Tyr Ser Leu Val Leu Ala Leu Leu Gly Leu Gly Val Val Leu Val Leu				
130 135 140				
tcc agc ttc ttt gca ctg ggg ttc gct gga act ttc cta ggt gat tac				543
Ser Ser Phe Phe Ala Leu Gly Phe Ala Gly Thr Phe Leu Gly Asp Tyr				
145 150 155				
ttc ggg atc ctc aag gag gcg aga gtg acc gtg ttc ccc ttc aac atc				591
Phe Gly Ile Leu Lys Glu Ala Arg Val Thr Val Phe Pro Phe Asn Ile				
160 165 170				
ctg gac aac ccc atg tac tgg gga agc aca gcc aac tac ctg ggc tgg				639
Leu Asp Asn Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp				
175 180 185 190				
gcc atc atg cac gcc agc ccc acg ggc ctg ctc ctg acg gtg ctg gtg				687
Ala Ile Met His Ala Ser Pro Thr Gly Leu Leu Leu Thr Val Leu Val				

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195      200      205
gcc ctc acc tac ata gtg gct ctc cta tac gaa gag ccc ttc acc gct      735
Ala Leu Thr Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala
      210      215      220
gag atc tac cgg cag aaa gcc tcc ggg tcc cac aag agg agc      777
Glu Ile Tyr Arg Gln Lys Ala Ser Gly Ser His Lys Arg Ser
      225      230      235
tgattgagct gcaacagctt tgctgaaggc ctggccagcc tcttgacctg ccccaagtgg      837
caggccctgc gcagggcgag aatggtgcct gctgctcagg gctcgcccc ggcgtgggct      897
gccccagtcg cttggaacct gctgccttgg ggacctgga cgtgccgaca tatggccatt      957
gagctccaac ccacacattc ccattcacca ataaaggcac cctgacctca aaaaaaaaaa      1017
aaaaaa                                           1023

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<213> Homo sapiens

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<400> 169
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caa cag ctt ctc cat cac gcc aga aat ggc aat gct gaa gaa gta aga      103
Gln Gln Leu Leu His His Ala Arg Asn Gly Asn Ala Glu Glu Val Arg
      10      15      20
caa cta tta gag acc atg gcg agt aat gaa gtg att gct gac att aat      151
Gln Leu Leu Glu Thr Met Ala Ser Asn Glu Val Ile Ala Asp Ile Asn
      25      30      35
tgc aaa gga aga agt aag tct aac ttg ggc tgg aca ccc cta cat ctg      199
Cys Lys Gly Arg Ser Lys Ser Asn Leu Gly Trp Thr Pro Leu His Leu
      40      45      50
gca tgc tat ttt gga cac aga caa gtg gtc cag gat ctg ttg aag gct      247
Ala Cys Tyr Phe Gly His Arg Gln Val Val Gln Asp Leu Leu Lys Ala
      55      60      65      70
ggg gca gaa gtg aat gtg ttg aat gac atg gga gac acg ccg ctt cat      295
Gly Ala Glu Val Asn Val Leu Asn Asp Met Gly Asp Thr Pro Leu His
      75      80      85
cga gct gcc ttt aca gga cga aag gtg aaa atc att cta tgt tca atg      343
Arg Ala Ala Phe Thr Gly Arg Lys Val Lys Ile Ile Leu Cys Ser Met
      90      95      100
ttt gta agt gag gta ttt gga gga gta gtt acc att gtt ttc tct gtt      391
Phe Val Ser Glu Val Phe Gly Gly Val Val Thr Ile Val Phe Ser Val
      105      110      115
ata acc atc tgaccagcaa ccgaagaaag ccacacaaaa aaatgtatac      440
Ile Thr Ile
      120
accagcactt tgggtcaaaa ggccacagga tcttttgagt ctgacagtga ggtccagtac      500
taaggtcatg gagaccccc ctctgtagca tccctgtgag gagatcattc cgtttctgct      560
tgtgtactcc agcaatgggg aactcctgat tattcttttt ttttaaaaaa aaatagcttc      620
attgaggtat aacttacatt gcataaactt cacctgtgat attgtgaaat atatatttgg      680
tctttgacct tgtacactaa agatgtacaa aaagatgact ggcaaccctt ggcttcagga      740
tggggggctgg tcaccagaaa gaccaaggca ggactagggg gttgggactt tcagccgaac      800
tttgcaacct ccagggaggg tagaggggct gaaggggaaa tggctcgcta atggccagtg      860
gtttcatcaa tcatgcctat ttaatggaac ctccataaaa acctgaaagg acaggggttct      920

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aggagctcct gggtagctga acacgtggag gttcttgaat gatcacaccc agggaggggca 980
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 <222> 63..572

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 Met Arg Leu Gln Gly Ala Ile Phe Val Leu Leu Pro His Leu Gly
 1 5 10 15
 ccc atc ctg gtc tgg ctg ttc act cgt gat cac atg tct ggt tgg tgt 155
 Pro Ile Leu Val Trp Leu Phe Thr Arg Asp His Met Ser Gly Trp Cys
 20 25 30
 gag ggc ccg agg atg ctg tcc tgg tgc cca ttc tac aaa gtc tta ttg 203
 Glu Gly Pro Arg Met Leu Ser Trp Cys Pro Phe Tyr Lys Val Leu Leu
 35 40 45
 ctt gta cag aca gcc atc tac tct gtc gtg ggc tat gcc tcc tac ctg 251
 Leu Val Gln Thr Ala Ile Tyr Ser Val Val Gly Tyr Ala Ser Tyr Leu
 50 55 60
 gtg tgg aag gac ctg gga ggg ggc ttg ggg tgg ccc ctg gcc ctg cct 299
 Val Trp Lys Asp Leu Gly Gly Gly Leu Gly Trp Pro Leu Ala Leu Pro
 65 70 75
 ctt ggc ctc tat gct gtt cag ctc acc atc agc tgg act gtc ctg gtt 347
 Leu Gly Leu Tyr Ala Val Gln Leu Thr Ile Ser Trp Thr Val Leu Val
 80 85 90 95
 ctc ttt ttc aca gtc cac aac cct ggt ctg gcc ctg ctg cac ctg ctg 395
 Leu Phe Phe Thr Val His Asn Pro Gly Leu Ala Leu Leu His Leu Leu
 100 105 110
 ctg ctg tat ggg ctg gtg gtg agc aca gca ctg atc tgg cat ccc atc 443
 Leu Leu Tyr Gly Leu Val Val Ser Thr Ala Leu Ile Trp His Pro Ile
 115 120 125
 aac aaa ctg gct gcc ctg tta ctg ctg ccc tac cta gcc tgg ctc acc 491
 Asn Lys Leu Ala Ala Leu Leu Leu Leu Pro Tyr Leu Ala Trp Leu Thr
 130 135 140
 gtg act tca gcc ctc acc tac cac ctg tgg agg gac agc ctt tgt cca 539
 Val Thr Ser Ala Leu Thr Tyr His Leu Trp Arg Asp Ser Leu Cys Pro
 145 150 155
 gtg cac cag cct cag ccc acg gag aag agt gac tgaggcccta gggcatggga 592
 Val His Gln Pro Gln Pro Thr Glu Lys Ser Asp
 160 165 170
 gaggagggac gcccagggtg gggaggaaga gtctgcaagc agggctgtgg agttaggggt 652
 caccccaatg ggaccaccct cctgggtccc ctggtgccgt ttttccttag aaatcagaga 712
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 aaaa 776

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<220>
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<400> 171

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ggtttccgga ggacagccaa caagcgatgc tgccgccgcc gtttcctgat tggttgtggg      120
tggctacctc ttcgttctga ttggccgcta gtgagcaag atg ctg agc aag ggt      174
                               Met Leu Ser Lys Gly
                               1           5
ctg aag cgg aaa cgg gag gag gag gag gag aag gaa cct ctg gca gtc      222
Leu Lys Arg Lys Arg Glu Glu Glu Glu Glu Lys Glu Pro Leu Ala Val
                               10           15           20
gac tcc tgg tgg cta gat cct ggc cac aca gcg gtg gca cag gca ccc      270
Asp Ser Trp Trp Leu Asp Pro Gly His Thr Ala Val Ala Gln Ala Pro
                               25           30           35
ccg gcc gtg gcc tct agc tcc ctc ttt gac ctc tca gtg ctc aag ctc      318
Pro Ala Val Ala Ser Ser Ser Leu Phe Asp Leu Ser Val Leu Lys Leu
                               40           45           50
cac cac agc ctg cag cag agt gag ccg gac ctg cgg cac ctg gtg ctg      366
His His Ser Leu Gln Gln Ser Glu Pro Asp Leu Arg His Leu Val Leu
                               55           60           65
gtc gtg aac act ctg cgg cgc atc cag gcg tcc atg gca ccc gcg gct      414
Val Val Asn Thr Leu Arg Arg Ile Gln Ala Ser Met Ala Pro Ala Ala
70                               75                               80           85
gcc ctg cca cct gtg cct agc cca cct gca gcc ccc agt gtg gct gac      462
Ala Leu Pro Pro Val Pro Ser Pro Pro Ala Ala Pro Ser Val Ala Asp
                               90           95           100
aac tta ctg gca agc tcg gac gct gcc ctt tca gcc tcc atg gcc agc      510
Asn Leu Leu Ala Ser Ser Asp Ala Ala Leu Ser Ala Ser Met Ala Ser
                               105           110           115
ctc ctg gag gac ctc agc cac att gag ggc ctg agt cag gct ccc caa      558
Leu Leu Glu Asp Leu Ser His Ile Glu Gly Leu Ser Gln Ala Pro Gln
120                               125           130
ccc ttg gca gac gag ggg cca cca ggc cgt agc atc ggg gga gca gcg      606
Pro Leu Ala Asp Glu Gly Pro Pro Gly Arg Ser Ile Gly Gly Ala Ala
135                               140           145
ccc agc ctg ggt gcc ttg gac ctg ctg ggc cca gcc act ggc tgt cta      654
Pro Ser Leu Gly Ala Leu Asp Leu Leu Gly Pro Ala Thr Gly Cys Leu
150                               155           160           165
ctg gac gat ggg ctt gag ggc ctg ttt gag gat att gac acc tct atg      702
Leu Asp Asp Gly Leu Glu Gly Leu Phe Glu Asp Ile Asp Thr Ser Met
170                               175           180
tat gac aat gaa ctt tgg gca cca gcc tct gag ggc ctc aaa cca ggc      750
Tyr Asp Asn Glu Leu Trp Ala Pro Ala Ser Glu Gly Leu Lys Pro Gly
185                               190           195
cct gag gat ggg ccg ggc aag gag gaa gct ccg gag ctg gac gag gcc      798
Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro Glu Leu Asp Glu Ala
200                               205           210
gaa ttg gac tac ctc atg gat gtg ctg gtg ggc aca cag gca ctg gag      846
Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly Thr Gln Ala Leu Glu
215                               220           225
cga ccg ccg ggg cca ggg cgc tgagccctcg tgctggaatg gttgtctggt      897
Arg Pro Pro Gly Pro Gly Arg
230                               235
atctgaactg agcctgctgg ctggaccaac tgcctcga aagacacagc tggcttcct      957
agtacagaga acagggcttg ggccactttg gagagacaga atctagtcct gggcaacttc      1017
acatccgtcc tctgtctca gggctggcag ggggagcctg gaattacccc ctagtgatgg      1077

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aatgacaggg tctggtgggg acttaattcc ctggccctgg ggtcatagct tgggctgttc 1137
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 atctcaaaaa aaaaaaaaaa aa 1219

<210> 172

<211> 1487

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 68..640

<400> 172

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 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu
 1 5 10
 ata aca ttt gta ttt caa gaa aag gaa gat ctt cct gtt aca gag gat 157
 Ile Thr Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp
 15 20 25 30
 aac ttt gtg aaa ctt caa gtt aaa gct tgt gct ctg agc cag ata aat 205
 Asn Phe Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn
 35 40 45
 aca aag ctt ctg gca gaa atg aag atg aaa aag gat tta ttt cct gtt 253
 Thr Lys Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val
 50 55 60
 ggg aga gaa att gct gga att gta tta gat gtt gga agc aag gta tca 301
 Gly Arg Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser
 65 70 75
 ttc ttt caa cca gat gat gaa gta gtt gga att ttg ccc ctg gac tct 349
 Phe Phe Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser
 80 85 90
 gaa gac cct gga ctt tgt gaa gtt gtt aga gta cat gag cat tac ttg 397
 Glu Asp Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu
 95 100 105 110
 gtt cat aaa cca gaa aag gtc aca tgg acg gaa gca gca gga agc att 445
 Val His Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile
 115 120 125
 cgg gat gga gtg cgt gcc tat aca gct ctg cat tat ctt tct cat ctc 493
 Arg Asp Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu
 130 135 140
 tct cct gga aaa tca gtg ctg ata atg gat gga gca agt gca ttt ggt 541
 Ser Pro Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly
 145 150 155
 aca ata gct att cag tta gca cat cat aga gga gcc aaa gta ttt caa 589
 Thr Ile Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Phe Gln
 160 165 170
 cag cat gca gcc ttg aag ata agc agt gcc ttg aaa gat tca gac ctc 637
 Gln His Ala Ala Leu Lys Ile Ser Ser Ala Leu Lys Asp Ser Asp Leu
 175 180 185 190
 cca tagcccgagt gattgatgta tctaattggga aagttcatgt tgctgaaagc 690
 Pro
 tgtttggaag aaacaggtgg cctgggagta gatattgtcc tagatgctgg agtgagatta 750
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<210> 173

<211> 1915

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 132..1298

<400> 173

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gcaccgcgcc c atg gca gag cca gac ccc tct cac cct ctg gag acc cag 170
Met Ala Glu Pro Asp Pro Ser His Pro Leu Glu Thr Gln
1 5 10
gca ggg aag gtg cag gag gct cag gac tca gat tca gac tct gag gga 218
Ala Gly Lys Val Gln Glu Ala Gln Asp Ser Asp Ser Asp Ser Glu Gly
15 20 25
gga gcc gct ggt gga gaa gca gac atg gac ttc ctg cgg aac tta ttc 266
Gly Ala Ala Gly Gly Glu Ala Asp Met Asp Phe Leu Arg Asn Leu Phe
30 35 40 45
tcc cag acg ctc agc ctg ggc agc cag aag gag cgt ctg ctg gac gag 314
Ser Gln Thr Leu Ser Leu Gly Ser Gln Lys Glu Arg Leu Leu Asp Glu
50 55 60
ctg acc ttg gaa ggg gtg gcc cgg tac atg cag agc gaa cgc tgt cgc 362
Leu Thr Leu Glu Gly Val Ala Arg Tyr Met Gln Ser Glu Arg Cys Arg
65 70 75
aga gtc atc tgt ttg gtg gga gct gga atc tcc aca tcc gca ggc atc 410
Arg Val Ile Cys Leu Val Gly Ala Gly Ile Ser Thr Ser Ala Gly Ile
80 85 90
ccc gac ttt cgc tct cca tcc acc ggc ctc tat gac aac cta gag aag 458
Pro Asp Phe Arg Ser Pro Ser Thr Gly Leu Tyr Asp Asn Leu Glu Lys
95 100 105
tac cat ctt ccc tac cca gag gcc atc ttt gag atc agc tat ttc aag 506
Tyr His Leu Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys
110 115 120 125
aaa cat ccg gaa ccc ttc ttc gcc ctc gcc aag gaa ctc tat cct ggg 554
Lys His Pro Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly
130 135 140
cag ttc aag cca acc atc tgt cac tac ttc atg cgc ctg ctg aag gac 602
Gln Phe Lys Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp
145 150 155
aag ggg cta ctc ctg cgc tgc tac acg cag aac ata gat acc ctg gag 650
Lys Gly Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu
160 165 170
cga ata gcc ggg ctg gaa cag gag gac ttg gtg gag gcg cac ggc acc 698
Arg Ile Ala Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr
175 180 185

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Phe Tyr Thr Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro	
190 195 200 205	
cta agc tgg atg aaa gag aag atc ttc tct gag gtg acg ccc aag tgt	794
Leu Ser Trp Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys	
210 215 220	
gaa gac tgt cag agc ctg gtg aag cct gat atc gtc ttt ttt ggt gag	842
Glu Asp Cys Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu	
225 230 235	
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Ser Leu Pro Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys	
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Val Asp Leu Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe	
255 260 265	
gcc tcc ctc atc agc aag gca ccc ctc tcc acc cct cgc ctg ctc atc	986
Ala Ser Leu Ile Ser Lys Ala Pro Leu Ser Thr Pro Arg Leu Leu Ile	
270 275 280 285	
aac aag gag aaa gct ggc cag tcg gac cct ttc ctg ggg atg att atg	1034
Asn Lys Glu Lys Ala Gly Gln Ser Asp Pro Phe Leu Gly Met Ile Met	
290 295 300	
ggc ctc gga gga ggc atg gac ttt gac tcc aag aag gcc tac agg gac	1082
Gly Leu Gly Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp	
305 310 315	
gtg gcc tgg ctg ggt gaa tgc gac cag ggc tgc ctg gcc ctt gct gag	1130
Val Ala Trp Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu	
320 325 330	
ctc ctt gga tgg aag aag gag ctg gag gac ctt gtc cgg agg gag cac	1178
Leu Leu Gly Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His	
335 340 345	
gcc agc ata gat gcc cag tcg ggg gcg ggg gtc ccc aac ccc agc act	1226
Ala Ser Ile Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr	
350 355 360 365	
tca gct tcc ccc aag aag tcc ccg cca cct gcc aag gac gag gcc agg	1274
Ser Ala Ser Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg	
370 375 380	
aca aca gag agg gag aaa ccc cag tgacagctgc atctcccagg cgggatgccg	1328
Thr Thr Glu Arg Glu Lys Pro Gln	
385	
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gtctggggag ctccagaacat cccccaatct cttacagctc cctccccaaa actgggggtcc	1448
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<210> 174

<211> 1990

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 259..1701

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 tatctgtctg agcagtggaa tgtgccagga aagaaggagc aaccactgac tgatgaacct 180
 ttgccagtct cccttccaag agggatgccca gagccttctg taagctcctc agatgtcact 240
 ggtatctagg caacaggg atg agc ctg aac ctc cct gag gcc agc tta ctt 291
 Met Ser Leu Asn Leu Pro Glu Ala Ser Leu Leu
 1 5 10
 agc aga gca tcc tgg cca gaa caa gcc aag gag cca aga cga gag gga 339
 Ser Arg Ala Ser Trp Pro Glu Gln Ala Lys Glu Pro Arg Arg Glu Gly
 15 20 25
 cac acg gac aaa caa cag aca gaa gac gta ctg gcc gct gga ctc cgc 387
 His Thr Asp Lys Gln Gln Thr Glu Asp Val Leu Ala Ala Gly Leu Arg
 30 35 40
 tgc ctc ccc cat ctc ccc gcc atc tgc gcc cgg agg atg agc cca gcc 435
 Cys Leu Pro His Leu Pro Ala Ile Cys Ala Arg Arg Met Ser Pro Ala
 45 50 55
 ttc agg gcc atg gat gtg gag ccc cgc gca aaa ggc gtc ctt ctg gag 483
 Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Val Leu Leu Glu
 60 65 70 75
 ccc ttt gtc cac cag gtc ggg ggg cac tca tgc gtg ctc cgc ttc aat 531
 Pro Phe Val His Gln Val Gly Gly His Ser Cys Val Leu Arg Phe Asn
 80 85 90
 gag aca acc ctg tgc aag ccc ctg gtc cca agg gaa cat cag ttc tac 579
 Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu His Gln Phe Tyr
 95 100 105
 gag acc ctc cct gct gag atg cgc aaa ttc act ccc cag tac aaa ggt 627
 Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro Gln Tyr Lys Gly
 110 115 120
 gtg gta tct gtg cgc ttt gaa gaa gat gaa gac agg aac ttg tgt cta 675
 Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg Asn Leu Cys Leu
 125 130 135
 ata gca tat cca ttg aaa ggg gac cat gga att gtg gac att gta gat 723
 Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val Asp Ile Val Asp
 140 145 150 155
 aat tca gac tgt gaa cca aaa agt aag ctc cta agg tgg aca aca aac 771
 Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Arg Trp Thr Thr Asn
 160 165 170
 aaa aaa cat cat gtc tta gaa aca gaa aag acc cct aag gac tgg gtg 819
 Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro Lys Asp Trp Val
 175 180 185
 cgt cag cac cgt aaa gag gag aaa atg aag agc cat aag tta gaa gaa 867
 Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His Lys Leu Glu Glu
 190 195 200
 gaa ttt gag tgg cta aag aaa tct gaa gtc ttg tac tac act gta gag 915
 Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr Tyr Thr Val Glu
 205 210 215
 aag aag ggg aat ata agt tcc cag ctt aaa cac tat aac cct tgg agc 963
 Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr Asn Pro Trp Ser
 220 225 230 235
 atg aaa tgt cac cag caa cag tta cag aga atg aag gag aat gca aag 1011
 Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys Glu Asn Ala Lys
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 cat cgg aac cag tac aaa ttt atc tta ctg gaa aac ctg act tcc cgc 1059
 His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn Leu Thr Ser Arg
 255 260 265
 tat gag gtg cct tgt gtc ctt gac ctc aag atg ggc aca cga caa cat 1107

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Gly	Asp	Asp	Ala	Ser	Glu	Glu	Lys	Ala	Ala	Asn	Gln	Ile	Arg	Lys	Cys		
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Gln	Gln	Ser	Thr	Ser	Ala	Val	Ile	Gly	Val	Arg	Val	Cys	Gly	Met	Gln		
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Val	Tyr	Gln	Ala	Gly	Ser	Gly	Gln	Leu	Met	Phe	Met	Asn	Lys	Tyr	His		
				320					325					330			
gga	cgg	aag	cta	tcg	gtg	cag	ggc	ttc	aag	gag	gca	ctt	ttc	cag	ttc	1299	
Gly	Arg	Lys	Leu	Ser	Val	Gln	Gly	Phe	Lys	Glu	Ala	Leu	Phe	Gln	Phe		
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ttc	cac	aat	ggg	cgg	tac	ctg	cgc	cgt	gaa	ctc	ctg	ggc	cct	gtg	ctc	1347	
Phe	His	Asn	Gly	Arg	Tyr	Leu	Arg	Arg	Glu	Leu	Leu	Gly	Pro	Val	Leu		
		350					355					360					
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Lys	Lys	Leu	Thr	Glu	Leu	Lys	Ala	Val	Leu	Glu	Arg	Gln	Glu	Ser	Tyr		
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cgc	ttc	tac	tca	agc	tcc	ctg	ctg	gtc	att	tat	gat	ggc	aag	gag	cgg	1443	
Arg	Phe	Tyr	Ser	Ser	Ser	Leu	Leu	Val	Ile	Tyr	Asp	Gly	Lys	Glu	Arg		
380					385					390					395		
ccc	gaa	gtg	gtc	ctg	gac	tca	gat	gct	gag	gat	ttg	gag	gac	ctg	tca	1491	
Pro	Glu	Val	Val	Leu	Asp	Ser	Asp	Ala	Glu	Asp	Leu	Glu	Asp	Leu	Ser		
				400					405					410			
gag	gaa	tca	gct	gat	gag	tct	gct	ggt	gcc	tat	gcc	tac	aaa	ccc	atc	1539	
Glu	Glu	Ser	Ala	Asp	Glu	Ser	Ala	Gly	Ala	Tyr	Ala	Tyr	Lys	Pro	Ile		
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ggc	gcc	agc	tct	gta	gat	gtg	cgc	atg	atc	gac	ttt	gca	cac	acc	acc	1587	
Gly	Ala	Ser	Val	Asp	Val	Arg	Met	Ile	Asp	Phe	Ala	His	Thr	Thr			
		430					435					440					
tgc	agg	ctg	tat	ggc	gag	gac	acc	gtg	gtg	cat	gag	ggc	cag	gat	gct	1635	
Cys	Arg	Leu	Tyr	Gly	Glu	Asp	Thr	Val	Val	His	Glu	Gly	Gln	Asp	Ala		
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Gly	Tyr	Ile	Phe	Gly	Leu	Gln	Ser	Leu	Ile	Asp	Ile	Val	Thr	Glu	Ile		
460					465					470					475		
agt	gag	gag	agt	ggg	gag	tgagcttgct	agctgctcca	gtacttgaga								1731	
Ser	Glu	Glu	Ser	Gly	Glu												
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gcgactctgt	gtcccaggma	cagctgtgct	gcgtcaggga	ggaagccagt	atggccaggt											1791	
ggtggctect	gcagcctgga	gctgatgtgc	agtggcctct	gtgagcccca	gcctgagcca											1851	
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cctggcagaa tcaagatgag gccctgtcat gcctccccag tgaggcctac agtctgagca	180
gacagcatgg cctgccaactg gcagtgaaca cc atg tct gca gga ggt ggc cgg	233
Met Ser Ala Gly Gly Gly Arg	
1 5	
gcc ttt gct tgg caa gtg ttc ccc ccc atg ccc act tgc cgg gtc tat	281
Ala Phe Ala Trp Gln Val Phe Pro Pro Met Pro Thr Cys Arg Val Tyr	
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ggc aca gtg gca cac caa gat ggg cac ctg ctg gtg ttg ggg ggt tgt	329
Gly Thr Val Ala His Gln Asp Gly His Leu Leu Val Leu Gly Gly Cys	
25 30 35	
ggc cgg gct gga ctg ccc ctg gac act gct gag aca ctg gac atg gcc	377
Gly Arg Ala Gly Leu Pro Leu Asp Thr Ala Glu Thr Leu Asp Met Ala	
40 45 50 55	
tcg cac aca tgg ctg gca ctg gca ccc ctg ccc act gcc cgg gct ggt	425
Ser His Thr Trp Leu Ala Leu Ala Pro Leu Pro Thr Ala Arg Ala Gly	
60 65 70	
gca gct gcg gta gtt ctg ggc aag cag gtg cta gtg gtg ggt ggt gtg	473
Ala Ala Ala Val Val Leu Gly Lys Gln Val Leu Val Val Gly Gly Val	
75 80 85	
gat gag gtc cag agc ccg gta gct gct gta gag gcc ttc ctg atg gat	521
Asp Glu Val Gln Ser Pro Val Ala Ala Val Glu Ala Phe Leu Met Asp	
90 95 100	
gag ggc cgc tgg gag cgt cgg gcc acc ctc cct caa gca gcc atg ggg	569
Glu Gly Arg Trp Glu Arg Arg Ala Thr Leu Pro Gln Ala Ala Met Gly	
105 110 115	
gtt gca act gtg gag aga gat ggt atg gtg tat gct ctg ggg gga atg	617
Val Ala Thr Val Glu Arg Asp Gly Met Val Tyr Ala Leu Gly Gly Met	
120 125 130 135	
ggc cct gac acg gcc ccc cag gcc cag gta cgt gtg tat gag ccc cgt	665
Gly Pro Asp Thr Ala Pro Gln Ala Gln Val Arg Val Tyr Glu Pro Arg	
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Arg Asp Cys Trp Leu Ser Leu Pro Ser Met Pro Thr Pro Cys Tyr Gly	
155 160 165	
gcc tcc acc ttc ctg cac ggg aac aag atc tat gtc ctg ggg ggc cgc	761
Ala Ser Thr Phe Leu His Gly Asn Lys Ile Tyr Val Leu Gly Gly Arg	
170 175 180	
cag ggc aag ctc ccg gtg act gct ttt gaa gcc ttt gat ctg gag gcc	809
Gln Gly Lys Leu Pro Val Thr Ala Phe Glu Ala Phe Asp Leu Glu Ala	
185 190 195	
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Arg Thr Trp Thr Arg His Pro Ser Leu Pro Ser Arg Arg Ala Phe Ala	
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Gly Cys Ala Met Ala Glu Gly Ser Val Phe Ser Leu Gly Gly Leu Gln	
220 225 230	
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Gln Pro Gly Pro His Asn Phe Tyr Ser Arg Pro His Phe Val Asn Thr	
235 240 245	
gtg gag atg ttt gac ctg gag cat ggg tcc tgg acc aaa ttg ccc cgc	1001
Val Glu Met Phe Asp Leu Glu His Gly Ser Trp Thr Lys Leu Pro Arg	
250 255 260	
agc ctg cgc atg agg gat aag agg gca gac ttt gtg gtt ggg tcc ctt	1049
Ser Leu Arg Met Arg Asp Lys Arg Ala Asp Phe Val Val Gly Ser Leu	
265 270 275	
ggg ggc cac att gtg gcc att ggg ggc ctt gga aac cag cca tgt cct	1097
Gly Gly His Ile Val Ala Ile Gly Gly Leu Gly Asn Gln Pro Cys Pro	

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Leu Gly Ser Val Glu Ser Phe Ser Leu Ala Arg Arg Arg Trp Glu Ala							
	300			305		310	
ttg cct gcc atg ccc act gcc cgc tgc tcc tgc tct agt ctg cag gct							1193
Leu Pro Ala Met Pro Thr Ala Arg Cys Ser Cys Ser Ser Leu Gln Ala							
	315			320		325	
ggg ccc cgg ctg ttt gtt att ggg ggt gtg gcc cag ggc ccc agt caa							1241
Gly Pro Arg Leu Phe Val Ile Gly Gly Val Ala Gln Gly Pro Ser Gln							
	330			335		340	
gcc gtg gag gca ctg tgt ctg cgt gat ggg gtc tgaaggcttg gtgggagctg							1294
Ala Val Glu Ala Leu Cys Leu Arg Asp Gly Val							
	345			350			
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tacctttatc accattcgtt catgaatcat gcctagctcc atccttgccc tgggacctac							1534
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tctctgtgcc tcagcatcct catctataaa tggggatctc tgaaaccttc ctaccctacc							1894
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 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu
 1 5 10
 ata aca ttt gta ttt caa taaaaggaag atcttctctgt tacagaggat 157
 Ile Thr Phe Val Phe Gln
 15 20
 aactttgtga aacttcaagt taaagcttgt gctctgagcc agataaatac aaagcttctg 217
 gcagaaatga agatgaaaaa ggatttattt cctgttgga gagaaattgc tggaattgta 277
 ttagatgttg gaagcaaggt atcattcctt caaccagatg atgaagtagt tggaattttg 337
 cccctggact ctgaagaccc tggactttgt gaagttgtta gagtacatga gcattacttg 397
 gttcataaac cagaaaaggt cacatggacg gaagcagcag gaagcattcg ggatggagtg 457
 cgtgcctata cagctctgca ttatctttct catctctctc ctggaaaatc agtgctgata 517
 atggatggag caagtgcatt tggtagaata gctattcagt tagcacatca tagaggagcc 577
 aaagtgattt caacagcatg cagccttgaa gataagcagt gccttgaaag attcagacct 637
 cccatagccc gagtgattga tgtatctaag gggaaagttc atgttgctga aagctgtttg 697
 gaagaaacag gtggcctggg agtagatatt gtccatagat ctggagttag attatatagt 757
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 gatagccact gcctttttcct caagggagca acgttagctt tcctgaatga tgaagtttgg 937
 aatttgtaaa atgtacaaca gggaamaata tctttgtatc ttaaaggatg tgatggagaa 997
 gttatcaact ggtgttttca gacctcagtt ggatgaaccc attccactgt atgaggcaaa 1057

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aagtaacgta ttaattttgt atcaactccg ttctcaacac cttccttaag tctttgctgt 1537
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<213> Homo sapiens

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<222> 65..1024

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Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile
1 5 10 15
aca ttt gta ttt caa gaa aag gaa gat ctt cct gtt aca gag gat aac 157
Thr Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn
20 25 30
ttt gtg aaa ctt caa gtt aaa gct tgt gct ctg agc cag ata aat aca 205
Phe Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn Thr
35 40 45
aag ctt ctg gca gaa atg aag atg aaa aag gat tta ttt cct gtt ggg 253
Lys Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val Gly
50 55 60
aga gaa att gct gga att gta tta gat gtt gga agc aag gta tca ttc 301
Arg Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser Phe
65 70 75
ttt caa cca gat gat gaa gta gtt gga att ttg ccc ctg gac tct gaa 349
Phe Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser Glu
80 85 90 95
gac cct gga ctt tgt gaa gtt gtt aga gta cat gag cat tac ttg gtt 397
Asp Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu Val
100 105 110
cat aaa cca gaa aag gtc aca tgg acg gaa gca gca gga agc att cgg 445
His Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile Arg
115 120 125
gat gga gtg cgt gcc tat aca gct ctg cat tat ctt tct cat ctc tct 493
Asp Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu Ser
130 135 140
cct gga aaa tca gtg ctg ata atg gat gga gca agt gca ttt ggt aca 541
Pro Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly Thr
145 150 155
ata gct att cag tta gca cat cat aga gga gcc aaa gtg att tca aca 589
Ile Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Ile Ser Thr
160 165 170 175
gca tgc agc ctt gaa gat aag cag tgc ctt gaa aga ttc aga cct ccc 637
Ala Cys Ser Leu Glu Asp Lys Gln Cys Leu Glu Arg Phe Arg Pro Pro
180 185 190

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195 200 205	
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Ser Cys Leu Glu Glu Thr Gly Gly Leu Gly Val Asp Ile Val Leu Asp	
210 215 220	
gct gga gtg aga tta tat agt aaa gat gat gaa cca gct gta aaa cta	781
Ala Gly Val Arg Leu Tyr Ser Lys Asp Asp Glu Pro Ala Val Lys Leu	
225 230 235	
caa cta cta cca cat aaa cat gat atc atc aca ctt ctt ggt gtt gga	829
Gln Leu Leu Pro His Lys His Asp Ile Ile Thr Leu Leu Gly Val Gly	
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Gly His Trp Val Thr Thr Glu Glu Asn Leu Gln Leu Asp Pro Pro Asp	
260 265 270	
agc cac tgc ctt ttc ctc aag gga gca acg tta gct ttc ctg aat gat	925
Ser His Cys Leu Phe Leu Lys Gly Ala Thr Leu Ala Phe Leu Asn Asp	
275 280 285	
gaa gtt tgg aat ttg tca aat gta caa cag gga aaa tat ctt tat ctt	973
Glu Val Trp Asn Leu Ser Asn Val Gln Gln Gly Lys Tyr Leu Tyr Leu	
290 295 300	
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Lys Gly Cys Asp Gly Glu Val Ile Asn Trp Cys Phe Gln Thr Ser Val	
305 310 315	
gga tgaacatatt ccagtatttg aagccagaat tttctttgga aattgttgag	1074
Gly	
320	
aaaaaccaag gaagataaaa caagttgcat ttttaagcac gtttctctgc taagacaaga	1134
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Met Glu Lys	
1	
ctg cgg cga gtc ctg agc ggc cag gac gac gag gag cag ggc ctg act	165
Leu Arg Arg Val Leu Ser Gly Gln Asp Asp Glu Glu Gln Gly Leu Thr	
5 10 15	
gcg cag gtc ctg gat gcc tca tcc ctt agt ttc aac acc aga ttg aaa	213
Ala Gln Val Leu Asp Ala Ser Ser Leu Ser Phe Asn Thr Arg Leu Lys	
20 25 30 35	
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Trp Phe Ala Ile Cys Phe Val Cys Gly Val Phe Phe Ser Ile Leu Gly	
40 45 50	
act gga ttg ctg tgg ctt ccg ggc ggc ata aag ctt ttt gca gtg ttt	309
Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe Ala Val Phe	

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Tyr Thr Leu		Gly Asn Leu Ala Ala		Leu Ala Ser Thr Cys Phe Leu Met		
	70		75		80	
gga cct gtg aag caa ctg aag aaa atg ttt gaa gca aca aga ttg ctt						405
Gly Pro Val Lys Gln Leu Lys Lys Met Phe Glu Ala Thr Arg Leu Leu						
	85		90		95	
gca aca att gtt atg ctt ttg tgt ttc ata ttt acc ctg tgt gct gct						453
Ala Thr Ile Val Met Leu Leu Cys Phe Ile Phe Thr Leu Cys Ala Ala						
	100		105		110	115
ctt tgg tgg cat aag aag gga ctg gct gtg tta ttc tgc ata ttg cag						501
Leu Trp Trp His Lys Lys Gly Leu Ala Val Leu Phe Cys Ile Leu Gln						
	120		125		130	
ttc ttg tca atg acc tgg tat agc ctg tgc tac atc cca tat gca agg						549
Phe Leu Ser Met Thr Trp Tyr Ser Leu Ser Tyr Ile Pro Tyr Ala Arg						
	135		140		145	
gat gca gtt att aaa tgc tgt tct tct cta agt tgaaaatcag						595
Asp Ala Val Ile Lys Cys Cys Ser Ser Leu Leu Ser						
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tccccataaa acactccagg aacaactgac gtgacagttg aagaccggtt tgtactaagt						715
ctcattttgt atactggtaa aaactacatg cttgattaaa ccattaaatg cttgtaactt						775
taaattcatt atgtgtcatt aatatacttt tccaaagata agatttttaa tcaactgccag						835
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Arg Ala Ala Arg Lys Arg Ala Gly Leu Ala Ala Gln Pro Pro Ala Ala		
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agt cag ggc gca caa acc cca gga gag aag ggc gaa gca gca gcg act		148
Ser Gln Gly Ala Gln Thr Pro Gly Glu Lys Ala Glu Ala Ala Ala Thr		
	25 30 35 40	
cta aag gca gcc cca ggc tgg cta aag cgg ttc ctg gta tgg aaa cct		196
Leu Lys Ala Ala Pro Gly Trp Leu Lys Arg Phe Leu Val Trp Lys Pro		
	45 50 55	
agg ccc gcg agt gcc cgg gcc cag ccc ggc cta gtt cag gaa gcg gct		244
Arg Pro Ala Ser Ala Arg Ala Gln Pro Gly Leu Val Gln Glu Ala Ala		
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cag ccc cag ggc agc aca tca gag aca cca tgg aac aca gcc att cct		292
Gln Pro Gln Gly Ser Thr Ser Glu Thr Pro Trp Asn Thr Ala Ile Pro		
	75 80 85	
ctg ccg tgc tgc tgg gac cag tct ttc ctg acc aat atc acc ttc ttg		340

Leu	Pro	Ser	Cys	Trp	Asp	Gln	Ser	Phe	Leu	Thr	Asn	Ile	Thr	Phe	Leu		
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Lys	Val	Leu	Leu	Trp	Leu	Val	Leu	Leu	Gly	Leu	Phe	Val	Glu	Leu	Glu		
105					110					115				120			
ttt	ggc	ctg	gca	tat	ttt	gtc	ctg	tcc	ttg	ttc	tat	tgg	atg	tac	gtc	436	
Phe	Gly	Leu	Ala	Tyr	Phe	Val	Leu	Ser	Leu	Phe	Tyr	Trp	Met	Tyr	Val		
			125						130					135			
ggg	aca	cga	ggc	cct	gaa	gag	aag	aaa	gag	gga	gag	aag	agc	gcc	tac	484	
Gly	Thr	Arg	Gly	Pro	Glu	Glu	Lys	Lys	Glu	Gly	Glu	Lys	Ser	Ala	Tyr		
			140					145						150			
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Ser	Val	Phe	Asn	Pro	Gly	Cys	Glu	Ala	Ile	Gln	Gly	Thr	Leu	Thr	Ala		
			155				160						165				
gag	cag	ttg	gag	cgc	gag	tta	cag	ttg	aga	ccc	ctg	gca	ggg	aga		577	
Glu	Gln	Leu	Glu	Arg	Glu	Gln	Leu	Arg	Pro		Leu	Ala	Gly	Arg			
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 <222> 23..451

<400> 180																	
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			1				5					10					
tcc	aca	gtg	ctc	tct	tca	ggt	ccc	ctt	caa	atg	ctg	ttt	tat	ctc	agc	100	
Ser	Thr	Val	Leu	Ser	Ser	Val	Pro	Leu	Gln	Met	Leu	Phe	Tyr	Leu	Ser		
			15						20						25		

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gga acg tac tac gcc ctg tat ttc ctc gcc acg ctc ctg atg atc acg      148
Gly Thr Tyr Tyr Ala Leu Tyr Phe Leu Ala Thr Leu Leu Met Ile Thr
      30      35      40
tat aaa agt cag gtg ttc agc tat cct cac cgc tac ctg gtc ctc gat      196
Tyr Lys Ser Gln Val Phe Ser Tyr Pro His Arg Tyr Leu Val Leu Asp
      45      50      55
ctt gct ctg ctg ttt ctg atg ggg att cta gaa gca gtt cgg tta tac      244
Leu Ala Leu Leu Phe Leu Met Gly Ile Leu Glu Ala Val Arg Leu Tyr
      60      65      70
ctg ggc acc agg ggc aac ctg aca gag gct gag agg ccg ctg gcc gcc      292
Leu Gly Thr Arg Gly Asn Leu Thr Glu Ala Glu Arg Pro Leu Ala Ala
      75      80      85      90
agc ctg gcc ctc acg gct ggc acc gcc ctc ctc tct gcc cac ttc ctg      340
Ser Leu Ala Leu Thr Ala Gly Thr Ala Leu Leu Ser Ala His Phe Leu
      95      100      105
ctt tgg cag gcc cta gtg ttg tgg gcg gac tgg gcc ctc agc gcc acg      388
Leu Trp Gln Ala Leu Val Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr
      110      115      120
ctc ctg gcc ctt cac ggc ctg gag gcc gtc ctg cag gtg gtt gcc atc      436
Leu Leu Ala Leu His Gly Leu Glu Ala Val Leu Gln Val Val Ala Ile
      125      130      135
gcg gcc ttc acc agg tagctacgga caccgaggat accccacact ggggccctcc      491
Ala Ala Phe Thr Arg
      140
tctctgggctt gaccagtccc ccagctgtca cctccccatt cctggacagg aagggcactt      551
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tagttcccca atggtcctaa tttgtgttct gagatcccag tttactctgt ggccaggccc      911
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accccagctc tgccctcacag gcaggcaggc ccggtgcaag agtggactct ggggttcctaa      1031
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gcttttgcac ggagtgtctaa acaaattcta gctctgtgtt tttttcccat tcccagattt      1271
actatcagtt ctcccttaaaa agtatctaag ctgttacagt agctttccct tcacttgatt      1331
ctattgtgtg ttttctatgt ttggaataat tacacccaaa tatctagata ttttctcttc      1391
accgcatttt gtaaataaag agatgtgtat gcctcaaaaa aaaaaaaaaa aa      1443

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<211> 605
<212> DNA
<213> Homo sapiens

<220>
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<222> 232..450

<400> 181
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attgttagac tgcctggcta ggagttcatt gttgttttct gaaggacgta accaaccact      120
ccaaaactta caggcttaaa acaacaaaca tgtatcattt cttatgattc tgtgggttgg      180
ctgggtggtt cttctagctg aggcaggatg gtctaggata gctacatcca c atg tct      237
Met Ser
      1
ggg gtc cca gct gag atg act ggg gct gtt gag gcc ttt ctc cct gtg      285

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ggc tgt gac agc ggc cac tgc agg att ctt ggc agg tac agc tta cta 1063
 Gly Cys Asp Ser Gly His Cys Arg Ile Leu Gly Arg Tyr Ser Leu Leu
 90 95 100

ggg tgg agt cag gga cat agg gca aga ggc aga ggt ggt gtt agt ctg 1111
 Gly Trp Ser Gln Gly His Arg Ala Arg Gly Arg Gly Gly Val Ser Leu
 105 110 115

aga gac aac acc ttc ttt cag gaa gcc agt gag ggc cag gga cag tgg 1159
 Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser Glu Gly Gln Gly Gln Trp
 120 125 130

ctc atg cct gta atc cca gca ttt taggaggctg agacaggtag atcacttgag 1213
 Leu Met Pro Val Ile Pro Ala Phe
 135 140

gtcaggtggt cgagaccagc ctggccaacg tgggtgaaacc tcgtctctac taaaaaatac 1273
 aaaaaattaa ctgggcgtgg tggcacacgc ctgtaatccc agctacatat gaggctgagg 1333
 caagagaata acttgaaccc aggaggcgga ggggtgcagtg agctgagatc ctgccgctgc 1393
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 ttcttccaag atgagaagca agccaggag gctcaggctc tgggatgggc agggctttga 1573
 tcaaaagaac acaggaagtg atttgctact tgaaagaaag gcaaccctc cccaaggaag 1633
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 gtatcgcaga ggacaaaaa aaaaaaaaaa a 1724

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 <213> Homo sapiens

<220>
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<400> 183
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 atggggtttc accatgttgg ccaggctggc cttgaactcc tgacctcagg tgatccgccc 180
 gcctcggcct cccaaagtgc tggggttaca ggcagagcc accgcacccg gcccccttcc 240
 ttcgtcttag tcaatcctat cccacctctt ctccaccag tccctcacc tgatgggtccc 300
 aacacttcat catccaccac ctccctggagg gggtaacccg aggtgctccg ctgggggactc 360
 tgctcattct ggggggtgcag ttgacggctg gtcgtgatct ttcccgtaat ctgtcccctc 420
 ttacggaacc tagtctccgt tctgtccatg gccttcttct ggacactgct aggatccaga 480
 agagt atg tta tca att ctc aag cct agg aga agt cag gag tgg aga aca 530
 Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr
 1 5 10 15

gct ctg aga aga tac tgt tgt cca act gat ctc cag gca cca cgg agt 578
 Ala Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser
 20 25 30

ccg gtc cct cca atc agg aag gtc gga atc tct gat gtc atc gtt cat 626
 Pro Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His
 35 40 45

gcc aac ctg gca acc agt ttg aaa aaa aac aca tgt aac tgc cag gct 674
 Ala Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala
 50 55 60

gat ctc ttg tcc tgg aga tcc tgg gtg aat ggt atc tcc tgc cac tgt 722
 Asp Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys
 65 70 75

ccc aac ctc aga cca ttg tcc aaa agc atc ttc agg gac tcc aca tcc 770
 Pro Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser
 80 85 90 95

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ctc tgt tcc ctg tcc cag cag agg ctg tgt cct ctc cac tca aag cct      818
Leu Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro
      100      105      110
gaa gca tgt tgg ggt ctc ttt gtc tct gta cat gcc cat ttc aga gtc      866
Glu Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val
      115      120      125
cag gct ggt ggg aga ggg aac aga gtg gga aag aaa act agg gta agc      914
Gln Ala Gly Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser
      130      135      140
aga aac gat gaa acc tta taagagtga attatcatgt gcaagagtga      962
Arg Asn Asp Glu Thr Leu
      145
gattatcatg tacaagagat cccaggaaat actgactttg atgaaaaagt cacatcagag      1022
cactcagttt tggcagagct ttttctgccg aatgtttact cacattcact gtccgagatt      1082
ctatactggg ggtacacacg tcctctgccg taaggcaatt ttgagtccaa gagacatttt      1142
gaggcctaaa aatcatagga aactgcccct gagctcacac atatttccaa tgggtgtcccc      1202
aatctcaggg aatccatgga ttacctaagc cagcccctcc agttcggcta agaaactcta      1262
gtctatatgt caagttttgt atcatatgta ttgctctgaa ctcagaaaatt tcccttccat      1322
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<212> DNA
<213> Homo sapiens

<220>
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<222> 80..304

<400> 184

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ccattagatc atttcacaa atg tat ctg cca cca aac agg tca gag ctt tgc      112
      1      5      10
aac ttt gct ttg tct ctt aac ctc tat ggc aaa ggg ttt ttt agc ctg      160
Asn Phe Ala Leu Ser Leu Asn Leu Tyr Gly Lys Gly Phe Phe Ser Leu
      15      20      25
gtg gaa aag cat aac agc agg gat tta gaa gat aga gct agt tct ggc      208
Val Glu Lys His Asn Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly
      30      35      40
cca tca ctt tca tct cca tca cac ccg gac tgg ggt tat ata gtt ctg      256
Pro Ser Leu Ser Ser Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu
      45      50      55
att tta gtg gca acc ctg ggg gaa ctt gat acc cag gta ggt ggt cac      304
Ile Leu Val Ala Thr Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His
      60      65      70      75
tgatcagtag ttgggagagg taggaattgg tgagtacagg taattagagg aaagtcttgt      364
gtcctgttcc ccccttttta attttatccc ttgctagaat taagatacta tatgacctcac      424
ttatcaatta cagtctaaat ccaaaagaaa aaaaaaaaaa      463

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<211> 773

<212> DNA
<213> Homo sapiens

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<222> 188..691

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aaaggactct ggattggttg gcagtcctgct tttttttttc caaggtgata actttactgt 180
agaagaa atg agg tta aca gaa aag agt gag gga gaa caa caa ctc aag 229
Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys
1 5 10
ccc aac aac tct aat gca ccc aat gaa gat caa gaa gaa gaa atc caa 277
Pro Asn Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln
15 20 25 30
cag tca gaa cag cat act cca gca agg cag cga aca caa aga gca gac 325
Gln Ser Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp
35 40 45
aca cag cca tcc aga tgt cga ttg cct tca cgt agg aca cct aca aca 373
Thr Gln Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr
50 55 60
tcc agc gac aga acg atc aac ctt ctt gaa gtc ctt ccg tgg cct act 421
Ser Ser Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr
65 70 75
gag tgg att ttc aac ccc tat cga ttg cct gct ctt ttt gag ctt tat 469
Glu Trp Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr
80 85 90
cct gaa ttt ctt ctg gtg ttt aaa gaa gcc ttc cat gac ata tcc cat 517
Pro Glu Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His
95 100 105 110
tgt ctg aaa gcc cag atg gaa aag atc gga ctg ccc atc ata ctc cac 565
Cys Leu Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His
115 120 125
ctc ttc gca ctc tcc acc ctc tac ttc tac aag ttt ttc ctt cct aca 613
Leu Phe Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr
130 135 140
att ctt tcc ctt tct ttc ttt att ctt ctt gta ctt ctg ctt ctg ctt 661
Ile Leu Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Leu
145 150 155
ttt att att gtc ttc att ctg atc ttc ttc tgattctttt gtttcaataa 711
Phe Ile Ile Val Phe Ile Leu Ile Phe Phe
160 165
acagcaatga gcatgaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 771
aa 773

<210> 186
<211> 753
<212> DNA
<213> Homo sapiens

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<221> CDS
<222> 94..573

<400> 186
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               Met Pro Arg Ser Ser Arg Ser
               1               5
cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga      162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg
               10               15               20
ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag      210
Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu
               25               30               35
gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac      258
Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn
               40               45               50               55
aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc      306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser
               60               65               70
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt      354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val
               75               80               85
ctg ttt aac acg tgc aga gac aga gtt tca cca tgt tgc cca ggc tgg      402
Leu Phe Asn Thr Cys Arg Asp Arg Val Ser Pro Cys Cys Pro Gly Trp
               90               95               100
tct caa act cca gtg atc ctc cca cct cag cct tcc gaa gtg ctg gga      450
Ser Gln Thr Pro Val Ile Leu Pro Pro Gln Pro Ser Glu Val Leu Gly
               105               110               115
tta cag atg caa gct gct gtg cca gaa gct cat gga gaa gac agg cat      498
Leu Gln Met Gln Ala Ala Val Pro Glu Ala His Gly Glu Asp Arg His
               120               125               130               135
tct gct cct ctg tgc ttt cgg tgt gtc cca ggg ccc tgc cca gtc cca      546
Ser Ala Pro Leu Cys Phe Arg Cys Val Pro Gly Pro Cys Pro Val Pro
               140               145               150
ggg gga ggt atc cct ggg ccc tgg cac tgattatagg acactgggca      593
Gly Gly Gly Ile Pro Gly Pro Trp His
               155               160
agacactgca ctgccacgtg actcagtttc cccatctgcc tgatgggtgt tgctgtgaga      653
attatgaaat gaaatgatga ccatgaaaat attgtagaag ccaagaaatg cttcagaagt      713
tataaagctc tccccaaacc gtgttaaaaa aaaaaaaaaa      753

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<210> 187

<211> 754

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 181..462

<400> 187

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attgagttat tacatatcaa ttgaacaagg tagttttaaa atgaaagaaa atcttgcaac      180
atg aat aaa gag ata gac tct ttg aat ctg gca tac agc ttt ccc ttc      228
Met Asn Lys Glu Ile Asp Ser Leu Asn Leu Ala Tyr Ser Phe Pro Phe
               1               5               10               15
ctt ctt cct gct ttc ctg gac aca ccg tgg aca gac cca ttt ccc tct      276
Leu Leu Pro Ala Phe Leu Asp Thr Pro Trp Thr Asp Pro Phe Pro Ser
               20               25               30
gga ttc atg gta agg tcc cga gtg ctt ctg ata cag ctg ctg agc aga      324
Gly Phe Met Val Arg Ser Arg Val Leu Leu Ile Gln Leu Leu Ser Arg

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ccc cgc tca tct cag gag tcc cga gga cac tcg ctt ccc tgc agc ccg      372
Pro Arg Ser Ser Gln Glu Ser Arg Gly His Ser Leu Pro Cys Ser Pro
      50      55      60
tcc gcc ctc cat aag cct ggg ggc atc tgc cct gca gca ctg ggg agg      420
Ser Ala Leu His Lys Pro Gly Gly Ile Cys Pro Ala Ala Leu Gly Arg
      65      70      75      80
agc cac ctc ctt gtc tgg gaa cag cca agc ctc cgt gac agc      462
Ser His Leu Leu Val Trp Glu Gln Pro Ser Leu Arg Asp Ser
      85      90
tgaggattct tgtggattgt tctttctgta actggacagc acatccggaa ttccttgcca      522
tagctctgtg ccttgctggg gtctgaggtt cacagggtcag atgctgctgt ctggtccttc      582
ccaattgcgg cgtgaattcc ttcacacctca ccagtagctt cttgctctcc ccaaggagg      642
cacgtgctta gtagggagag aggcctacca aggttgccat ctgccatggg ctcaattgtg      702
tccccaaccc ccttgcaaat tatatattga agtcccaaaa aaaaaaaaaa aa      754

<210> 188
<211> 998
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 6..290

<220>
<221> misc_feature
<222> 871
<223> n=a, g, c or t

<400> 188
gattc atg aag gcc tcg ggt cct gac ctc tct gat gga ctc cac tgc ccc      50
Met Lys Ala Ser Gly Pro Asp Leu Ser Asp Gly Leu His Cys Pro
      1      5      10      15
agt cta att aga cat tta aga acc ttc tct gca gct gct gcc tta gcc      98
Ser Leu Ile Arg His Leu Arg Thr Phe Ser Ala Ala Ala Ala Leu Ala
      20      25      30
cca aga tac cca acc aga ctt ccc agt tca ctg ctt cta tgg cac ctc      146
Pro Arg Tyr Pro Thr Arg Leu Pro Ser Ser Leu Leu Leu Trp His Leu
      35      40      45
tgc cag tgc ctc cat ctc ctc tat gca gtt tct acc tca tgc aac agc      194
Cys Gln Cys Leu His Leu Leu Tyr Ala Val Ser Thr Ser Cys Asn Ser
      50      55      60
cat ggg aag aga tcg gct gcc tgg gca atg acc aga aca gaa gac aca      242
His Gly Lys Arg Ser Ala Ala Trp Ala Met Thr Arg Thr Glu Asp Thr
      65      70      75
gat gcg cta aca gat tcc ttc gat gac agt ttc atc agt tct gca gat      290
Asp Ala Leu Thr Asp Ser Phe Asp Asp Ser Phe Ile Ser Ser Ala Asp
      80      85      90      95
taaagacttt caccagaaaa aaaaattacc tgattttgcc ctgaggcagc cagggagggc      350
tttgtccttg acaatcccac tgacttattt aacaggtagc tcaaaaccca acaaaaactg      410
gaggaggctg ctccactgca gggatgggtt caattcggtg actggagtat tgtactctcc      470
ttgcacctg gctcatcccc acaaaaagacc tttcaaagaa aacacttaat tacctccttg      530
cacaagccct gtaagcccta aggtgaaaag aaactcagca gacaagggtc acagagaagg      590
agaaggcaca attcagtagg gacctacgct cagcaccagg ataaagaaac tgtccattcc      650
tgccacctcc taggaagcta aaagaattaa ggggaggccg ggcacgggtg ctcacgcctg      710
taatcccagc actttgggag gccgaggcgg gtggatcatg aggtcaggag atcgagacca      770
tcctggctaa catggtgaaa ccccatctct actaaaaata caaaaaatta gccgggcgtg      830

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gtggcgggcg ccctgtagtc ccagctactc gggaggctga nggcaggaga atggtgtgaa 890
 cctgggagggc ggagcttgca gtgagccgag attgcgccct gctccactcc agcctgagcg 950
 acagagcgag actccgtctc aaaaaaaaaa argaaaaaaaaa aaaaaaaaaa 998

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 <213> Homo sapiens

<220>
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 <222> 115..411

<400> 189
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 ggacaggaag aaccacagat accagatacg ggtactgttg taactctggt ctcc atg 117
 Met
 1
 aaa aaa aag gaa gaa aca aca ctt tca gag atg gag cct gtt gag cca 165
 Lys Lys Lys Glu Glu Thr Thr Leu Ser Glu Met Glu Pro Val Glu Pro
 5 10 15
 cag tac caa cta gtc aat gct gaa tcg act tct ccc ttt cta cat tgc 213
 Gln Tyr Gln Leu Val Asn Ala Glu Ser Thr Ser Pro Phe Leu His Cys
 20 25 30
 ctg aga gaa gtc att ggg gaa tac tct gta cac gaa ttt tca ctg ttg 261
 Leu Arg Glu Val Ile Gly Glu Tyr Ser Val His Glu Phe Ser Leu Leu
 35 40 45
 ggg aaa aca gag agt caa ggg att gga ttg tgg att gca ttg gtg gtt 309
 Gly Lys Thr Glu Ser Gln Gly Ile Gly Leu Trp Ile Ala Leu Val Val
 50 55 60 65
 ttc ctc agt ttc ctc atc ttc tcc aca agt ttc tac ata tcg aat gca 357
 Phe Leu Ser Phe Leu Ile Phe Ser Thr Ser Phe Tyr Ile Ser Asn Ala
 70 75 80
 gag cag ccc ttc ttc aaa gaa cct cct acg gaa gct gct aag gaa ctc 405
 Glu Gln Pro Phe Phe Lys Glu Pro Pro Thr Glu Ala Ala Lys Glu Leu
 85 90 95
 agt ctg tagctctgcg tggagccatg tgtaaact gaactgagac ctgccacctc 461
 Ser Leu
 ctactaccta agggccatt ttcactgat atcatcccc agaaacaaac tcatgatgac 521
 ttccatgttt ttttagatt agatacatgg agaattttcc tttcccttag aattaaaac 581
 ctgcattcta aaaaaaaaaa aaaa 605

<210> 190
 <211> 526
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 3..368

<400> 190
 ag atc cga gcg acc atg gtg gcc cgg gtg tgg tcg ctg atg agg ttc 47
 Ile Arg Ala Thr Met Val Ala Arg Val Trp Ser Leu Met Arg Phe
 1 5 10 15
 ctc atc aag gga agt gtg gct ggg ggc gcc gtc tac ctg gtg tac gac 95
 Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr Asp
 20 25 30

cag gag ctg ctg ggg ccc agc gac aag agc cag gca gcc cta cag aag	143
Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln Lys	
35 40 45	
gct ggg gag gtg gtc ccc ccc gcc atg tac cag ttc agc cag tac gtg	191
Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr Val	
50 55 60	
tgt cag cag aca ggc ctg cag ata ccc cag ctc cca gcc cct cca aag	239
Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro Lys	
65 70 75	
att tac ttt ccc atc cgt gac tcc tgg aat gca ggc atc atg acg gtg	287
Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr Val	
80 85 90 95	
atg tca gct ctg tgc gtg gcc ccc tcc aag gcc cgc gag tac tcc aag	335
Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser Lys	
100 105 110	
gag ggc tgg gag tat gtg aag gcg cgc acc aag tagcgagtca gcaggggccc	388
Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys	
115 120	
cctgcccccg ccagaacggg cagggtctgcc actgacctga agactccgga ctgggacccc	448
actccgaggg cagctcccg ccttgccggc ccaataaagg acttcagaag tgaaaaaaaa	508
ataaaaaaaaa aaaaaaaaa	526
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<211> 910	
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<213> Homo sapiens	
<220>	
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<222> 174..527	
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attttcctgt taggccaaga gagaagagga tccttctctca gagcctccag cctcccttga	60
tcccttgctt gtgggcatat gtgggtcata tttccctccc atcaccctct gcacgccacc	120
cccatcaccg ccacagaccc ccagcccttc agttgccctg cacctccttg gtg atg	176
Met	
1	
cag ccg tcc ttg tta agg tca tac agg ttg aag gcc caa tta agc ctg	224
Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser Leu	
5 10 15	
tca tct aca gtt ccc cga aga atc acg gac aaa cca gcc aca aag tcc	272
Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys Ser	
20 25 30	
tgg gaa gga ggc agg agg gag ctg tgt cct cgg gta ctc ttc acc caa	320
Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr Gln	
35 40 45	
ctc ctt ctc tgg gtt tgg cct gga gat cct ggc cct gaa ctc cag gaa	368
Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln Glu	
50 55 60 65	
aca ggc ttc cct ggc cca cct cgc cca gct cac ctc aaa act gac cga	416
Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp Arg	
70 75 80	
gcc atc atg gtt ggt gtc aaa ggc att gaa gag aaa agt ggc ata ggt	464
Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile Gly	
85 90 95	
gct gga gtc tgc agg gtg agt gtg gag aag ttg gct tcc aca cag gag	512
Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln Glu	
100 105 110	

agg act tcc tcc ctc taaggagctc cccataccccc ccatcacctt ggcattccca 567
Arg Thr Ser Ser Leu

115

gctcctccag aatccctccc tccttcagcc tagagaagga caactgcttc cccttggggc 627
ttgtcccttc acctccttga ggaaagaact gggagtaaact ctgcttgaag ttctcctcat 687
tgacaattcc gctgggacat tcctggaagg agagggcacc aggctgaggg cagagacaaa 747
atcccccttc gttcaccgcc cccaccctcc atggcccaag actcccaggg agggggataa 807
tcttcaagcc tccagaggac tcaccacgtg gctcatgtga tgggagggaa gacttctttc 867
ccagtgcaca aataaaaaaac atggaacgaa aaaaaaaaaa aaa 910

<210> 192

<211> 668

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 57..203

<400> 192

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Met

1

gag ctc gag gcc atg agc aga tat acc agc cca gtg aac cca cct gtc 107
Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Pro Val

5

10

15

ttc ccc cat ctg acc gtg gtg ctt ttg gcc att ggc atg ttc ttc acc 155
Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr

20

25

30

gcc tgg ttc ttc gtg tat cct ttc act gag cag cca gag gac cag cat 203
Ala Trp Phe Phe Val Tyr Pro Phe Thr Glu Gln Pro Glu Asp Gln His

35

40

45

tagtgatgtg ggaagctcag ggagaaacca cgctaggtac atggaccccg ccggttttgt 263
acattggatt ggggctgaga gaagattgcc gtgggctggg ctctctgcac tccacagtcc 323
acccttcgc tttgccttaa ctgctgtgcc cagttacgag gtcacctcta ccaagtacac 383
tcgtgatatc tataaagagc tcctcatctc attagtggcc tcactcttca tgggcttttg 443
agtcctcttc ctgctgtctc gggttggcat ctacgtgtga gcacccaagg gtaacaacca 503
gatggcttca ctgaaacctg cttttgtaaa ttactttttt ttactgttgc tggaagtgtc 563
ccacctgtcg ctcataataa atgcagatgt atagcaaaaa aaaaaaaaaa aaaaaaaaaa 623
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 668

<210> 193

<211> 637

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 68..334

<400> 193

agttatgaag ttctaaaagc aagtcttaat caggaagtgt ccttgatcac caacggctcg 60
cccaggc atg ctg gct ctc ttc cac ttc cac ctt cca cca tgg gat gac 109
Met Leu Ala Leu Phe His Phe His Leu Pro Pro Trp Asp Asp

1

5

10

gca gta aga agg cca tca gta gat gcc agt ccc tca acc ttg aac ttt 157
Ala Val Arg Arg Pro Ser Val Asp Ala Ser Pro Ser Thr Leu Asn Phe

15

20

25

30

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cca gac gca gaa ctt tat gcc tcc att ttc ctc tgc tgc atg gcc cca 205
Pro Asp Ala Glu Leu Tyr Ala Ser Ile Phe Leu Cys Cys Met Ala Pro
          35          40          45
gga gag att tta att agc ttt cta acc ttg gtc cag att gca cat gca 253
Gly Glu Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala
          50          55          60
aat ggt aga gga tgc aac acc ccc gct tgt gga gct gcc gct tgt gtc 301
Asn Gly Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Ala Cys Val
          65          70          75
tgg cat gaa aat tca caa gaa gag agg aaa tac tgaggagaaa atggcagatt 354
Trp His Glu Asn Ser Gln Glu Glu Arg Lys Tyr
          80          85
gtgttttgctg aatttgattg acgaagaagt caccatgaaa atcacagtga accatttgga 414
aagcaaaactg ccaaaaaaat aatagttagt catgctctca ggctgggtgt tttggctgtt 474
gtgggtttct tgcatttcca gatgattgca aagagctgtt tctcaatttc tgcaacaagt 534
gccagctgaa attttggtac cagtttcatt aaatatgtat aacaaaakaa aaaaaaaaaa 594
aaaaaaaaaa aaaaaaaaaa aaaaaaagaa aaaaaaaaaa aaa 637

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<210> 194
 <211> 706
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 183..443

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<400> 194
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cacagaaacc cagggccgaa gcaaagtccc aatcccagag aggctggggc acacctacaa 120
ctgaaaggag gcttagaaaat ccttcagaga ccaccctatc ggttctctc cacctggaca 180
gg atg agc cag caa cac aga agg aag cct tcc tcc gaa aga aaa 227
Met Ser Gln Gln His Arg Arg Lys Arg Pro Ser Ser Glu Arg Lys
  1          5          10          15
agc aca aga aag atg gac aca tgg cag agt ctt aaa gtc aaa gaa gta 275
Ser Thr Arg Lys Met Asp Thr Trp Gln Ser Leu Lys Val Lys Glu Val
          20          25          30
ttc tgt aag cat aat tct tcc tat gaa tgc ctt ctc tat aaa gag gtt 323
Phe Cys Lys His Asn Ser Ser Tyr Glu Cys Leu Leu Tyr Lys Glu Val
          35          40          45
gaa gca aga cag gtt tct aag aca gcc acc gat ggg tcc tac ctc ctc 371
Glu Ala Arg Gln Val Ser Lys Thr Ala Thr Asp Gly Ser Tyr Leu Leu
          50          55          60
gta ttc aca tcc tat gta atc tcc tcc cca gtg tgg act gga cct ggt 419
Val Phe Thr Ser Tyr Val Ile Ser Ser Pro Val Trp Thr Gly Pro Gly
          65          70          75
gac ttg ctt cca gtg aat aga ata tagcaaaagt gattgatgtc acctccaaga 473
Asp Leu Leu Pro Val Asn Arg Ile
          80          85
ttcagctata gaagactatg actatgactt tcctcttggc tagcattctc gctaaccctt 533
cctgcttgct tgtactgagc tgccctatga agaggcccat gtaggggtggc ctgggtgggg 593
gtgatctgtg gccaacagcc agcaaggaac taaatcctgt ttacaaccac atgagcttgg 653
aaggagatcc ttccccagta aagccaggag atgaatacaa aaaaaaaaaa aaa 706

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<210> 195
 <211> 670
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 94..228

<400> 195

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catctccatc cccaatccta aagaaggaaa tcg atg cca cgg tcc tca agg agc 114
                               Met Pro Arg Ser Ser Arg Ser
                               1           5
cct ggg gac cca ggc gcc cta ctc gaa gat ggc cca caa tcc cag acc 162
Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Gly Pro Gln Ser Gln Thr
      10           15           20
ccg gag gat tgc cca gcg agg ccg gaa cac cag cag gat ggc aga gga 210
Pro Glu Asp Cys Pro Ala Arg Pro Glu His Gln Gln Asp Gly Arg Gly
      25           30           35
cac ctc ccc aaa cat gaa tgacaacatc ctgttgccctg tccgcaacaa 258
His Leu Pro Lys His Glu
      40           45
tgaccaagcc ctaggcctga ctgagtgcat gctgggatgt gtgtcctggt tcacctgttt 318
tgacctgctcc ctgagaactc aggccagca ggttctgttt aacacgtgca gatgcaagct 378
gctgtgccag aagctcatgg agaagacagg cattctgctc ctctgtgctt tcggtgtgtc 438
ccagggccct gccagtcctc aggtggaagg taccctggg ccctggcact gattatagga 498
cactgggcaa gacactgcac cgccacgtga ctgagtttcc ccatctgcct gatgggtgtt 558
gctgtgagaa ttatgaaatg aaatgatgac catgaaaata ttgtagaagc caagaaatgc 618
ttcagaagtt ataaagctct ccccaaaccg tggtatgaaa aaaaaaaaaa aa 670
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<210> 196

<211> 510

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 133..327

<400> 196

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ctccaatacc caaacagggt gtagttgcct aatccatcct catgtggata gctctttact 120
taggaaacct tg atg gct tat ttg gat gac aaa ggt tcc ctt ttg gcg ata 171
                               Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile
                               1           5           10
cat agc cat gcg aga caa cat agc cat gaa aca aac caa gtc cac cag 219
His Ser His Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln
      15           20           25
tgg ctt cct agg aac aca ttt gct ttc ctg ata aaa gag gac aga tgc 267
Trp Leu Pro Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys
      30           35           40           45
agt tgc aga agt acc tgt gcc tct ttt tct ttt tct tct tct ttt tct 315
Ser Cys Arg Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Ser Phe Ser
      50           55           60
ttt tta atc tct taaatgcaga tataagaact ggtactgaag cagccatctt 367
Phe Leu Ile Ser
      65
gtgaccataa ggaagaagcc aagaacatca gaaccagtgg cctagccatt gcacagtcac 427
ctaaacacac ctctggactt gttattatgt aaaaaaaaaa aaacacctgc tcttgttatt 487
tgcaatccaa aaaaaaaaaa aaa 510
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06706-0601

000769-000001

06706-0601

06706-0601

06706-0601

06706-0601

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cag atc tct agc tac ctc tac tta aat act gct ctt gtg gac ttg cct			240
Gln Ile Ser Ser Tyr Leu Tyr Leu Asn Thr Ala Leu Val Asp Leu Pro			
65	70	75	
ggt gtg gcg gcc tcc cag gca tgt gac tct cag cag gtg act tgg ctt			288
Gly Val Ala Ala Ser Gln Ala Cys Asp Ser Gln Gln Val Thr Trp Leu			
80	85	90	95
ctc tac gtt gct aat ggt gcc tac tcg gca tgt aac agg cct gga			333
Leu Tyr Val Ala Asn Gly Ala Tyr Ser Ala Cys Asn Arg Pro Gly			
100	105	110	
tgaacggttag ctgctgcggt tacattatta gcttcagttt gcccgcccag gctagatggt			393
taatcagatt tcacagactt cacagtgtga gttggggatg tgacttcgta tgaagtgaa			453
ggaactcagg ctccagagagg gtgagacgta ggagcatggc cactgcgcga gctcggggct			513
ggctgtgggt ttctcccat tccctgccc tctgggaagt cgctgccacc ccctacgctt			573
gtctgtgac tccagtcctt cctaaccctt cagaatgtaa acagcagcag atgaacaaaa			633
ataaaaaatc aaaaggccga aaaaaaaaaa aaaa			667
<210> 199			
<211> 514			
<212> DNA			
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<220>			
<221> CDS			
<222> 1..363			
<400> 199			
acg agt tct tcc ggg gcg gag gtc acc atg gca gct gcc ttg gct cgg			48
Thr Ser Ser Ser Gly Ala Glu Val Thr Met Ala Ala Ala Leu Ala Arg			
1	5	10	15
ctt ggt ctg cgg cct gtc aaa cag gtt cgg gtt cag ttc tgt ccc ttc			96
Leu Gly Leu Arg Pro Val Lys Gln Val Arg Val Gln Phe Cys Pro Phe			
20	25	30	
gag aaa aac gtg gaa tcg acg agg acc ttc ctg cag acg gtg agc agt			144
Glu Lys Asn Val Glu Ser Thr Arg Thr Phe Leu Gln Thr Val Ser Ser			
35	40	45	
gag aag gtc cgc tcc act aat ctc aac tgc tca gtg att gcg gac gtg			192
Glu Lys Val Arg Ser Thr Asn Leu Asn Cys Ser Val Ile Ala Asp Val			
50	55	60	
agg cat gac ggc tcc gag ccc tgc gtg gac gtg ctg ttc gga gac ggg			240
Arg His Asp Gly Ser Glu Pro Cys Val Asp Val Leu Phe Gly Asp Gly			
65	70	75	80
cat cgc ctg att atg cgc ggc gct cat ctc acc gct ctg gaa atg ctc			288
His Arg Leu Ile Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu			
85	90	95	
acc gcc ttc gcc tcc cac atc cgg gcc agg gac gcg gcg ggc agc ggg			336
Thr Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ala Gly Ser Gly			
100	105	110	
gac aag ccg ggc gct gat act ggt cgc tgacagcgcc aaagagacca			383
Asp Lys Pro Gly Ala Asp Thr Gly Arg			
115	120		
acaagatgat ttgcgtggac taggacactt aacctaagaa gagtttcaact taatcattca			443
aatcactatc tgaagggtca cggagcgcaa aataaagttt aaaaccctgc taccaaaaaa			503
aaaaaaaaa a			514
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<213> Homo sapiens

<220>

<221> CDS

<222> 41..337

<400> 200

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Met Leu Ala Arg Ala
1 5
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Thr Phe Arg Ala Ala Ser Ala Pro Thr Leu Val Ala Arg Arg Gly Phe
10 15 20
cag tcg acc cgc gcg caa atg gcc agc cca tac cac tac ccc gag ggt 151
Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr His Tyr Pro Glu Gly
25 30 35
cct cgc agc aac ttg cca ttc gac ccg ctg aag aag ggc ttt gct ttc 199
Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys Lys Gly Phe Ala Phe
40 45 50
aag tac tgg ggc ttt atg ggc acc gga ttc gcc ctt ccc ttc ctc ctt 247
Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala Leu Pro Phe Leu Leu
55 60 65
gct gtc tgg caa aca gaa caa gcc gta aat gcg ctg aga cac ggc gtg 295
Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala Leu Arg His Gly Val
70 75 80 85
gac atg cgt atc ggg atc ccg ggg aac acg gca ttt gta gat 337
Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala Phe Val Asp
90 95
taggtggagg gcccgcatcac ggctatacta gacatcacag catcaatttc attgtctgtc 397
ccccaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 457
aaaaa 462

<210> 201

<211> 551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 1..549

<400> 201

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tcg gcc atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttc 96
Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe
20 25 30
cca ctc ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag 144
Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu
35 40 45
ccg ggc tgc ctg gac atc agc gac ttc ggc tgc cag ctg tcc tcc tgc 192
Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys
50 55 60
cat cgc acc gac ccg ctc cac cgc ttc cac acc aag tgg aac cta 240
His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu
65 70 75 80
act tct tgt gga aca agt gtt gcc agc tca gaa ggc agt gag gag ctg 288

Thr	Ser	Cys	Gly	Thr	Ser	Val	Ala	Ser	Ser	Glu	Gly	Ser	Glu	Glu	Leu	
				85					90					95		
ttt	tca	tct	gtg	tct	gtt	gga	gat	caa	gat	gat	tgc	tat	tcc	ctg	tta	336
Phe	Ser	Ser	Val	Ser	Val	Gly	Asp	Gln	Asp	Asp	Cys	Tyr	Ser	Leu	Leu	
			100				105					110				
gat	gat	cag	gac	ttc	act	tct	ttt	gat	tta	ttt	cct	gag	ggg	agt	gtc	384
Asp	Asp	Gln	Asp	Phe	Thr	Ser	Phe	Asp	Leu	Phe	Pro	Glu	Gly	Ser	Val	
		115					120				125					
tgc	agt	gat	gtc	tct	tct	tct	att	agc	act	tac	tgg	gat	tgg	tca	gat	432
Cys	Ser	Asp	Val	Ser	Ser	Ser	Ile	Ser	Thr	Tyr	Trp	Asp	Trp	Ser	Asp	
	130					135					140					
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Ser	Glu	Phe	Glu	Trp	Gln	Leu	Pro	Gly	Ser	Asp	Ile	Ala	Ser	Gly	Ser	
	145				150				155					160		
gat	gta	ctt	tct	gat	gtc	ata	ccc	agt	att	cca	agt	tca	cct	tgc	ctg	528
Asp	Val	Leu	Ser	Asp	Val	Ile	Pro	Ser	Ile	Pro	Ser	Ser	Pro	Cys	Leu	
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ctt	cct	aaa	aaa	aaa	aaa	aa										551
Leu	Pro	Lys	Lys	Lys	Lys	Lys										
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				1				5								
atc	act	tcc	tac	gag	aag	ttt	cta	acc	ccc	gag	gag	ccc	ttc	cca	ctc	102
Ile	Thr	Ser	Tyr	Glu	Lys	Phe	Leu	Thr	Pro	Glu	Glu	Pro	Phe	Pro	Leu	
		10				15						20				
ctg	gga	cct	cct	cgc	ggg	gtg	ggc	acc	tgc	ccg	agc	gag	gag	ccg	ggc	150
Leu	Gly	Pro	Pro	Arg	Gly	Val	Gly	Thr	Cys	Pro	Ser	Glu	Glu	Pro	Gly	
	25				30				35							
tgc	ctg	gac	atc	agc	gac	ttc	ggc	tgc	cag	ctg	tcc	tcc	tgc	cat	cgc	198
Cys	Leu	Asp	Ile	Ser	Asp	Phe	Gly	Cys	Gln	Leu	Ser	Ser	Cys	His	Arg	
	40			45				50						55		
acc	gac	ccg	ctc	cac	cgc	ttc	cac	acc	aac	agg	tgg	aac	cta	act	tct	246
Thr	Asp	Pro	Leu	His	Arg	Phe	His	Thr	Asn	Arg	Trp	Asn	Leu	Thr	Ser	
			60			65						70				
tgt	gga	aca	agt	gtt	gcc	agc	tca	gaa	ggc	agt	gag	gag	ctg	ttt	tca	294
Cys	Gly	Thr	Ser	Val	Ala	Ser	Ser	Glu	Gly	Ser	Glu	Glu	Leu	Phe	Ser	
			75			80						85				
tct	gtc	tgt	tgg	aga	tca	aga	tgattgctat	tcctgttag	atgatcagga							345
Ser	Val	Cys	Trp	Arg	Ser	Arg										
			90													
cttcacttct	tttgatttat	ttcctgaggg	gagtgctctgc	agtgatgtct	cttcttctat											405

tagcacttac tgggattggt cagatagcga gtttgaatgg cagttaccag gcagtgcacat 465
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 ctg agc gac cca gcc cgc gag cga ggt gag atg ccg gtg gcc gtg ggt 96
 Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly
 20 25 30
 ccc tac gga cag tcc cag cca agc tgc ttc gac cgt gtc aaa atg ggc 144
 Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly
 35 40 45
 ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc ggg gcg ctc ttc ggc 192
 Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly
 50 55 60
 acc ttt tcc tgt ctc agg atc gga atg cgg ggt cga gag ctg atg ggc 240
 Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly
 65 70 75 80
 ggc att ggg aaa acc atg atg cag agt ggc ggc acc ttt ggc aca ttc 288
 Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe
 85 90 95
 atg gcc att ggg atg ggc atc cga tgc taaccatggt tgccaactac 335
 Met Ala Ile Gly Met Gly Ile Arg Cys
 100 105
 atctgtccct tcccatcaat cccagcccat gtactaataa aagaaagtct ttgagcaaaa 395
 aaaaaaaaaa aaa 408

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 <222> 94..582

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 Met Pro Arg Ser Ser Arg Ser
 1 5
 cct ggg gac cca ggc gcc cta ctc gaa gat gtg gcc cac aat ccc aga 162
 Pro Gly Asp Pro Gly Ala Leu Leu Glu Asp Val Ala His Asn Pro Arg
 10 15 20
 ccc cgg agg att gcc cag cga ggc cgg aac acc agc agg atg gca gag 210
 Pro Arg Arg Ile Ala Gln Arg Gly Arg Asn Thr Ser Arg Met Ala Glu
 25 30 35

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gac acc tcc cca aac atg aat gac aac atc ctg ttg cct gtc cgc aac      258
Asp Thr Ser Pro Asn Met Asn Asp Asn Ile Leu Leu Pro Val Arg Asn
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aat gac caa gcc cta ggc ctg act cag tgc atg ctg gga tgt gtg tcc      306
Asn Asp Gln Ala Leu Gly Leu Thr Gln Cys Met Leu Gly Cys Val Ser
60          65          70
tgg ttc acc tgt ttt gcc tgc tcc ctg aga act cag gcc cag cag gtt      354
Trp Phe Thr Cys Phe Ala Cys Ser Leu Arg Thr Gln Ala Gln Gln Val
75          80          85
ctg ttt aac acg tgc aga tgc aag ctg tgc cag aag ctc atg gag      402
Leu Phe Asn Thr Cys Arg Cys Lys Leu Leu Cys Gln Lys Leu Met Glu
90          95          100
aag aca ggc att ctg ctc ctc tgt gct ttc ggt gtg tcc cag ggc cct      450
Lys Thr Gly Ile Leu Leu Leu Cys Ala Phe Gly Val Ser Gln Gly Pro
105          110          115
gcc cag tcc cag gtg gag gta tcc ctg ggc cct ggc act gat tat agg      498
Ala Gln Ser Gln Val Glu Val Ser Leu Gly Pro Gly Thr Asp Tyr Arg
120          125          130          135
aca ctg ggc aag aca ctg cac tgc cac gtg act cag ttt ccc cat ctg      546
Thr Leu Gly Lys Thr Leu His Cys His Val Thr Gln Phe Pro His Leu
140          145          150
cct gat ggg tgt tgc tgt gag aat tat gaa atg aaa tgatgaccat      592
Pro Asp Gly Cys Cys Cys Glu Asn Tyr Glu Met Lys
155          160
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<222> 540..923

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ccaaggcagc atttcagaag gtgatccacg gcaaagccgt cccttcaaata cegtctttgt      180
gccccactgcc atagtcaacc ccgtgagaag cacagccggc cctgggactt taggacaagg      240
gtctcttcgg aaagggcgga gcagcatgag aaagagtaag tgggtggcaga gagatggatc      300
cctgcagaga cccctccagt ccgggatccc cactctcgtg gtaggctccc tcagacgcag      360
ccccaccatg gtccttcggc ctgagcagtt ccaattctac cagccacagg ggatcacctc      420
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cctcacgtgc atcagcaggg gcagtgaggc ggatccactc cgcggccagc tccctcatt      539
atg gaa gac aaa gaa atc ccc atc aag agt gag cct ctg cca aaa ccg      587
Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro
1          5          10          15
ccc gca tct gcc cca cca tcc atc ctg gtg aaa cca gaa aac tca aga      635
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg
20          25          30
aat gga atc gaa aag caa gtc aaa acc gtg aga ttt cag aat tac agc      683
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser
35          40          45
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Met Gly Lys Ile Ala Leu Gln Leu Lys Ala Thr Leu Glu Asn Ile
1 5 10 15
acc aac ctc cgg ccc gtg ggc gag gac ttc cgg tgg tac ctg aag atg 157
Thr Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met
20 25 30
aaa tgt ggc aac tgt ggt gag att tcg gac aag tgg cag tac atc cgg 205
Lys Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg
35 40 45
ctg atg gac agt gtg gca ctg aag ggg ggc cgt ggc agt gct tcc atg 253
Leu Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met
50 55 60
gtc cag aag tgc aag ctg tgt gca aga gaa aat tcc atc gag att tta 301
Val Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu
65 70 75
agc agc acc atc aag cct tac aat gct gaa gac aat gag aac ttc aag 349
Ser Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys
80 85 90 95
aca ata gtg gag ttt gag tgc cgg ggc ctt gaa cca gtt gat ttc cag 397
Thr Ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln
100 105 110
ccg cas gwg rtw ttg ctg ctg aag gtg tgg agt cag gga cag cct tca 445
Pro Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser
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Val Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys
130 135 140
gcc cag gag tct gtg gga atc tat gag gtc acc cac cag ttt gtg aag 541
Ala Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys
145 150 155
tgc tgatccctct tccttcccag ttgcccttaa gaactgagaa aggacaaagt 594
Cys
160
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<222> 117..467

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gac tcc ctg gct gct gga gag ttg aat gcc agc cac cag cca tgg gtg 167
Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp Val
5 10 15
cca gag ttt gta gcc tat tgg agg aaa aca cac caa gat cac ctc tgc 215
Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu Cys

aac tcc tcc cag gag acg tgc acc cgg gcc aga gag ttg gcc cag cag	1090
Asn Ser Ser Gln Glu Thr Cys Thr Arg Ala Arg Glu Leu Ala Gln Gln	
55 60 65	
att gga agc cac cac atc agt ctc aac atc gat cca gcc gtg aag gcc	1138
Ile Gly Ser His His Ile Ser Leu Asn Ile Asp Pro Ala Val Lys Ala	
70 75 80	
gtc atg ggc atc ttc agc ctg gtg acg ggg aag agc cct ctg ttt gca	1186
Val Met Gly Ile Phe Ser Leu Val Thr Gly Lys Ser Pro Leu Phe Ala	
85 90 95	
gct cat gga gga agc agc agg gaa aac ctg gcg ctg caa aat gtg cag	1234
Ala His Gly Gly Ser Ser Arg Glu Asn Leu Ala Leu Gln Asn Val Gln	
100 105 110	
gct cga ata cgg atg gtc ctc gcc tat ctg ttt gct cag ttg agc ctc	1282
Ala Arg Ile Arg Met Val Leu Ala Tyr Leu Phe Ala Gln Leu Ser Leu	
115 120 125 130	
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Trp Ser Arg Gly Val His Gly Gly Leu Leu Val Leu Gly Ser Ala Asn	
135 140 145	
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Val Asp Glu Ser Leu Leu Gly Tyr Leu Thr Lys Tyr Asp Cys Ser Ser	
150 155 160	
gcg gac atc aac ccc ata ggc ggg atc agc aag acg gac ctc agg gcc	1426
Ala Asp Ile Asn Pro Ile Gly Gly Ile Ser Lys Thr Asp Leu Arg Ala	
165 170 175	
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Phe Val Gln Phe Cys Ile Gln Arg Phe Gln Leu Pro Ala Leu Gln Ser	
180 185 190	
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Ile Leu Leu Ala Pro Ala Thr Ala Glu Leu Glu Pro Leu Ala Asp Gly	
195 200 205 210	
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Gln Val Ser Gln Thr Asp Glu Glu Asp Met Gly Met Thr Tyr Ala Glu	
215 220 225	
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Leu Ser Val Tyr Gly Lys Leu Arg Lys Val Ala Lys Met Gly Pro Tyr	
230 235 240	
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Ser Met Phe Cys Lys Leu Leu Gly Met Trp Arg His Ile Cys Thr Pro	
245 250 255	
aga cag gtc gct gac aaa gtg aag cgg ttt ttc tcc aag tac tcc atg	1714
Arg Gln Val Ala Asp Lys Val Lys Arg Phe Phe Ser Lys Tyr Ser Met	
260 265 270	
aac aga cac aag atg acc acg ctc aca ccc gcg tac cac gcc gag aac	1762
Asn Arg His Lys Met Thr Thr Leu Thr Pro Ala Tyr His Ala Glu Asn	
275 280 285 290	
tac agc cct gag gac aac agg ttt gat ctg cga cca ttt ctg tac aac	1810
Tyr Ser Pro Glu Asp Asn Arg Phe Asp Leu Arg Pro Phe Leu Tyr Asn	
295 300 305	
aca agc tgg cct tgg cag ttt cgg tgc ata gaa aat cag gtg cta cag	1858
Thr Ser Trp Pro Trp Gln Phe Arg Cys Ile Glu Asn Gln Val Leu Gln	
310 315 320	
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Leu Glu Arg Ala Glu Pro Gln Ser Leu Asp Gly Val Asp	
325 330 335	
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gccaagggtg ggagccctac actaggagcc caggatggga cggcgcatca gccgagagg	2027
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<222> 85..342

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Met Cys Trp Val Ile Asn His Ala Ile
1 5
ctc cct aga atg aga atg cac agc aag cgg cag aca atc acc cgg cat 159
Leu Pro Arg Met Arg Met His Ser Lys Arg Gln Thr Ile Thr Arg His
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tcg gca tct ctt tct ttt cac gcg ctc cct cgc tcc gcc ttt ctc cag 207
Ser Ala Ser Leu Ser Phe His Ala Leu Pro Arg Ser Ala Phe Leu Gln
30 35 40
ctc tgc ctt ctc agg cag ata cat cag ata cct tgt tta tcc atc ttc 255
Leu Cys Leu Leu Arg Gln Ile His Gln Ile Pro Cys Leu Ser Ile Phe
45 50 55
agc tcc act ctg agg gcg cag acg cac gat tcc ggg atc ggg tgc acc 303
Ser Ser Thr Leu Arg Ala Gln Thr His Asp Ser Gly Ile Gly Cys Thr
60 65 70
acg gcg aas cca ggc ggg aga cgg cag gag cag ctc agg taaccagggg 352
Thr Ala Xaa Pro Gly Gly Arg Arg Gln Glu Gln Leu Arg
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atttggtctgc taacctcaca cagctgagcc ttcc atg aaa att gct ctc tgc caa 175
Met Lys Ile Ala Leu Cys Gln
1 5
aga gaa ctt cct agt cca agg tca tgt cta ctc tcc aga gat gtg act 223
Arg Glu Leu Pro Ser Pro Arg Ser Cys Leu Leu Ser Arg Asp Val Thr
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gga gtg att tgc acc cgg atg cct aga ctc gcc atc tgc tca aag act 271
Gly Val Ile Cys Thr Arg Met Pro Arg Leu Ala Ile Cys Ser Lys Thr
25 30 35
gct cag aaa gcc ctc cca tgc att ccc ctg ctg cat acc agc cca ctc 319
Ala Gln Lys Ala Leu Pro Cys Ile Pro Leu Leu His Thr Ser Pro Leu
40 45 50 55
tgc ctg cag ctg ctg tct gca gga ctt cat atc tat gcc aca ctg tgt 367

Cys Leu Gln Leu Leu Ser Ala Gly Leu His Ile Tyr Ala Thr Leu Cys
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Lys Ser Cys Ala Ser Arg Asn His Lys Asn Ile Phe Leu His Leu Leu
75 80 85
cac agc ctg agt gcg gca taagttgacc ttgcttgcta agaaatgggg 463
His Ser Leu Ser Ala Ala
90
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Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys
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Phe Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser
20 25 30
gag aac ttc tac agt gtg ttc gag ggc gag ctc tcc gat acc atc ccc 203
Glu Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro
35 40 45
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Val Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys
50 55 60
gtg gga gac aga aga aat tct ggc aga tgt gct caa ggt gga agt ctt 299
Val Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu
65 70 75
cag aca gac agt ggc cga cca ggt gct agt agg aag cta ctg tgt ctt 347
Gln Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu
80 85 90 95
cag caa tca ggg agg gct ggt gca tcc caa gac ttc aat tgaagaccag 396
Gln Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn
100 105
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gacctctttg	gtgctgtaaa	tcctggatat	actgtagatg	agtactgcgt	ttttctttta	420
tggactctct	tcagcttctg	gagacctcac	tatcctatt	atg tct ttg tgt gaa		474
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gac atg ctg ctt tgt aat tat cga aag tgt cgc atc aaa ctc tct ggc						522
Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg Ile Lys Leu Ser Gly						
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tat gca tgg gtc act gcc tgc tct cac atc ttc tgt gat cag cat ggc						570
Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe Cys Asp Gln His Gly						
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agt ggt gag ttt agt cgc tca cca gct atc tgt cct gcc tgc aac agt						618
Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys Pro Ala Cys Asn Ser						
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acc ctt tct gga aag cta gat att gtc cgc aca gaa ctc agt cca tca						666
Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr Glu Leu Ser Pro Ser						
	55		60		65	
gag gaa tat aaa gct atg gta ttg gca gga ctg cga cca gag atc gtg						714
Glu Glu Tyr Lys Ala Met Val Leu Ala Gly Leu Arg Pro Glu Ile Val						
	70		75		80	85
ttg gac att agc tcc cga gcg ctg gcc ttc tgg aca tat cag gta cat						762
Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp Thr Tyr Gln Val His						
	90		95		100	
cag gaa cgt ctc tat caa gaa tac aat ttc agc aag gct gag ggc cat						810
Gln Glu Arg Leu Tyr Gln Glu Tyr Asn Phe Ser Lys Ala Glu Gly His						
	105		110		115	
ctg aaa cag atg gag aag ata tat act cag caa ata caa agc aag gat						858
Leu Lys Gln Met Glu Lys Ile Tyr Thr Gln Gln Ile Gln Ser Lys Asp						
	120		125		130	
gta gaa ttg acc tct atg aaa ggg gag gtt acc tcc atg aag aaa gta						906
Val Glu Leu Thr Ser Met Lys Gly Glu Val Thr Ser Met Lys Lys Val						
	135		140		145	
cta gaa gaa tac aag aaa aag ttc agt gac atc tct gag aaa ctt atg						954
Leu Glu Glu Tyr Lys Lys Lys Phe Ser Asp Ile Ser Glu Lys Leu Met						
	150		155		160	165
gag cgc aat cgt cag tat caa aag ctc caa ggc ctc tat gat agc ctt						1002
Glu Arg Asn Arg Gln Tyr Gln Lys Leu Gln Gly Leu Tyr Asp Ser Leu						
	170		175		180	
agg cta cga aac atc act att gct aac cat gaa ggc acc ctt gaa cca						1050
Arg Leu Arg Asn Ile Thr Ile Ala Asn His Glu Gly Thr Leu Glu Pro						
	185		190		195	
tcc atg att gca cag tct ggt gtt ctt ggc ttc cca tta ggt aac aac						1098
Ser Met Ile Ala Gln Ser Gly Val Leu Gly Phe Pro Leu Gly Asn Asn						
	200		205		210	

tcc aag ttt cct ttg gat aat aca cct gtt cga aat cgg ggc gat gga	1146
Ser Lys Phe Pro Leu Asp Asn Thr Pro Val Arg Asn Arg Gly Asp Gly	
215 220 225	
gat gga gat ttt cag ttc aga cca ttt ttt gcg ggt tct ccc aca gca	1194
Asp Gly Asp Phe Gln Phe Arg Pro Phe Phe Ala Gly Ser Pro Thr Ala	
230 235 240 245	
cct gaa ccc agc aac agc ttt ttt agt ttt gtc tct cca agt cgt gaa	1242
Pro Glu Pro Ser Asn Ser Phe Phe Ser Phe Val Ser Pro Ser Arg Glu	
250 255 260	
tta gag cag cag caa gtt tct agc agg gcc ttc aaa gta aaa aga att	1290
Leu Glu Gln Gln Gln Val Ser Ser Arg Ala Phe Lys Val Lys Arg Ile	
265 270 275	
tgagccacgc atagtgtcac gcacctgtga tcccagctac ttaggaggtt gaggctggga	1350
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ggt tac cta acc ttc tat gga gaa gtt gaa gat gaa tta ctt cat gcc	101
Gly Tyr Leu Thr Phe Tyr Gly Glu Val Glu Asp Glu Leu Leu His Ala	
15 20 25	
tac agc aaa gtg tat aca tta gac atc cct ctt ctc atg gtt cgc ctg	149
Tyr Ser Lys Val Tyr Thr Leu Asp Ile Pro Leu Leu Met Val Arg Leu	
30 35 40	
gca gtc ctt gtg gca gta aca cta act gtg ccc att gtc ctc ttc cca	197
Ala Val Leu Val Ala Val Thr Leu Thr Val Pro Ile Val Leu Phe Pro	
45 50 55	
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Ile Arg Thr Ser Val Ile Thr Leu Leu Phe Pro Lys Arg Pro Phe Ser	
60 65 70 75	
tgg ata cga cat ttc ctg att gca gct gtg ctt att gca ctt aat aat	293
Trp Ile Arg His Phe Leu Ile Ala Ala Val Leu Ile Ala Leu Asn Asn	
80 85 90	
gtt ctg gtc atc ctt gtg cca act ata aaa tac atc ttc gga ttc ata	341
Val Leu Val Ile Leu Val Pro Thr Ile Lys Tyr Ile Phe Gly Phe Ile	
95 100 105	
ggg gct tct tct gcc act atg ctg att ttt att ctt cca gca gtt ttt	389
Gly Ala Ser Ser Ala Thr Met Leu Ile Phe Ile Leu Pro Ala Val Phe	
110 115 120	
tat ctt aaa ctt gtc aag aaa gaa act ttt agg tca ccc caa aag gtc	437
Tyr Leu Lys Leu Val Lys Lys Glu Thr Phe Arg Ser Pro Gln Lys Val	
125 130 135	
ggg gct tta att ttc ctt gtg gtt gga ata ttc ttc atg att gga agc	485
Gly Ala Leu Ile Phe Leu Val Val Gly Ile Phe Phe Met Ile Gly Ser	
140 145 150 155	
atg gca ctc att ata att gac tgg att tat gat cct cca aat tcc aag	533

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Met Ala Leu Ile Ile Ile Asp Trp Ile Tyr Asp Pro Pro Asn Ser Lys
      160              165              170
cat cac taacacaagg aaaaatactt tctttttcta ttggaaatgg ttacaagtta      589
His His
tactccaaaa gatatttgaa ttatcttgat tggaatgtta ttcataggaa ataacaggaa      649
gattccaaag acgtttacca gtmatatcac caggcacctg cagaagagga aaatcactgt      709
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aaaaaaa      776

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      1              5
ggg gtc ttc gtg ctg tcc ctc tcg gcc atc ccg gtc acc tat gtc ttc      102
Gly Val Phe Val Leu Ser Leu Ser Ala Ile Pro Val Thr Tyr Val Phe
      10              15              20
aac cac ctg gcg gcc cag cat gat tcc tgg act att gta ggg gtt gct      150
Asn His Leu Ala Ala Gln His Asp Ser Trp Thr Ile Val Gly Val Ala
      25              30              35
gcc ctc atc ctg ttc ctg gta gca ctg ctg gct cgt gtc ctc gtc aaa      198
Ala Leu Ile Leu Phe Leu Val Ala Leu Leu Ala Arg Val Leu Val Lys
      40              45              50              55
aga aaa cca ccc cgg gac cca ctg ttc tat gtg tat gca gtt ttt gga      246
Arg Lys Pro Pro Arg Asp Pro Leu Phe Tyr Val Tyr Ala Val Phe Gly
      60              65              70
ttt acc agc gtg gtg aac ctc atc ata gga ctg gag caa gat gga atc      294
Phe Thr Ser Val Val Asn Leu Ile Ile Gly Leu Glu Gln Asp Gly Ile
      75              80              85
att gac ggg ttc atg aca cac tac ttg aga gag ggt gaa ccg tat ctg      342
Ile Asp Gly Phe Met Thr His Tyr Leu Arg Glu Gly Glu Pro Tyr Leu
      90              95              100
aac acc gca tat ggg cac atg atc tgc tac tgg gat ggc tct gct cat      390
Asn Thr Ala Tyr Gly His Met Ile Cys Tyr Trp Asp Gly Ser Ala His
      105              110              115
tat ctg atg tac ctg gtg atg gtg gca gcc ata gca tgg gag gaa act      438
Tyr Leu Met Tyr Leu Val Met Val Ala Ala Ile Ala Trp Glu Glu Thr
      120              125              130              135
tat aga acc att ggc cta tat tgg gtt gga tct att att atg agt gtt      486
Tyr Arg Thr Ile Gly Leu Tyr Trp Val Gly Ser Ile Ile Met Ser Val
      140              145              150
gtt gtt ttt gtg cca gga aac att gta ggg aag tat gga aca cga att      534
Val Val Phe Val Pro Gly Asn Ile Val Gly Lys Tyr Gly Thr Arg Ile
      155              160              165
tgc cct gct ttt ttc tta agc ata cca tat act tgt ctt cct gtc tgg      582
Cys Pro Ala Phe Phe Leu Ser Ile Pro Tyr Thr Cys Leu Pro Val Trp
      170              175              180
gct ggt ttc aga atc tat aat cag cca tca gaa aat tat aat tac ccc      630
Ala Gly Phe Arg Ile Tyr Asn Gln Pro Ser Glu Asn Tyr Asn Tyr Pro
      185              190              195

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09376997-060601

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Ser Lys Val Ile Gln Glu Ala Gln Ala Lys Asp Leu Leu Arg Arg Pro	
200 205 210 215	
ttt gat tta atg ttg gtt gtg tgt ctc ctc ctg gca act gga ttt tgc	726
Phe Asp Leu Met Leu Val Val Cys Leu Leu Leu Ala Thr Gly Phe Cys	
220 225 230	
ctg ttc aga ggt ttg att gct ttg gat tgc cca tct gag ctc tgc cga	774
Leu Phe Arg Gly Leu Ile Ala Leu Asp Cys Pro Ser Glu Leu Cys Arg	
235 240 245	
tta tat acg caa ttt caa gag ccc tat cta aag gat cct gct gct tat	822
Leu Tyr Thr Gln Phe Gln Glu Pro Tyr Leu Lys Asp Pro Ala Ala Tyr	
250 255 260	
cct aaa att cag atg ctg gca tat atg ttc tat tct gtt cct tac ttt	870
Pro Lys Ile Gln Met Leu Ala Tyr Met Phe Tyr Ser Val Pro Tyr Phe	
265 270 275	
gtg act gca ctg tat ggc tta gtg gtt cct gga tgt tcc tgg atg cct	918
Val Thr Ala Leu Tyr Gly Leu Val Val Pro Gly Cys Ser Trp Met Pro	
280 285 290 295	
gac atc aca ttg ata cat gct gga ggt ctg gct cag gct cag ttt tct	966
Asp Ile Thr Leu Ile His Ala Gly Gly Leu Ala Gln Ala Gln Phe Ser	
300 305 310	
cac att ggt gca tct ctt cat gct aga act gct tat gtc tac aga gtc	1014
His Ile Gly Ala Ser Leu His Ala Arg Thr Ala Tyr Val Tyr Arg Val	
315 320 325	
cct gaa gaa gca aaa atc ctt ttt tta gca tta aac ata gca tat gga	1062
Pro Glu Glu Ala Lys Ile Leu Phe Leu Ala Leu Asn Ile Ala Tyr Gly	
330 335 340	
gtt ctt cct cag ctc ttg gcc tat cgt tgt atc tac aaa cca gag ttc	1110
Val Leu Pro Gln Leu Leu Ala Tyr Arg Cys Ile Tyr Lys Pro Glu Phe	
345 350 355	
ttc ata aaa aca aag gca gaa gaa aaa gtg gaa taaaaatatt acttcatgtt	1163
Phe Ile Lys Thr Lys Ala Glu Glu Lys Val Glu	
360 365 370	
cctccttttct aaattactaa cttttgttat actggtactg atattttgtc ccatttcact	1223
ctcttctcat acgtgagtagt ttaagaatat gtacattctt gctctgcact gtatgtgtga	1283
gctatatggt attgtgtaaa ttttttttga aggaaaatgg aaattcttga gaaacagttt	1343
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aaaaaaaaa	1412

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1 5 10 15	
gag ccc cgg cca gga ttt cat ggt gtc ttg ggt atc aat tcc atc act	98
Glu Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr	
20 25 30	
ggg aag gag gag cct ctg tac ccc agc tac aag aga cag ttg cgc att	146
Gly Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile	
35 40 45	


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His Ile Gln Met Lys Leu Ala Arg Leu Glu Phe Glu Ser Leu Glu Ala
      355      360      365
ctc aag cag cag caa atg aag ctc gtg acc gag aac ctg aag gag gaa      1154
Leu Lys Gln Gln Gln Met Lys Leu Val Thr Glu Asn Leu Lys Glu Glu
      370      375      380
cca atg gaa agc ggg aag gag aag gca acc tgagtgccca gcgtgcccag      1204
Pro Met Glu Ser Gly Lys Glu Lys Ala Thr
      385      390
ctgccctgtt ggcagaggcc tgtgtctgtg ccacacctgc caccgtggca ggggggggtac      1264
ccggggcagc atcgtggctc ctgaaccag acccaatgct tagccaaacg aagtggctcc      1324
catgtggcaa gcacccttct cagtttcgca gtggcttggc tcgggatacct tggcagttcc      1384
cccagcccca cctgtctgtc tccttcccag ttccttcccg ggccccacac gctgctccag      1444
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agtgcagcgg gtacagtaag gcagtgttcc ccacactgga cctctttcct ggttctcttt      1684
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              Met Val Gly Gly Glu Ala Ala Ala
              1              5
gca gtg gag gag ctg gtt tcg ggg gtg cgg cag gcg gcc gac ttc gcg      100
Ala Val Glu Glu Leu Val Ser Gly Val Arg Gln Ala Ala Asp Phe Ala
      10      15      20
gag cag ttc cgc tcc tac tca gag agc gag aag caa tgg aag gcc cgc      148
Glu Gln Phe Arg Ser Tyr Ser Glu Ser Glu Lys Gln Trp Lys Ala Arg
      25      30      35      40
atg gaa ttc atc ctg cgc cac ctg ccc gac tac cgc gac ccg ccc gac      196
Met Glu Phe Ile Leu Arg His Leu Pro Asp Tyr Arg Asp Pro Pro Asp
      45      50      55
ggc agt ggc cgc ctg gac cag ctg ctc tcc ctc tcc atg gtc tgg gcc      244
Gly Ser Gly Arg Leu Asp Gln Leu Leu Ser Leu Ser Met Val Trp Ala
      60      65      70
aac cat ctc ttc cta ggc tgc agt tac aat aaa gac ctt tta gac aag      292
Asn His Leu Phe Leu Gly Cys Ser Tyr Asn Lys Asp Leu Leu Asp Lys
      75      80      85
gtg atg gaa atg gcc gat ggg att gaa gtg gaa gac ctg cca caa ttt      340
Val Met Glu Met Ala Asp Gly Ile Glu Val Glu Asp Leu Pro Gln Phe
      90      95      100
act acc aga agt gaa tta atg aaa aag cat caa agc taagccagaa      386
Thr Thr Arg Ser Glu Leu Met Lys Lys His Gln Ser
      105      110      115
gatttatcac attttcatca tcagctacag gattagaaag gaggctggga tgaatgtgac      446
atagaccaca gcagctctct taagactcct ggtattacca acataaagag gcaggtggaa      506
tgagaaggac tctgtctaga ttggcttttt taacattctc attttcccag gagttatcac      566
tgtaaaagta tgcattgata tttatgtatt tataaatcat gcaactctaag atgagttcat      626
caacattgta aaagccctct tttctgtttt cagggttttt tttttcttat cgacaaggtc      686

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tcactctgtc	gcccaggcag	aatcacaaag	gtgcattatt	ggctcattgc	agcctcgaac	746
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gaattttttgt	ttaaaatgcc	tttttgggct	gggccacagt	ggccttatgc	ccataataat	926
cccagcactt	tgggaggccg	aggtgagcag	atcacctgag	gttaggagtt	tgagaccagc	986
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gtggcggaca	tctgtaatcc	cagctactca	ggaggctgaa	gcagaagaac	tgcttgaacc	1106
tgggaggtgg	agggttcagt	gagccaagat	cgcaccattg	cactccatcc	tgggcgacaa	1166
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<211> 894

<212> DNA

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<221> CDS

<222> 78..566

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		Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu				
		1 5 10				
ctc cca gcg cct tcc cca atg ccc cag cta cct cct gat acc ctt gag						158
Leu Pro Ala Pro Ser Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu						
	15	20	25			
atg cgg gtc cga gat ggc agc aaa att cgc aac ctg ctg ggg ttg gct						206
Met Arg Val Arg Asp Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala						
	30	35	40			
ctg ggt cgg ttg gag ggc ggc agt gct cgg cat gta gtg ttc tca ggt						254
Leu Gly Arg Leu Glu Gly Gly Ser Ala Arg His Val Val Phe Ser Gly						
	45	50	55			
tct ggc agg gct gca gga aag gct gtc agc tgc gct gag att gtc aag						302
Ser Gly Arg Ala Ala Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys						
	60	65	70	75		
cgg cgg gtc cca ggc ctg cac cag ctc acc aag cta cgt ttc ctt cag						350
Arg Arg Val Pro Gly Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln						
	80	85	90			
act gag gac agc tgg gtc cca gcc tca cct gac aca ggg cta gac ccc						398
Thr Glu Asp Ser Trp Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro						
	95	100	105			
ctc aca gtg cgc cgc cat gtg cct gca gtg tgg gtg ctg ctc agc cgg						446
Leu Thr Val Arg Arg His Val Pro Ala Val Trp Val Leu Leu Ser Arg						
	110	115	120			
gac ccc ctg gac ccc aat gag tgt ggt tac caa ccc cca gga gca ccc						494
Asp Pro Leu Asp Pro Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro						
	125	130	135			
cct ggc ctg ggt tcc atg ccc agc tcc agc tgt ggc cct cgt tcc cga						542
Pro Gly Leu Gly Ser Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg						
	140	145	150	155		
aga agg gct cga gac acc cga tcg tgaagacctg ctgagccagc ctgttctccg						596
Arg Arg Ala Arg Asp Thr Arg Ser						
	160					
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ccatcaaggt ttgagtcac aaaagtggac ctccctatca tgcttccct tccctctagc						716
atgtgggaag ggactgctgt gaagaatgac agatgtgggg cctctgccaa gttctgcatt						776

gctaaataag ggcttcctct gccttctacc tacagtgcac ttgaactgcc ttctgaaaga 836
 ggtccaggga gggatttagg aaataaagtt tctacctatt taaaaaaaaa aaaaaaaa 894

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 Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val
 15 20 25
 ttc aag atg gca gca tct atg cat ggt cag ccc agt cct tct cta gaa 147
 Phe Lys Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu
 30 35 40
 gat gca aaa ctc aga aga cca atg gtc ata gaa atc ata gaa aaa aat 195
 Asp Ala Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn
 45 50 55 60
 ttt gac tat ctt aga aaa gaa atg aca caa aat ata tat caa atg gcg 243
 Phe Asp Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala
 65 70 75
 aca ttt gga aca aca gct ggt ttc tct gga ata ttc tca aac ttc ctg 291
 Thr Phe Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu
 80 85 90
 ttc aga cgc tgc ttc aag gtt aaa cat gat gct ttg aag aca tat gca 339
 Phe Arg Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala
 95 100 105
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 Ser Leu Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu
 110 115 120
 ttt gta att gat gct ttg tat tca gat aat ata agc aag gaa aac tgt 435
 Phe Val Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys
 125 130 135 140
 gtt ttc aga agc tca ctg att ggc ata gtt tgt ggt gtt ttc tat ccc 483
 Val Phe Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro
 145 150 155
 agt tct ttg gct ttt act aaa aat gga cgc ctg gca acc aag tat cat 531
 Ser Ser Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His
 160 165 170
 acc gtt cca ctg cca cca aaa gga agg gtt tta atc cat tgg atg acg 579
 Thr Val Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr
 175 180 185
 ctt tgt caa aca caa atg aaa tta atg gcg att cct cta gtc ttt cag 627
 Leu Cys Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln
 190 195 200
 att atg ttt gga ata tta aat ggt cta tac cat tat gca gta ttt gaa 675
 Ile Met Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu
 205 210 215 220
 gag aca ctt gag aaa act ata cat gaa gag taacacaaaaa aatgaatggg 725
 Glu Thr Leu Glu Lys Thr Ile His Glu Glu
 225 230

tgctaactta gcaaaatgaa gtttctataa agaggactca ggcattgctg aaagagttaa 785
aagtaactgt gaacaaataa tttgttctgt gccttttgcc tggtatatag caaatactca 845
aaaaatattc aataattcaa tcaataaata taagtttcat cttacaccaa aaaaaaaaaa 905
aaaaa 910

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<213> Homo sapiens

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Met Glu Arg Pro
1
gat aag gcg gcg ctg aac gca ctg cag cct cct gag ttc aga aat gaa 162
Asp Lys Ala Ala Leu Asn Ala Leu Gln Pro Pro Glu Phe Arg Asn Glu
5 10 15 20
agc tca tta gca tct aca ctg aag acg ctc ctg ttc ttc aca gct tta 210
Ser Ser Leu Ala Ser Thr Leu Lys Thr Leu Phe Phe Thr Ala Leu
25 30 35
atg atc act gtt cct att ggg tta tat ttc aca act aaa tct tac ata 258
Met Ile Thr Val Pro Ile Gly Leu Tyr Phe Thr Thr Lys Ser Tyr Ile
40 45 50
ttt gaa ggc gcc ctt ggg atg tcc aat agg gac agc tat ttt tac gct 306
Phe Glu Gly Ala Leu Gly Met Ser Asn Arg Asp Ser Tyr Phe Tyr Ala
55 60 65
gct att gtt gca gtg gtc gcc gtc cat gtg gtg ctg gcc ctc ttt gtg 354
Ala Ile Val Ala Val Val Ala Val His Val Val Leu Ala Leu Phe Val
70 75 80
tat gtg gcc tgg aat gaa ggc tca cga cag tgb cgt gaa ggc aaa cag 402
Tyr Val Ala Trp Asn Glu Gly Ser Arg Gln Xaa Arg Glu Gly Lys Gln
85 90 95 100
gat taaagtgaac atcacctttt tatagcatta aattcatttt ttaaaatgat 455
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aatgctggag ggggccatct gatttgaata aagttgaaag aacatgtaaa aaaaaaaaaa 515
aaaaa 519

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Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met
1 5 10
ctg ggc gca ggg gct ggc gtg ggc tac gcg ctc ctc gtt atc gtg acc 158
Leu Gly Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr

15	20	25	
ccg gga gag cgg cgg aag cag gaa atg cta aag gag atg cca ctg cag			206
Pro Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln			
30	35	40	45
gac cca agg agc aga gag gag gcg gcc agg acc cag cag cta ttg ctg			254
Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu			
50	55	60	
gcc act ctg cag gag gca gcg acc acg cag gag aac gtg gcc tgg agg			302
Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg			
65	70	75	
aag aac tgg atg gtt ggc ggc gaa ggc ggc gcc ggc ggg agg tca ccg			350
Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Gly Gly Arg Ser Pro			
80	85	90	
tgagaccgga cttgcctccg tgggcgcgcg accttggtt gggcgcagga atccgaggca			410
gcctttctcc ttcgtgggcc cagcggagag tccggaccga gataccatgc caggactctc			470
cggggtcctg tgagctgcgc tcgggtgagc acgtttcccc caaaccttg actgactgct			530
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Ile Val Leu Ala Asp Leu Asn Phe Pro Ala Ser Ser Ile Cys Gln Cys			
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ggg ccc atg gag atc cgt gca gac ggc ctg ggc atc ccg cag ctc ctg			151
Gly Pro Met Glu Ile Arg Ala Asp Gly Leu Gly Ile Pro Gln Leu Leu			
25	30	35	
gag gcc gtg ctg aag ctg ctg ccc ctg gac acc tat gtg gag agt ccg			199
Glu Ala Val Leu Lys Leu Leu Pro Leu Asp Thr Tyr Val Glu Ser Pro			
40	45	50	
gct gca gtc atg gag ctg gtg ccc agc gac aag gag agg ggc ctg cag			247
Ala Ala Val Met Glu Leu Val Pro Ser Asp Lys Glu Arg Gly Leu Gln			
55	60	65	70
acc cca gtg tgg acg gag tac gag tcc atc cta cgc agg gcc ggc tgt			295
Thr Pro Val Trp Thr Glu Tyr Glu Ser Ile Leu Arg Arg Ala Gly Cys			
75	80	85	
gtg aga gcc ctg gca aag ata gag agg ttt gag ttt tat gaa cgg gct			343
Val Arg Ala Leu Ala Lys Ile Glu Arg Phe Glu Phe Tyr Glu Arg Ala			
90	95	100	
aag aag gct ttt gct gtt gtg gca acg ggg gag acg gcc ctc tac gga			391
Lys Lys Ala Phe Ala Val Val Ala Thr Gly Glu Thr Ala Leu Tyr Gly			
105	110	115	
aac ctc atc ctc agg aag ggg gtg ctt gcc ctc aac ccc ctg ctg			436
Asn Leu Ile Leu Arg Lys Gly Val Leu Ala Leu Asn Pro Leu Leu			
120	125	130	
taggcctggt gaagaccacc tgggcgcgaa gaggaactgg gggcacctg agctccagta			496
ccaccactca caacaggcct ccagtgga gctccagac ctgggcctg gccagggtc			556

taggggccgg	cagtcttggg	gtgggccctg	ccaattggga	cgagtatccc	tgattttgtga	616
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<213> Homo sapiens
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Ile Val Leu Ala Asp Leu Asn Phe Pro Ala Ser Ser Ile Cys Gln Cys																	
10 15 20																	
ggg ccc atg gag atc cgt gca gac ggc ctg ggc atc ccg cag ctc ctg																	151
Gly Pro Met Glu Ile Arg Ala Asp Gly Leu Gly Ile Pro Gln Leu Leu																	
25 30 35																	
gag gcc gtg cta gct gct gcc cct gga cac cta tgt gga gag tcc ggc																	199
Glu Ala Val Leu Ala Ala Ala Pro Gly His Leu Cys Gly Glu Ser Gly																	
40 45 50																	
tgc agt cat gga gct ggt gcc cag cga caa gga gag ggg cct gca gac																	247
Cys Ser His Gly Ala Gly Ala Gln Arg Gln Gly Glu Gly Pro Ala Asp																	
55 60 65 70																	
ccc agt gtg gac gga gta cga gtc cat cct acg cag ggc cgg ctg tgt																	295
Pro Ser Val Asp Gly Val Arg Val His Pro Thr Gln Gly Arg Leu Cys																	
75 80 85																	
gag agc cct ggc aaa gat aga gag gtt tgagttttat gaacgggcta																	342
Glu Ser Pro Gly Lys Asp Arg Glu Val																	
90 95																	
agaaggcttt tgctgttgtg gcaacggggg agacggccct ctacggaaac ctcatcctca																	402
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aagaggaact gggggcaccc tgagctccag taccaccact cacaacaggc ctcccagtg																	522
cagctcccag acctgggccc tggccagggc tctagggggc ggcagtcttg ggggtgggccc																	582
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aaaaaaaa																	650

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<212> DNA
<213> Homo sapiens
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<221> CDS
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ctatagaaca acagatgtag tctccttatt aagtctgaag accaaacttc ttagtgcaaa      180
gcagtcaagt cttttctcaa c   atg acc cca atc aag ctt ttg aac tta aca      231
                               Met Thr Pro Ile Lys Leu Leu Asn Leu Thr
                               1           5               10
tca aga tat aac ttc aga aga acg ttt gga ata gag ctc agt tca aac      279
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Ser	Ser	Tyr	Cys	Lys	Arg	Gly	Asn	Gly	Tyr	Arg	Ser	Arg	Val	Pro	Lys		
			30					35					40				
gaa	tgc	gaa	tgc	aac	tgg	ctt	cat	ctt	gaa	agc	gac	act	ctg	aag	aaa		375
Glu	Cys	Glu	Cys	Asn	Trp	Leu	His	Leu	Glu	Ser	Asp	Thr	Leu	Lys	Lys		
			45				50					55					
tta	ccc	ata	att	tct	ccc	tct	tgg	aca	tgc	aga	att	atc	ctg	ttc	ttg		423
Leu	Pro	Ile	Ile	Ser	Pro	Ser	Trp	Thr	Cys	Arg	Ile	Ile	Leu	Phe	Leu		
	60					65				70							
tat	ttt	tct	ggc	cag	ctt	ctc	caa	ctt	tcc	ctt	tct	tgt	ttg	caa	cta		471
Tyr	Phe	Ser	Gly	Gln	Leu	Leu	Gln	Leu	Ser	Leu	Ser	Cys	Leu	Gln	Leu		
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tgagctctga	ttcaagtgcc	tgccctctgcc	ccttggtggg	ctgaagcttc	atg gag												176
					Met Glu												
					1												
gta	tcc	acc	aac	ccc	tcc	tcc	aac	atc	gat	cca	ggc	aac	tat	gtt	gaa		224
Val	Ser	Thr	Asn	Pro	Ser	Ser	Asn	Ile	Asp	Pro	Gly	Asn	Tyr	Val	Glu		
		5					10					15					
atg	aat	gat	tca	atc	acc	cac	cta	ccc	tct	aaa	gtg	gtg	ata	caa	gat		272
Met	Asn	Asp	Ser	Ile	Thr	His	Leu	Pro	Ser	Lys	Val	Val	Ile	Gln	Asp		
	20					25				30							
att	act	atg	gag	cta	cac	tgc	cct	ctg	tgc	aat	gat	tgg	ttc	cga	gac		320
Ile	Thr	Met	Glu	Leu	His	Cys	Pro	Leu	Cys	Asn	Asp	Trp	Phe	Arg	Asp		
	35				40					45				50			
cca	ctg	atg	cta	agc	tgt	ggc	cac	aac	ttc	tgt	gaa	gcc	tgt	atc	caa		368
Pro	Leu	Met	Leu	Ser	Cys	Gly	His	Asn	Phe	Cys	Glu	Ala	Cys	Ile	Gln		
				55				60					65				
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Asp	Phe	Trp	Arg	Leu	Gln	Ala	Lys	Glu	Thr	Phe	Cys	Pro	Glu	Cys	Lys		
		70					75					80					
atg	cta	tgt	cag	tat	aac	aac	tgt	aca	ttc	aac	cct	gta	ctg	gac	aag		464
Met	Leu	Cys	Gln	Tyr	Asn	Asn	Cys	Thr	Phe	Asn	Pro	Val	Leu	Asp	Lys		
	85				90					95							
ttg	gta	gag	aag	att	aag	aag	tta	ccc	tta	ctc	aag	ggc	cat	cca	cag		512
Leu	Val	Glu	Lys	Ile	Lys	Lys	Leu	Pro	Leu	Leu	Lys	Gly	His	Pro	Gln		
	100					105					110						
tgc	cca	gag	cat	gga	gag	aac	ctg	aaa	ctg	ttc	agt	aaa	cca	gat	ggg		560
Cys	Pro	Glu	His	Gly	Glu	Asn	Leu	Lys	Leu	Phe	Ser	Lys	Pro	Asp	Gly		
	115				120				125						130		
aaa	ctg	atc	tgc	ttt	caa	tgc	aag	gat	gct	cgg	ttg	tct	gtg	ggg	cag		608
Lys	Leu	Ile	Cys	Phe	Gln	Cys	Lys	Asp	Ala	Arg	Leu	Ser	Val	Gly	Gln		

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Ser	Lys	Glu	Phe	Leu	Gln	Ile	Ser	Asp	Ala	Val	His	Phe	Phe	Met	Glu																					
			150							155							160																			
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Glu	Leu	Ala	Ile	Gln	Gln	Gly	Gln	Leu	Glu	Thr	Thr	Leu	Lys	Glu	Leu																					
			165							170							175																			
cag	acc	ctg	agg	aac	atg	cag	aag	gaa	gct	att	gct	gct	cac	aag	gaa	752																				
Gln	Thr	Leu	Arg	Asn	Met	Gln	Lys	Glu	Ala	Ile	Ala	Ala	His	Lys	Glu																					
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Asn	Lys	Leu	His	Leu	Gln	Gln	His	Val	Ser	Met	Glu	Phe	Leu	Lys	Leu																					
			195							200							210																			
cat	cag	ttc	ctg	cac	agc	aaa	gaa	aag	gac	att	tta	act	gag	ctc	cgg	848																				
His	Gln	Phe	Leu	His	Ser	Lys	Glu	Lys	Asp	Ile	Leu	Thr	Glu	Leu	Arg																					
			215							220							225																			
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Glu	Glu	Gly	Lys	Ala	Leu	Asn	Glu	Glu	Met	Glu	Leu	Asn	Leu	Ser	Gln																					
			230							235							240																			
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Leu	Gln	Glu	Gln	Cys	Leu	Leu	Ala	Lys	Asp	Met	Leu	Val	Ser	Ile	Gln																					
			245							250							255																			
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Ala	Lys	Thr	Glu	Gln	Gln	Asn	Ser	Phe	Asp	Phe	Leu	Lys	Asp	Ile	Thr																					
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Thr	Leu	Leu	His	Ser	Leu	Glu	Gln	Gly	Met	Lys	Val	Leu	Ala	Thr	Arg																					
			275							280							290																			
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Glu	Leu	Ile	Ser	Arg	Lys	Leu	Asn	Leu	Gly	Gln	Tyr	Lys	Gly	Pro	Ile																					
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cag	tac	atg	gta	tgg	agg	gaa	atg	cag	gac	act	ctc	tgc	cca	ggc	ctg	1136																				
Gln	Tyr	Met	Val	Trp	Arg	Glu	Met	Gln	Asp	Thr	Leu	Cys	Pro	Gly	Leu																					
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tct	cca	cta	act	ctg	gac	cct	aaa	aca	gct	cac	cca	aat	ctg	gtg	ctc	1184																				
Ser	Pro	Leu	Thr	Leu	Asp	Pro	Lys	Thr	Ala	His	Pro	Asn	Leu	Val	Leu																					
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Ser	Lys	Ser	Gln	Thr	Ser	Val	Trp	His	Gly	Asp	Ile	Lys	Lys	Ile	Met																					
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Pro	Asp	Asp	Pro	Glu	Arg	Phe	Asp	Ser	Ser	Val	Ala	Val	Leu	Gly	Ser																					
			355							360							370																			
aga																																				

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gga gga cag ttg tcc ttc tac aat gct aaa acc atg act cac att tac      1568
Gly Gly Gln Leu Ser Phe Tyr Asn Ala Lys Thr Met Thr His Ile Tyr
                                455                                460                                465
acc ttc agt aac act ttc atg gag aaa ctt tat ccc tac ttc tgc ccc      1616
Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe Cys Pro
                                470                                475                                480
tgc ctt aat gat ggt aga gag aat aaa gaa cca ttg cac atc tta cat      1664
Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile Leu His
                                485                                490                                495
cca cag taatgagtca taatattata caaattcaga gtgttattaa agagggttttg      1720
Pro Gln
500
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aaaataagga atgaaatggt ttctgatgat gattttttgt tttcatctga taataatttt      180
atatatcaca gaaacagc atg gtt ctt act aaa cct ctt caa aga aat ggc      231
                                Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly
                                1                                5                                10
agc atg atg agc ttt gaa aat gtg aaa gaa aag agc aga gaa gga ggg      279
Ser Met Met Ser Phe Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly
                                15                                20                                25
ccc cat gca cac aca ccc gaa gaa gaa ttg tgt ttc gtg gta aca cac      327
Pro His Ala His Thr Pro Glu Glu Glu Leu Cys Phe Val Val Thr His
                                30                                35                                40
tac cct cag gtt cag acc aca ctc aac ctg ttt ttc cat ata ttc aag      375
Tyr Pro Gln Val Gln Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys
                                45                                50                                55
gtt ctt act caa cca ctt tcc ctt ctg tgg ggt tgt gat cag aag cct      423
Val Leu Thr Gln Pro Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro
60                                65                                70                                75
cgt act gtt cct acc ctt gga aac ggc gca tgg gat acc tgc caa caa      471
Arg Thr Val Pro Thr Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln
                                80                                85                                90
cac ata cgc act tca tca tgg aca gca aac aca ctc gtc att caa aac      519
His Ile Arg Thr Ser Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn
                                95                                100                                105
cag cat tca cgg gaa agc act gtt tct gtt tgc ctt ttt atg tta atc      567
Gln His Ser Arg Glu Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile
                                110                                115                                120
cgc atg caa cat att ttg aaa aca gat aca ctt caa cag ttc aga ata      615
Arg Met Gln His Ile Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile
125                                130                                135
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Cys
140

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 <213> Homo sapiens

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 <222> 182..481

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 aggccctatt ctctgcctc acagggaccg gccaggatct ctatccttac agcacgttgg 180
 a atg tat atg ctg ctg tcc cca cat cgc ctt agg gag cag gca ggt gtc 229
 Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val
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 Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile
 20 25 30
 cga gag gct gag tca ctt cca caa agt aac aca gct gat ttt aaa tgc 325
 Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys
 35 40 45
 ctg cat tca gca tcc ctg cag cag gct cca ggt gga att cta atg gga 373
 Leu His Ser Ala Ser Leu Gln Ala Pro Gly Gly Ile Leu Met Gly
 50 55 60
 cca gcc tcc agt ccc tgg acc tta gcc gtg gaa gga gag aag agg aca 421
 Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr
 65 70 75 80
 tct gca cct cct ctg aga gaa agc ctg atg cct act aaa gga ctt ggg 469
 Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly
 85 90 95
 tgg tgg acg cag tgacctcag tctggagctt gttcactgaa cattggagac 521
 Trp Trp Thr Gln
 100
 tatcatttgc gcagatgggc ttgggcctct atgagcagca ggctgcaccc cacagtgacc 581
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 cctccctcog cccgcgcctc tcttagtcc ttgagatgag atg gca agt tac agc 175
 Met Ala Ser Tyr Ser
 1 5
 ggc ttc tcc ggc ctg ctg gag att cgc tac ggg cca gga cac cgc agc 223

Gly	Phe	Ser	Gly	Leu	Leu	Glu	Ile	Arg	Tyr	Gly	Pro	Gly	His	Arg	Ser		
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Cys	Leu	Pro	Gln	Phe	Ala	Phe	Phe	Pro	Gln	Pro	Pro	Leu	Pro	Arg	Pro		
			25					30					35				
cgg	atc	tgc	atg	tgg	gtg	ctg	gct	gag	ctg	ctg	gag	cta	ggg	tgt	cct		319
Arg	Ile	Cys	Met	Trp	Val	Leu	Ala	Glu	Leu	Leu	Glu	Leu	Gly	Cys	Pro		
		40					45				50						
gag	cag	agc	ctg	agg	gac	gcc	atc	acc	ctg	gac	ctc	ttc	tgc	cac	gcg		367
Glu	Gln	Ser	Leu	Arg	Asp	Ala	Ile	Thr	Leu	Asp	Leu	Phe	Cys	His	Ala		
		55				60				65							
ctc	att	ttc	tgc	cgc	cag	cag	ggc	ttc	tca	ctg	gag	cag	acg	tca	gcg		415
Leu	Ile	Phe	Cys	Arg	Gln	Gln	Gly	Phe	Ser	Leu	Glu	Gln	Thr	Ser	Ala		
		70			75					80					85		
gct	tgt	gcc	ctg	ctc	cag	gat	ctt	cac	aag	gct	tgt	att	ggg	gag	agg		463
Ala	Cys	Ala	Leu	Leu	Gln	Asp	Leu	His	Lys	Ala	Cys	Ile	Gly	Glu	Arg		
			90						95					100			
ggg	cag	cta	cca	ggt	ttg	agc	ccc	agg	gag	aag	agg	aac	cgg	gcc	tgg		511
Gly	Gln	Leu	Pro	Gly	Leu	Ser	Pro	Arg	Glu	Lys	Arg	Asn	Arg	Ala	Trp		
			105					110					115				
cac	aag	tgaccatggg	aagcagaagc	aggggatttc	tgccctggaat	atgtcattat											567
His	Lys																
tagtagcatc	atcatcacaca	agccatcagc	tttccaatcc	actgcttcct	tatctagaaa												627
ttaaggatac	agcacacatt	ttacaggact	gttctgagaa	ataatatatg	caaatatatg												687
catagtgcac	aataaaaaaaaa	aaaaaaaaaa															716

<210> 229
 <211> 654
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 86..505

<400> 229

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ccggtgaatc	ctgccgctgg	cgtgg	atg	aga	agt	gaa	tgc	gtg	ctc	gga	gct						112
			Met	Arg	Ser	Glu	Cys	Val	Leu	Gly	Ala						
			1				5										
gcg	agt	gac	agc	ggg	cag	gag	gcg	ccc	agg	gac	act	tgg	ttt	ctc	cag		160
Ala	Ser	Asp	Ser	Gly	Gln	Glu	Ala	Pro	Arg	Asp	Thr	Trp	Phe	Leu	Gln		
				15						20					25		
ggc	tgg	aag	gct	tct	aga	agg	ttc	ctc	atc	aag	gga	agt	gtg	gct	ggg		208
Gly	Trp	Lys	Ala	Ser	Arg	Arg	Phe	Leu	Ile	Lys	Gly	Ser	Val	Ala	Gly		
			30						35					40			
ggc	gcc	gtc	tac	ctg	gtg	tac	gac	cag	gag	ctg	ctg	ggg	ccc	agc	gac		256
Gly	Ala	Val	Tyr	Leu	Val	Tyr	Asp	Gln	Glu	Leu	Leu	Gly	Pro	Ser	Asp		
			45					50					55				
aag	agc	cag	gca	gcc	cta	cag	aag	gct	ggg	gag	gtg	gtc	ccc	ccc	gcc		304
Lys	Ser	Gln	Ala	Ala	Leu	Gln	Lys	Ala	Gly	Glu	Val	Val	Pro	Pro	Ala		
			60				65					70					
atg	tac	cag	ttc	agc	cag	tac	gtg	tgt	cag	cag	aca	ggc	ctg	cag	ata		352
Met	Tyr	Gln	Phe	Ser	Gln	Tyr	Val	Cys	Gln	Gln	Thr	Gly	Leu	Gln	Ile		
			75				80					85					
ccc	cag	ctc	cca	gcc	cct	cca	aag	att	tac	ttt	ccc	atc	cgt	gac	tcc		400
Pro	Gln	Leu	Pro	Ala	Pro	Pro	Lys	Ile	Tyr	Phe	Pro	Ile	Arg	Asp	Ser		
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[illegible]

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<221> CDS
<222> 56..382
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<210> 231
<211> 634
<212> DNA
<213> Homo sapiens
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246

<221> CDS
<222> 56..355

<400> 231

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Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala Ser
                    5                    10                    15
cag act gtt aag aca ttt tca caa aac aga cca gca gca gct agg aca      154
Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg Thr
                    20                    25                    30
ttt caa cag att cgt gct att ctg cac ctg ttg ctg ctg agc cct ttc      202
Phe Gln Gln Ile Arg Ala Ile Leu His Leu Leu Leu Leu Ser Pro Phe
                    35                    40                    45
tca gtg gga cta gtt cga act atg tgg agg aga tgt act gtg ctt ggc      250
Ser Val Gly Leu Val Arg Thr Met Trp Arg Arg Cys Thr Val Leu Gly
50                    55                    60                    65
tgg aaa acc cca aaa gtg tac ata aga cag ggt ccc act gtt gtc cag      298
Trp Lys Thr Pro Lys Val Tyr Ile Arg Gln Gly Pro Thr Val Val Gln
                    70                    75                    80
gct gga gtg cag tgg cgg gat ctc ggc ttg ctg caa cct ccg act cct      346
Ala Gly Val Gln Trp Arg Asp Leu Gly Leu Leu Gln Pro Pro Thr Pro
                    85                    90                    95
ggg ttc aag tgattcttat gcctcagcct cccgagtaac tgggactaca      395
Gly Phe Lys
100
ggtgcacgctc accacgcctg actagttttt gtatttttag tagagatggg attttacttt      455
gttggccagg ctggtcttga acccctggcc tcaagtgatc caccacctt ggccctccaa      515
agtgtgga ttacaggtat gatcaaccac gcctggccat gtcatgcctt gtgacagaat      575
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<210> 232

<211> 583

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 76..498

<400> 232

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tcgagattgc gggct atg gcg ccg aag gtt ttt cgt cag tac tgg gat atc      111
                Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile
                1                5                10
ccc gat ggc acc gat tgc cac cgc aaa gcc tac agc acc acc agt att      159
Pro Asp Gly Thr Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile
                15                20                25
gcc agc gtc gct ggc ctg acc gcc gct gcc tac aga gtc aca ctc aat      207
Ala Ser Val Ala Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn
                30                35                40
cct ccg ggc acc ttc ctt gaa gga gtg gct aag gtt gga caa tac acg      255
Pro Pro Gly Thr Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr
45                50                55                60
ttc act gca gct gct gtc ggg gcc gtg ttt ggc ctc acc acc tgc atc      303
Phe Thr Ala Ala Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile

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 aaaaaaaaaa aaa 753

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 <211> 762
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 211..612

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 acgtgggagc gagaacgtca cactggaggc agctgggtggc acgatggggg acagagtga 180
 aggtagcaag tcaagagcct tcgtgtcacc atg gcc aca cac ccc gat ggc ttc 234
 Met Ala Thr His Pro Asp Gly Phe
 1 5
 cgg ctt gag gga ccc ctg gct gca gcg cac agc cct ggg cct tgc act 282
 Arg Leu Glu Gly Pro Leu Ala Ala Ala His Ser Pro Gly Pro Cys Thr
 10 15 20
 gtg ctc tac gaa ggc cct gtc cgt ggg ctc tgc ccc ttt gcc ccg cga 330
 Val Leu Tyr Glu Gly Pro Val Arg Gly Leu Cys Pro Phe Ala Pro Arg
 25 30 35 40
 aat tcc aac acc atg tcg gcg gct gcc ctg gct gcc ccc agc ctg ggc 378
 Asn Ser Asn Thr Met Ser Ala Ala Ala Leu Ala Ala Pro Ser Leu Gly
 45 50 55
 ttc gat ggg gtg att ggg gtg ctc gtg gct gat acc agc ctc acg gac 426
 Phe Asp Gly Val Ile Gly Val Leu Val Ala Asp Thr Ser Leu Thr Asp
 60 65 70
 atg cac gtg gtg gat gta gag ctg agc gga ccc cgg ggc ccc acg tgc 474
 Met His Val Val Asp Val Glu Leu Ser Gly Pro Arg Gly Pro Thr Cys
 75 80 85
 cga agc ttt gct gtg cac acc cgc aga gag aac cct gcc gag cca ggc 522
 Arg Ser Phe Ala Val His Thr Arg Arg Glu Asn Pro Ala Glu Pro Gly
 90 95 100
 gcg gtc acc ggc tcc gcc acc gtc acg gcc ttc tgg cgg agc ctc ctg 570
 Ala Val Thr Gly Ser Ala Thr Val Thr Ala Phe Trp Arg Ser Leu Leu
 105 110 115 120
 gcc tgc tgc cag ctc ccc tcc agg ccg ggg atc cat ctc tgc 612
 Ala Cys Cys Gln Leu Pro Ser Arg Pro Gly Ile His Leu Cys
 125 130
 tgagaagcct cctccctccc gagacaagat catctgcttg gcctctcacc accaccatcc 672
 caccctgcc ctgccccact tccccagggt ctcccttctg actcagtaaa gatcaccgct 732
 gcctcccccc gccaaaaaaaa aaaaaaaaaa 762

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..259

<400> 235
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	1					5				10					15	
ggt	gga	gag	ccc	cgg	act	gga	gct	cct	gcg	aac	tcc	cct	tcc	tgc	cct	97
Gly	Gly	Glu	Pro	Arg	Thr	Gly	Ala	Pro	Ala	Asn	Ser	Pro	Ser	Cys	Pro	
				20					25					30		
cag	gag	atg	cca	ctg	cag	gac	cca	agg	agc	agg	gag	gag	gcg	gcc	agg	145
Gln	Glu	Met	Pro	Leu	Gln	Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	
			35					40					45			
acc	cag	cag	cta	ttg	ctg	gcc	act	ctg	cag	gag	gca	gcg	acc	acg	cag	193
Thr	Gln	Gln	Leu	Leu	Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	
			50				55					60				
gag	aac	gtg	gcc	tgg	agg	aag	aac	tgg	atg	gtt	ggc	ggc	gaa	ggc	ggc	241
Glu	Asn	Val	Ala	Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	
	65				70					75						
gcc	agc	ggg	agg	tca	cgg	tgagaccgga	cttgccctccg	tgggcgccggg								289
Ala	Ser	Gly	Arg	Ser	Pro											
80					85											
accttggcctt	gggcgcagga	atccgaggca	gcctttctcc	ttcgtgggcc	cagcggagag											349
tccggaccga	gataccatgc	caggactctc	cggggctcctg	tgagctgccg	tccgggtgagc											409
acgtttcccc	caaaccctgg	actgaactgt	ttaaggctccg	caaggcgggc	cagggccgag											469
acgcgagtcg	gatgtggtga	actgaaagaa	ccaataaaat	catgttcctc	caaaaaaaaa											529
aaaaaaaa																537
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<213>	Homo sapiens															
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<222>	23..370															
<400>	236															
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			Met	Gly	Arg	Pro	Trp	Met	Val	Met	Ile	Leu				
			1				5				10					
gag	tca	aaa	tct	gaa	gaa	aag	atg	tgg	tat	ggt	gta	ttc	ctg	tgg	gca	100
Glu	Ser	Lys	Ser	Glu	Glu	Lys	Met	Trp	Tyr	Gly	Val	Phe	Leu	Trp	Ala	
			15					20					25			
ctg	gtg	tct	tct	ctc	ttc	ttt	cat	gtc	cct	gct	gga	tta	ctg	gcc	ctc	148
Leu	Val	Ser	Ser	Leu	Phe	Phe	His	Val	Pro	Ala	Gly	Leu	Leu	Ala	Leu	
			30					35					40			
ttc	acc	ctc	aga	cat	cac	aaa	tat	ggt	agg	ttc	atg	tct	gta	agc	atc	196
Phe	Thr	Leu	Arg	His	His	Lys	Tyr	Gly	Arg	Phe	Met	Ser	Val	Ser	Ile	
	</															

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ttcttagttc ttcaaaggga agcaacttgg atgaacagga acatgaagga caacacatct 510
cagccttttc ttcatattga agctcctaga attgaagact tatgtggact cctattgttc 570
tcaaccaaaa caagtctttt ggctttcttt tttgtagata ttttaatttaa gcagttttca 630
tgtgtacctt tacccaagcc aagtcaacag tgtctctggg gtggcatcct ttgcactgaa 690
atttacagta ttctgtgaga tgtcgcata tttgaagaaa ccgtggaaga tactggttta 750
tttcaaataa gcagagtatg ttgtattaaa atcttatcta atcttgatta aaatttggca 810
aactcttttc tttgctacat cttagtgaca ataaatgcc aataggtttt gggttgagtat 870
agttttgaaa acaaatttgg tgaaataaag caggaaaaaa aatttaagta taactcaagt 930
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<210> 237
 <211> 662
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 41..352

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ggc aag ata ttt gtc tct gtc atg gtt aaa ttg caa aaa aat aaa ctt 103
Gly Lys Ile Phe Val Ser Val Met Val Lys Leu Gln Lys Asn Lys Leu
                        10                15                20
acc tcc ttc ccc agg cag cca ttg tta aca ttt ttt gaa tat cta gaa 151
Thr Ser Phe Pro Arg Gln Pro Leu Leu Thr Phe Phe Glu Tyr Leu Glu
                        25                30                35
aaa gtc ctt tgt tca gga tta ttt tcc cac tct gcc aag agt cac cat 199
Lys Val Leu Cys Ser Gly Leu Phe Ser His Ser Ala Lys Ser His His
                        40                45                50
gac ctg ctc aca cgc cac cct tat gaa act gcc gcg cca ctt ctc agc 247
Asp Leu Leu Thr Arg His Pro Tyr Glu Thr Ala Ala Pro Leu Leu Ser
                        55                60                65
tcc cat ttg att ctc aca gaa gct cta cga aat ggg ttg ggc aaa tgt 295
Ser His Leu Ile Leu Thr Glu Ala Leu Arg Asn Gly Leu Gly Lys Cys
                        70                75                80                85
cat gat cct cat ttc aca ggg gaa gaa act gag gcc cag agg ggg aaa 343
His Asp Pro His Phe Thr Gly Glu Glu Thr Glu Ala Gln Arg Gly Lys
                        90                95                100
ctg act acc taaaattgcc atgtaggccg gcgcgggtggc tcacgcctgt 392
Leu Thr Thr
aatcccagca ctgtgggagg ccaaggcggg tggatcgga ggtcaggaga tcgagaccat 452
cctggctggc acttgaagcc ccgtctctac tagggataca aataattggc cgggtgtggt 512
ggcgggcgcc tgtgkwccca gctgttcggc aggctgagga gggcgaatgg tgtgagcctg 572
ggaggcggag cttgcgggtg gccgggattg cgccactgca ctccagcctg ggcgacagag 632
ccagattccg tccaaaaaaa aaaaaaaaaa 662

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 <211> 1829
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 3..1319

<400> 238

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ctg tgg ggt ggg gtg gtg aag agt tgt ttt gag gga aaa ggc cca caa	95
Leu Trp Gly Gly Val Val Lys Ser Cys Phe Glu Gly Lys Gly Pro Gln	
20 25 30	
aga gaa gcc caa cca gcc agc ccc cag gcc gcc ccg cca gga ccc acc	143
Arg Glu Ala Gln Pro Ala Ser Pro Gln Ala Ala Pro Pro Gly Pro Thr	
35 40 45	
aat gag gca cag atg gca gcc gct gcc gcc cta gcc cgg ctg gag cag	191
Asn Glu Ala Gln Met Ala Ala Ala Ala Ala Leu Ala Arg Leu Glu Gln	
50 55 60	
aag cag tcc cgg gcc tgg ggc ccc aca tcg cag gac acc atc cga aac	239
Lys Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg Asn	
65 70 75	
cag gtg aga aag gaa ctt caa gcc gaa gcc acc gtc agc ggg agc ccc	287
Gln Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser Pro	
80 85 90 95	
gag gcc cca ggg acc aac gtg gta tct gag ccc aga gag gaa ggc tct	335
Glu Ala Pro Gly Thr Asn Val Val Ser Glu Pro Arg Glu Glu Gly Ser	
100 105 110	
gcc cac ctg gct gtg cct ggc gtg tac ttc acc tgt ccg ctc act ggg	383
Ala His Leu Ala Val Pro Gly Val Tyr Phe Thr Cys Pro Leu Thr Gly	
115 120 125	
gcc acc ctg agg aag gac cag cgg gac gcc tgc atc aag gag gcc att	431
Ala Thr Leu Arg Lys Asp Gln Arg Asp Ala Cys Ile Lys Glu Ala Ile	
130 135 140	
ctc ttg cac ttc tcc acc gac cca gtg gcc gcc tcc atc atg aag atc	479
Leu Leu His Phe Ser Thr Asp Pro Val Ala Ala Ser Ile Met Lys Ile	
145 150 155	
tac acg ttc aac aaa gac cag gac cgg gtg aag ctg ggt gtg gac acc	527
Tyr Thr Phe Asn Lys Asp Gln Asp Arg Val Lys Leu Gly Val Asp Thr	
160 165 170 175	
att gcc aag tac ctg gac aac atc cac ctg cac ccc gag gag gag aag	575
Ile Ala Lys Tyr Leu Asp Asn Ile His Leu His Pro Glu Glu Glu Lys	
180 185 190	
tac cgg aag atc aag ctg cag aac aag gtg ttt cag gag cgc att aac	623
Tyr Arg Lys Ile Lys Leu Gln Asn Lys Val Phe Gln Glu Arg Ile Asn	
195 200 205	
tgc ctg gaa ggg acc cac gag ttt ttt gag gcc att ggg ttc cag aag	671
Cys Leu Glu Gly Thr His Glu Phe Phe Glu Ala Ile Gly Phe Gln Lys	
210 215 220	
gtg ttg ctt ccc gcc cag gat cag gag gac ccc gag gag ttc tac gtg	719
Val Leu Leu Pro Ala Gln Asp Gln Glu Asp Pro Glu Glu Phe Tyr Val	
225 230 235	
ctg agc gag acc acc ttg gcc cag ccc cag agc ctg gag agg cac aag	767
Leu Ser Glu Thr Thr Leu Ala Gln Pro Gln Ser Leu Glu Arg His Lys	
240 245 250 255	
gaa cag ctg ctg gct gcg gag ccc gtg cgc gcc aag ctg gac agg cag	815
Glu Gln Leu Leu Ala Ala Glu Pro Val Arg Ala Lys Leu Asp Arg Gln	
260 265 270	
cgc cgc gtc ttc cag ccc tcg ccc ctg gcc tcg cag ttc gaa ctg cct	863
Arg Arg Val Phe Gln Pro Ser Pro Leu Ala Ser Gln Phe Glu Leu Pro	
275 280 285	
ggg gac ttc ttc aac ctc aca gca gag gag atc aag cgg gag cag agg	911
Gly Asp Phe Phe Asn Leu Thr Ala Glu Glu Ile Lys Arg Glu Gln Arg	

290	295	300	
ctc agg tcc gag gcg gtg gag cgg ctg agc gtg ctg cgg acc aag gcc			959
Leu Arg Ser Glu Ala Val Glu Arg Leu Ser Val Leu Arg Thr Lys Ala			
305	310	315	
atg cgg gag aag gag gag cag cgg ggg ctg cgc aag tac aac tac acg			1007
Met Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr			
320	325	330	335
ctg ctg cgc gtg cgc ctc ccc gat ggc tgc ctc ctg cag ggc act ttc			1055
Leu Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe			
340	345	350	
tac gct cgg gag cgg ctg ggg gcg gtg tac ggg ttc gtc cgg gag gcc			1103
Tyr Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu Ala			
355	360	365	
ctg cag agc gac tgg ctg cct ttt gag ctg ctg gcc tcg gga ggg cag			1151
Leu Gln Ser Asp Trp Leu Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln			
370	375	380	
aag ctg tcc gag gac gag aac ctg gcc ttg aac gag tgc ggg ctg gtg			1199
Lys Leu Ser Glu Asp Glu Asn Leu Ala Leu Asn Glu Cys Gly Leu Val			
385	390	395	
ccc tct gcc ctc ctg acc ttc tcg tgg gac atg gct gtg ctg gag gac			1247
Pro Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu Asp			
400	405	410	415
atc aag gcc gcg ggg gcc gag ccg gac tcc atc ctg aaa ccc gag ctc			1295
Ile Lys Ala Ala Gly Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu			
420	425	430	
ctg tca gcc atc gag aag ctc ttg tgaaataaaa gcagggttgg cctcagccct			1349
Leu Ser Ala Ile Glu Lys Leu Leu			
435			
gtgggtctgt ctcagtctct ccctgttctt ctccccgcca cccaggggcc tccaagccac			1409
ctctggaaat acttggctct gccccatggg caccggaggg gcgccagccg tggagctgtg			1469
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tctgtggatg tgggtgacaa cggcaggagg ggacgtggc cttcctgcac atagacctgc			1769
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ttgatttgat tcatgaccct catctggaca caagctctaa aatacttgag ccttggcaga			240
aatggctgat agagtccaca gaacacgtg tcctcatctc agagaggaga actctgaacc			300
cagaggggaa ggatttacct gcagttgtat ggcaagccag aggtaggcgc tgcactggaa			360
cgcagcctaa ccagcctaaa gaaaccatgg gaggagaggc tcttaccctc tcctttgcag			420
atg tgg gcc cgg ctg cct cac act cca gag cag atg ggc cac agg ctt			468
Met Trp Ala Arg Leu Pro His Thr Pro Glu Gln Met Gly His Arg Leu			
1 5 10 15			
ata ggt ccc aag gaa gct tca ctt cat gtg gta ccc age tgg cca gcc			516

Ile Gly Pro Lys Glu Ala Ser Leu His Val Val Pro Ser Trp Pro Ala	
20 25 30	
agg aag atg gag ggg ctt ctg gct ggc ctc tct tcc tct cct aga aag	564
Arg Lys Met Glu Gly Leu Leu Ala Gly Leu Ser Ser Ser Pro Arg Lys	
35 40 45	
tca tgc tgg ccc ttt tgg gtc cat ggg cca aag gtt cat gaa ggt ggc	612
Ser Cys Trp Pro Phe Trp Val His Gly Pro Lys Val His Glu Gly Gly	
50 55 60	
tct gcc tgt gag aca tca agc tcc tgg gtt gaa gga ctt gga tta aga	660
Ser Ala Cys Glu Thr Ser Ser Trp Val Glu Gly Leu Gly Leu Arg	
65 70 75 80	
aga gtg aca tca gtg cac agt tta tgc caa ggg ctt ggg gcc tca gtc	708
Arg Val Thr Ser Val His Ser Leu Cys Gln Gly Leu Gly Ala Ser Val	
85 90 95	
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Gln Leu Leu Pro Gly Pro Pro Pro Thr Thr Thr Ser Asp Lys Asn Asn	
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 184. **Funding**
 185. **Data Availability Statement**
 186. **References**
 187. **Appendix**
 188. **Tables**
 189. **Figures**
 190. **Supplementary Materials**
 191. **Notes**
 192. **Abbreviations**
 193. **Conflicts of Interest**
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 196. **Funding**
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 Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr
 5 10 15
 Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu Leu Asp Ala
 20 25 30 35
 Glu Val Leu Glu Val Phe His Pro Thr His Glu Trp Gln Ala Leu Gln
 40 45 50
 Pro Gly Gln Ala Val Pro Ala Gly Ser His Val Arg Leu Asn Leu Gln
 55 60 65
 Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn
 70 75 80
 Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn Thr Asn Thr Tyr Thr Ser
 85 90 95
 Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe Lys Glu Gly Ala Glu Met
 100 105 110 115
 Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln Ala Glu Val Lys Arg Leu
 120 125 130
 Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val
 135 140 145
 Val Ile Glu Thr Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe
 150 155 160
 Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp
 165 170 175
 Leu Glu Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser
 180 185 190 195
 Phe Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro
 200 205 210
 Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser Ser
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 Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu Gln Lys
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 Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala Lys Lys Lys
 245 250 255
 Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe Pro Tyr Ala Gln
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 Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln Val Leu Arg Thr Leu Val
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 Gln Glu Lys Gly Thr Glu Val Leu Ala Val Arg Val Val Thr Leu Leu
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Tyr Asp Leu Val Thr Glu Lys Met Phe Ala Glu Glu
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-20					-15					-10					-5
Ala	Leu	Arg	Ala	Leu	Gln	Glu	Cys	Gln	Arg	Gln	Gln	Val	Arg	Pro	Val
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Ile	Ala	Phe	Gln	Gly	His	Arg	Gly	Tyr	Leu	Arg	Leu	Pro	Gly	Pro	Gly
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Trp	Ser	Cys	Leu	Phe	Ser	Phe	Ile	Val	Ser	Gln	Cys	Cys	Gln	Glu	Gly
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Ala	Gly	Gly	Ser	Leu	Asp	Leu	Val	Cys	Gln	Arg	Phe	Leu	Arg	Ser	Gly
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Pro	Asn	Ser	Leu	His	Cys	Leu	Gly	Ser	Leu	Arg	Glu	Arg	Leu	Ile	Ile
				65						70				75	
Trp	Ala	Ala	Met	Asp	Ser	Ile	Pro	Ala	Pro	Ser	Ser	Val	Gln	Gly	His
			80					85					90		
Asn	Leu	Thr	Glu	Asp	Ala	Arg	His	Pro	Glu	Ser	Trp	Gln	Asn	Thr	Gly
		95					100					105			
Gly	Tyr	Ser	Glu	Gly	Asp	Ala	Val	Ser	Gln	Pro	Gln	Met	Ala	Leu	Glu
	110					115					120				
Glu	Val	Ser	Val	Ser	Asp	Pro	Leu	Ala	Ser	Asn	Gln	Gly	Gln	Ser	Leu
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Pro	Gly	Ser	Ser	Arg	Glu	His	Met	Ala	Gln	Trp	Glu	Val	Arg	Ser	Gln
				145					150					155	
Thr	His	Val	Pro	Asn	Arg	Glu	Pro	Val	Gln	Ala	Leu	Pro	Ser	Ser	Ala
			160					165					170		
Ser	Arg	Lys	Arg	Leu	Asp	Lys	Lys	Arg	Ser	Val	Pro	Val	Ala	Thr	Val
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Glu	Leu	Glu	Glu	Lys	Arg	Phe	Arg	Thr	Leu	Pro	Leu	Val	Pro	Ser	Pro
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Leu	Gln	Gly	Leu	Thr	Asn	Gln	Asp	Leu	Gln	Glu	Gly	Glu	Asp	Trp	Glu
205					210					215					220
Gln	Glu	Asp	Glu	Asp	Met	Asp	Pro	Arg	Leu	Glu	His	Ser	Ser	Ser	Val
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Gln	Glu	Asp	Ser	Glu	Ser	Pro	Ser	Pro	Glu	Asp	Ile	Pro	Asp	Tyr	Leu
			240					245					250		
Leu	Gln	Tyr	Arg	Ala	Ile	His	Ser	Ala	Glu	Gln	Gln	His	Ala	Tyr	Glu
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Gln	Asp	Phe	Glu	Thr	Asp	Tyr	Ala	Glu	Tyr	Arg	Ile	Leu	His	Ala	Arg
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Val	Gly	Thr	Ala	Ser	Gln	Arg	Phe	Ile	Glu	Leu	Gly	Ala	Glu	Ile	Lys
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Arg	Val	Arg	Arg	Gly	Thr	Pro	Glu	Tyr	Lys	Val	Leu	Glu	Asp	Lys	Ile
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 Ser Ser Ser
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 Tyr Gly Asn Pro Ile Glu Ala Ser Ser Tyr Gly Leu Asp Leu Asp Cys
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 Gly Ala Pro Gly Thr Pro Glu Ala His Val Cys Phe Asp Pro Cys Gln
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 Asn Tyr Thr Leu Leu Asp Leu Gly Pro Ile Thr Arg Arg Gly Ala Gln
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 Arg Leu Gln Ser Pro Gln Gly Phe Asn Lys Ala Gly Gly Phe His Gly
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 Ile Tyr Ala Gly Val Pro Ser Ala Ala Ile Gly Ser Phe Pro Asn Gly
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 Cys Leu Pro Asp Ser Ser Ser Ile
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 Val Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala
 5 10 15
 Gln Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala
 20 25 30
 Glu Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser
 35 40 45
 Ala Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu
 50 55 60 65
 Leu Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu
 70 75 80
 Gln Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly
 85 90 95
 Gly Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu
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 Lys Lys Phe Ser Leu Leu Lys Pro Trp Ala
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 Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu
 5 10 15
 Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg
 20 25 30
 Ile Ser Ala Ile Ala His Arg Gly Gly Ser Xaa Xaa Ala Pro Glu Asn
 35 40 45

Thr Leu Ala Ala Ile Arg Gln Leu Arg Met Glu Gln Gln Ala Trp Ser
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 Trp Thr Leu Ser Leu Leu Leu Thr Gly Phe Leu Ser
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 -5 1 5
 Phe Leu Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg
 10 15 20
 Tyr Cys Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys
 25 30 35 40
 Asp Ile Asn Thr Phe Ile His Gly Asn Lys Arg Thr Ile Lys Ala Ile
 45 50 55
 Cys Glu Asn Lys Asn Gly Asn Pro His Arg Glu Asn Leu Arg Ile Ser
 60 65 70
 Lys Ser Ser Phe Gln Val Thr Thr Cys Lys Leu His Gly Gly Ser Pro
 75 80 85
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 Ala Thr Arg Ile Pro Leu Asn Gly Thr Trp Leu Phe Thr Pro Val Ser
 1 5 10 15
 Lys Met Ala Thr Val Lys Ser Glu Leu Ile Glu Arg Phe Thr Ser Glu
 20 25 30
 Lys Pro Val His Ser Lys Val Ser Ile Ile Gly Thr Gly Ser Val
 35 40 45
 Gly Met Ala Cys Ala Ile Ser Ile Leu Leu Lys Gly Leu Ser Asp Glu
 50 55 60
 Leu Ala Leu Val Asp Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met

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Asp 80	Leu	Gln	His	Gly	Ser 85	Pro	Phe	Thr	Lys	Met 90	Pro	Asn	Ile	Val	Cys 95	
Ser	Lys	Asp	Tyr	Phe 100	Val	Thr	Ala	Asn	Ser 105	Asn	Leu	Val	Ile	Ile	Thr	
Ala	Gly	Ala	Arg	Gln 115	Glu	Lys	Gly	Glu	Thr 120	Arg	Leu	Asn	Leu	Val	Gln	
Arg	Asn	Val	Ala	Ile 130	Phe	Lys	Leu	Met	Ile 135	Ser	Ser	Ile	Val	Gln	Tyr	
Ser	Pro	His	Cys	Lys 145	Leu	Ile	Ile	Val	Ser 150	Asn	Pro	Val	Asp	Ile	Leu	
Thr 160	Tyr	Val	Ala	Trp 165	Lys	Leu	Ser	Ala	Phe 170	Pro	Lys	Asn	Arg	Ile	Ile 175	
Gly	Ser	Gly	Cys	Asn 180	Leu	Asp	Thr	Ala	Arg 185	Phe	Arg	Phe	Leu	Ile	Gly 190	
Gln	Lys	Leu	Gly	Ile 195	His	Ser	Glu	Ser	Cys 200	His	Gly	Trp	Ile	Leu	Gly 205	
Glu	His	Gly	Asp	Ser 210	Ser	Val	Pro	Val	Trp 215	Ser	Gly	Val	Asn	Ile	Ala 220	
Gly	Val	Pro	Leu	Lys 225	Asp	Leu	Asn	Ser	Asp 230	Ile	Gly	Thr	Asp	Lys	Asp 235	
Pro 240	Glu	Gln	Trp	Lys 245	Asn	Val	His	Lys	Glu 250	Val	Thr	Ala	Thr	Ala	Tyr 255	
Glu	Ile	Ile	Lys	Met 260	Lys	Gly	Tyr	Thr	Ser 265	Trp	Ala	Ile	Gly	Leu	Ser 270	
Val	Ala	Asp	Leu	Thr 275	Glu	Ser	Ile	Leu	Lys 280	Asn	Leu	Arg	Arg	Ile	His 285	
Pro	Val	Ser	Thr	Ile 290	Ile	Lys	Gly	Leu	Tyr 295	Gly	Ile	Asp	Glu	Glu	Val 300	
Phe	Leu	Ser	Ile	Pro 305	Cys	Ile	Leu	Gly	Glu 310	Asn	Gly	Ile	Thr	Asn	Leu 315	
Ile 320	Lys	Ile	Lys	Leu 325	Thr	Pro	Glu	Glu	Glu 330	Ala	His	Leu	Lys	Lys	Ser 335	
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Ala	Thr	Arg	Ile	Pro	Leu	Asn	Gly	Thr	Trp	Leu	Phe	Thr	Pro	Val	Ser	
	1				5					10					15	
Lys	Met	Ala	Thr	Val	Lys	Ser	Glu	Leu	Ile	Glu	Arg	Phe	Thr	Ser	Glu	
				20					25					30		
Lys	Pro	Val	His	His	Ser	Lys	Val	Ser	Ile	Ile	Gly	Thr	Gly	Ser	Val	
			35					40					45			
Gly	Met	Ala	Cys	Ala	Ile	Ser	Ile	Leu	Leu	Lys	Gly	Leu	Ser	Asp	Glu	
		50					55					60				

Leu Ala Leu Val Asp Leu Asp Glu Asp Lys Leu Lys Gly Glu Thr Met
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Asp Leu Gln His Gly Ser Pro Phe Thr Lys Met Pro Ile Leu Phe Val
80 85 90 95
Ala Lys Ile Thr Leu Ser Gln Gln Thr Pro Thr
100 105

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Leu Asn Glu Asp Val Asn Lys Gln Glu Glu Lys Asn Glu Asp His Thr
20 25 30
Pro Asn Tyr Ala Pro Ala Asn Glu Lys Asn Gly Asn Tyr Tyr Lys Asp
35 40 45 50
Ile Lys Gln Tyr Val Phe Thr Thr Gln Asn Pro Asn Gly Thr Glu Ser
55 60 65
Glu Ile Ser Val Arg Ala Thr Thr Asp Leu Asn Phe Ala Leu Lys Asn
70 75 80
Gly Ser Thr Pro Asn Val Pro Ala Phe Trp Thr Met Leu Ala Lys Ala
85 90 95
Ile Asn Gly Thr Ala Val Val Met Asp Asp Lys Asp Gln Leu Phe His
100 105 110
Pro Ile Pro Glu Ser Asp Val Asn Ala Thr Gln Gly Glu Asn Gln Pro
115 120 125 130
Asp Leu Glu Asp Leu Lys Ile Lys Ile Met Leu Gly Ile Ser Leu Met
135 140 145
Thr Leu Leu Leu Phe Val Val Leu Leu Ala Phe Cys Ser Ala Thr Leu
150 155 160
Tyr Lys Leu Arg His Leu Ser Tyr Lys Ser Cys Glu Ser Gln Tyr Ser
165 170 175
Val Asn Pro Glu Leu Ala Thr Met Ser Tyr Phe His Pro Ser Glu Gly
180 185 190
Val Ser Asp Thr Ser Phe Ser Lys Ser Ala Glu Ser Ser Thr Phe Leu
195 200 205 210
Gly Thr Thr Ser Ser Asp Met Arg Arg Ser Gly Thr Arg Thr Ser Glu
215 220 225
Ser Lys Ile Met Thr Asp Ile Ile Ser Ile Gly Ser Asp Asn Glu Met
230 235 240
His Glu Asn Asp Glu Ser Val Thr Arg
245 250

<210> 258
<211> 200
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -20...-1

<400> 258
Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
-20 -15 -10 -5
Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
1 5 10
Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
15 20 25
Ile Leu Gly Thr Ile Gln Ile Leu Phe Gly Ile Met Thr Phe Ser Phe
30 35 40
Gly Val Ile Phe Leu Phe Thr Leu Leu Lys Pro Tyr Pro Arg Phe Pro
45 50 55 60
Phe Ile Phe Leu Ser Gly Tyr Pro Phe Trp Gly Ser Val Leu Phe Ile
65 70 75
Asn Ser Gly Ala Phe Leu Ile Ala Val Lys Arg Lys Thr Thr Glu Thr
80 85 90
Leu Ile Ile Leu Ser Arg Ile Met Asn Phe Leu Ser Ala Leu Gly Ala
95 100 105
Ile Ala Gly Ile Ile Leu Leu Thr Phe Gly Phe Ile Leu Asp Gln Asn
110 115 120
Tyr Ile Cys Gly Tyr Ser His Gln Asn Ser Gln Cys Lys Ala Val Thr
125 130 135 140
Val Leu Phe Leu Gly Ile Leu Ile Thr Leu Met Thr Phe Ser Ile Ile
145 150 155
Glu Leu Phe Ile Ser Leu Pro Phe Ser Ile Leu Gly Cys His Ser Glu
160 165 170
Asp Cys Asp Cys Glu Gln Cys Cys
175 180

<210> 259
<211> 394
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39...-1

<400> 259
Met Ala Thr Ala Gln Leu Gln Arg Thr Pro Met Ser Ala Leu Val Phe
-35 -30 -25
Pro Asn Lys Ile Ser Thr Glu His Gln Ser Leu Val Leu Val Lys Arg
-20 -15 -10
Leu Leu Ala Val Ser Val Ser Cys Ile Thr Tyr Leu Arg Gly Ile Phe
-5 1 5
Pro Glu Cys Ala Tyr Gly Thr Arg Tyr Leu Asp Asp Leu Cys Val Lys
10 15 20 25
Ile Leu Arg Glu Asp Lys Asn Cys Pro Gly Ser Thr Gln Leu Val Lys
30 35 40
Trp Ile Leu Gly Cys Tyr Asp Ala Leu Gln Lys Lys Tyr Leu Arg Met
45 50 55
Val Val Leu Ala Val Tyr Thr Asn Pro Glu Asp Pro Gln Thr Ile Ser
60 65 70
Glu Cys Tyr Gln Phe Lys Phe Lys Tyr Thr Asn Asn Gly Pro Leu Met
75 80 85
Asp Phe Ile Ser Lys Asn Gln Ser Asn Glu Ser Ser Met Leu Ser Thr

90					95					100				105
Asp	Thr	Lys	Lys	Ala	Ser	Ile	Leu	Leu	Ile	Arg	Lys	Ile	Tyr	Ile
				110						115				120
Met	Gln	Asn	Leu	Gly	Pro	Leu	Pro	Asn	Asp	Val	Cys	Leu	Thr	Met
			125					130					135	
Leu	Phe	Tyr	Tyr	Asp	Glu	Val	Thr	Pro	Pro	Asp	Tyr	Gln	Pro	Pro
		140					145					150		
Phe	Lys	Asp	Gly	Asp	Cys	Glu	Gly	Val	Ile	Phe	Glu	Gly	Glu	Pro
	155					160					165			
Tyr	Leu	Asn	Val	Gly	Glu	Val	Ser	Thr	Pro	Phe	His	Ile	Phe	Lys
170					175					180				185
Lys	Val	Thr	Thr	Glu	Arg	Glu	Arg	Met	Glu	Asn	Ile	Asp	Ser	Thr
				190					195					200
Leu	Ser	Pro	Lys	Gln	Ile	Lys	Thr	Pro	Phe	Gln	Lys	Ile	Leu	Arg
			205					210					215	
Lys	Asp	Val	Glu	Asp	Glu	Gln	Glu	His	Tyr	Thr	Ser	Asp	Asp	Leu
	220						225					230		
Ile	Glu	Thr	Lys	Met	Glu	Glu	Gln	Glu	Lys	Asn	Pro	Ala	Ser	Ser
	235					240					245			
Leu	Glu	Glu	Pro	Ser	Leu	Val	Cys	Glu	Glu	Asp	Glu	Ile	Met	Arg
250					255					260				265
Lys	Glu	Ser	Pro	Asp	Leu	Ser	Ile	Ser	His	Ser	Gln	Val	Glu	Gln
				270					275					280
Val	Asn	Lys	Thr	Ser	Glu	Leu	Asp	Met	Ser	Glu	Ser	Lys	Thr	Arg
		285					290					295		
Gly	Lys	Val	Phe	Gln	Asn	Lys	Met	Ala	Asn	Gly	Asn	Gln	Pro	Val
	300						305					310		
Ser	Ser	Lys	Glu	Asn	Arg	Lys	Arg	Ser	Gln	His	Glu	Ser	Gly	Arg
	315					320				325				
Val	Leu	His	His	Phe	Asp	Ser	Ser	Ser	Gln	Glu	Ser	Val	Pro	Lys
330					335					340				345
Arg	Lys	Phe	Ser	Glu	Pro	Lys	Glu	His	Ile					
				350					355					

<210> 260
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 260

Met	Ala	Leu	Glu	Val	Leu	Met	Leu	Leu	Ala	Val	Leu	Ile	Trp	Thr	Gly
	-15						-10					-5			
Ala	Glu	Asn	Leu	His	Val	Lys	Ile	Ser	Cys	Ser	Leu	Asp	Trp	Leu	Met
1				5					10					15	
Val	Ser	Val	Ile	Pro	Val	Ala	Glu	Ser	Arg	Asn	Leu	Tyr	Ile	Phe	Ala
				20					25					30	
Asp	Glu	Leu	His	Leu	Gly	Met	Gly	Cys	Pro	Ala	Asn	Arg	Ile	His	Thr
		35					40					45			
Tyr	Val	Tyr	Glu	Phe	Ile	Tyr	Leu	Val	Arg	Asp	Cys	Gly	Ile	Arg	Thr
	50					55						60			
Arg	Val	Val	Ser	Glu	Glu	Thr	Leu	Phe	Gln	Thr	Glu	Leu	Tyr	Phe	
	65					70				75					
Thr	Pro	Arg	Asn	Ile	Asp	His	Asp	Pro	Gln	Glu	Ile	His	Leu	Glu	Cys
80					85					90					95

Ser Thr Ser Arg Lys Ser Val Trp Leu Thr Pro Val Ser Thr Glu Asn
 100 105 110
 Glu Ile Lys Leu Asp Pro Ser Pro Phe Ile Ala Asp Phe Gln Thr Thr
 115 120 125
 Ala Glu Glu Leu Gly Leu Leu Ser Ser Ser Pro Asn Leu Leu
 130 135 140

<210> 261
 <211> 233
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 261
 Met Ala Thr Pro Pro Phe Arg Leu Ile Arg Lys Met Phe Ser Phe Lys
 -30 -25 -20
 Val Ser Arg Trp Met Gly Leu Ala Cys Phe Arg Ser Leu Ala Ala Ser
 -15 -10 -5
 Ser Pro Ser Ile Arg Gln Lys Lys Leu Met His Lys Leu Gln Glu Glu
 1 5 10 15
 Lys Ala Phe Arg Glu Glu Met Lys Ile Phe Arg Glu Lys Ile Glu Asp
 20 25 30
 Phe Arg Glu Glu Met Trp Thr Phe Arg Gly Lys Ile His Ala Phe Arg
 35 40 45
 Gly Gln Ile Leu Gly Phe Trp Glu Glu Glu Arg Pro Phe Trp Glu Glu
 50 55 60
 Glu Lys Thr Phe Trp Lys Glu Glu Lys Ser Phe Trp Glu Met Glu Lys
 65 70 75 80
 Ser Phe Arg Glu Glu Lys Thr Phe Trp Lys Lys Tyr Arg Thr Phe
 85 90 95
 Trp Lys Glu Asp Lys Ala Phe Trp Lys Glu Asp Asn Ala Leu Trp Glu
 100 105 110
 Arg Asp Arg Asn Leu Leu Gln Glu Asp Lys Ala Leu Trp Glu Glu Glu
 115 120 125
 Lys Ala Leu Trp Val Glu Glu Arg Ala Leu Leu Glu Gly Glu Lys Ala
 130 135 140
 Leu Trp Glu Asp Lys Thr Ser Leu Trp Glu Glu Asn Ala Leu Trp
 145 150 155 160
 Glu Glu Glu Arg Ala Phe Trp Met Glu Asn Asn Gly His Ile Ala Gly
 165 170 175
 Glu Gln Met Leu Glu Asp Gly Pro His Asn Ala Asn Arg Gly Gln Arg
 180 185 190
 Leu Leu Ala Phe Ser Arg Gly Arg Ala
 195 200

<210> 262
 <211> 67
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 262

Met Asp Ser Ser Thr Ala His Ser Pro Val Phe Leu Val Phe Pro Pro
 -20 -15 -10 -5
 Glu Ile Thr Ala Ser Glu Tyr Glu Ser Thr Glu Leu Ser Ala Thr Thr
 1 5 10
 Phe Ser Thr Gln Ser Pro Leu Gln Lys Leu Phe Ala Arg Lys Met Lys
 15 20 25
 Ile Leu Gly Asp Ile His Ser Gly Ala Leu Phe Cys Ser Leu Ile Leu
 30 35 40
 Glu Pro Ser
 45

<210> 263
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 263
 Met Cys Phe Leu Val Ser Phe Asn Leu Pro Ile His Ile Ser Leu Ser
 -25 -20 -15 -10
 His Leu Phe Leu Asp Leu Ser Arg Ser Leu Trp Phe Leu Ala Cys Pro
 -5 1 5
 Gly Leu Asn Leu Val Tyr Leu Ala Leu Asp Ser Phe Ser Asp Leu Arg
 10 15 20
 Pro Ser Leu Asn Leu Leu Phe Tyr Phe Val Pro Gly Phe Gly Val Ser
 25 30 35
 Lys Tyr Leu Thr Ser Ala Gln Pro Val Leu Gly Phe Leu Leu Leu Pro
 40 45 50 55
 Asp Ile Asp Asn Pro Ala Leu Leu Gly Thr Glu Arg Trp Ser
 60 65

<210> 264
 <211> 174
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<400> 264
 Met Phe Leu Thr Val Lys Leu Leu Leu Gly Gln Arg Cys Ser Leu Lys
 -15 -10 -5
 Val Ser Gly Gln Glu Ser Val Ala Thr Leu Lys Arg Leu Val Ser Arg
 1 5 10
 Arg Leu Lys Val Pro Glu Glu Gln Gln His Leu Leu Phe Arg Gly Gln
 15 20 25
 Leu Leu Glu Asp Asp Lys His Leu Ser Asp Tyr Cys Ile Gly Pro Asn
 30 35 40 45
 Ala Ser Ile Asn Val Ile Met Gln Pro Leu Glu Lys Met Ala Leu Lys
 50 55 60
 Glu Ala His Gln Pro Gln Thr Gln Pro Leu Trp His Gln Leu Gly Leu
 65 70 75
 Val Leu Ala Lys His Phe Glu Pro Gln Asp Ala Lys Ala Val Leu Gln
 80 85 90

Leu Leu Arg Gln Glu His Glu Glu Arg Leu Gln Lys Ile Ser Leu Glu
 95 100 105
 His Leu Glu Gln Leu Ala Glu Tyr Leu Leu Ala Glu Glu Pro His Val
 110 115 120 125
 Glu Pro Ala Gly Glu Arg Glu Leu Glu Ala Lys Ala Arg Pro Gln Ser
 130 135 140
 Ser Cys Asp Met Glu Glu Lys Glu Glu Ala Ala Ala Asp Gln
 145 150 155

<210> 265
 <211> 106
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 265
 Met Ala Leu Glu Val Leu Met Leu Leu Ala Val Leu Ile Trp Thr Gly
 -15 -10 -5
 Ala Glu Asn Leu His Val Lys Ile Ser Cys Ser Leu Asp Trp Leu Met
 1 5 10 15
 Val Ser Val Ile Pro Val Ala Glu Ser Arg Asn Leu Tyr Ile Phe Ala
 20 25 30
 Asp Glu Leu His Leu Gly Met Gly Cys Pro Ala Asn Arg Ile His Thr
 35 40 45
 Tyr Val Tyr Glu Phe Ile Tyr Leu Val Arg Asp Cys Gly Ile Arg Thr
 50 55 60
 Arg Val Arg Thr Val Ile Val Cys Lys Lys Tyr Cys Met Phe Cys Gln
 65 70 75
 Thr Phe Met Pro Ser Ile Lys Ile Val Phe
 80 85

<210> 266
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -18...-1

<400> 266
 Met Val Leu Cys Trp Leu Leu Leu Leu Val Met Ala Leu Pro Pro Gly
 -15 -10 -5
 Thr Thr Gly Val Lys Asp Cys Val Phe Cys Glu Leu Thr Asp Ser Met
 1 5 10
 Gln Cys Pro Gly Thr Tyr Met His Cys Gly Asp Asp Glu Asp Cys Phe
 15 20 25 30
 Thr Gly His Gly Val Ala Pro Gly Thr Gly Pro Val Ile Asn Lys Gly
 35 40 45
 Cys Leu Arg Ala Thr Ser Cys Gly Leu Glu Glu Pro Val Ser Tyr Arg
 50 55 60
 Gly Val Thr Tyr Ser Leu Thr Thr Asn Cys Cys Thr Gly Arg Leu Cys
 65 70 75
 Asn Arg Ala Pro Ser Ser Gln Thr Val Gly Ala Thr Thr Ser Leu Ala
 80 85 90

Figure 1 consists of 11 sub-graphs labeled (a) through (k). Each graph plots the percentage of total protein (Y-axis, 0 to 100) against time in hours (X-axis, 0 to 24). The graphs show the distribution of protein fractions (A, B, C, D, E, F, G, H, I, J, K) over time for different treatments (Control, 100 μg/ml, 200 μg/ml, 400 μg/ml, 800 μg/ml, 1600 μg/ml, 3200 μg/ml, 6400 μg/ml, 12800 μg/ml, 25600 μg/ml, 51200 μg/ml). The graphs show the distribution of protein fractions over time for each treatment group.

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<220>
<221> SIGNAL
<222> -16..-1
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<210> 268
<211> 76
<212> PRT
<213> Homo sapiens
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<400> 268

Met Cys Met Ser Leu Ser Met Lys Val Pro Cys Cys Leu Cys Ala Leu
 -25 -20 -15 -10
 Leu Ser Asn Phe Cys Pro Ser Thr Thr Val Lys Gly Asp Val Val Thr
 -5 1 5
 Ser Phe Phe Arg Ala Asp Tyr Asp Leu Ala Ser Arg Ser Ala Asp Gln
 10 15 20
 Ser Ser Gln Lys Val Lys Leu Arg Met Phe Thr Gly Arg Leu Pro Ile
 25 30 35
 Gly Pro Phe Ala Ser Val Gly Asn Ala Ala Glu Leu
 40 45 50

<210> 269
 <211> 199
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 269
 Met Glu Thr Phe Pro Leu Leu Leu Leu Ser Leu Gly Leu Val Leu Ala
 -15 -10 -5
 Glu Ala Ser Glu Ser Thr Met Lys Ile Ile Lys Glu Glu Phe Thr Asp
 1 5 10 15
 Glu Glu Met Gln Tyr Asp Met Ala Lys Ser Gly Gln Glu Lys Gln Thr
 20 25 30
 Ile Glu Ile Leu Met Asn Pro Ile Leu Leu Val Lys Asn Thr Ser Leu
 35 40 45
 Ser Met Ser Lys Asp Asp Met Ser Ser Thr Leu Leu Thr Phe Arg Ser
 50 55 60
 Leu His Tyr Asn Asp Pro Lys Gly Asn Ser Ser Gly Asn Asp Lys Glu
 65 70 75 80
 Cys Cys Asn Asp Met Thr Val Trp Arg Lys Val Ser Glu Ala Asn Gly
 85 90 95
 Ser Cys Lys Trp Ser Asn Asn Phe Ile Arg Ser Ser Thr Glu Val Met
 100 105 110
 Arg Arg Val His Arg Ala Pro Ser Cys Lys Phe Val Gln Asn Pro Gly
 115 120 125
 Ile Ser Cys Cys Glu Ser Leu Glu Leu Glu Asn Thr Val Cys Gln Phe
 130 135 140
 Thr Thr Gly Lys Gln Phe Pro Arg Cys Gln Tyr His Ser Val Thr Ser
 145 150 155 160
 Leu Glu Lys Ile Leu Thr Val Leu Thr Gly His Ser Leu Met Ser Trp
 165 170 175
 Leu Val Cys Gly Ser Lys Leu
 180

<210> 270
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -36...-1

<400> 270

Met Ala Ser Val Val Pro Val Lys Asp Lys Lys Leu Leu Glu Val Lys
 -35 -30 -25
 Leu Gly Glu Leu Pro Ser Trp Ile Leu Met Arg Asp Phe Ser Pro Ser
 -20 -15 -10 -5
 Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr Tyr Arg Tyr Tyr Asn Lys
 1 5 10
 Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser Gly Ile Thr Met Val Leu
 15 20 25
 Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe Ser Tyr Lys His Leu Lys
 30 35 40
 His Glu Arg Leu Arg Lys Tyr His
 45 50

<210> 271
 <211> 481
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 271
 Met Gly Ala Leu Ala Arg Ala Leu Pro Ser Ile Leu Leu Ala Leu Leu
 -25 -20 -15 -10
 Leu Thr Ser Thr Pro Glu Ala Leu Gly Ala Asn Pro Gly Leu Val Ala
 -5 1 5
 Arg Ile Thr Asp Lys Gly Leu Gln Tyr Ala Ala Gln Glu Gly Leu Leu
 10 15 20
 Ala Leu Gln Ser Glu Leu Leu Arg Ile Thr Leu Pro Asp Phe Thr Gly
 25 30 35
 Asp Leu Arg Ile Pro His Val Gly Arg Gly Arg Tyr Glu Phe His Ser
 40 45 50 55
 Leu Asn Ile His Ser Cys Glu Leu Leu His Ser Ala Leu Arg Pro Val
 60 65 70
 Pro Gly Gln Gly Leu Ser Leu Ser Ile Ser Asp Ser Ser Ile Arg Val
 75 80 85
 Gln Gly Arg Trp Lys Val Arg Lys Ser Phe Phe Lys Leu Gln Gly Ser
 90 95 100
 Phe Asp Val Ser Val Lys Gly Ile Ser Ile Ser Val Asn Leu Leu Leu
 105 110 115
 Gly Ser Asp Ser Ser Gly Arg Pro Thr Val Thr Ala Ser Ser Cys Ser
 120 125 130 135
 Ser Asp Ile Ala Asp Val Glu Val Asp Met Ser Gly Asp Leu Gly Trp
 140 145 150
 Leu Leu Asn Leu Phe His Asn Gln Ile Glu Ser Lys Phe Gln Lys Val
 155 160 165
 Leu Glu Ser Arg Ile Cys Glu Met Ile Gln Lys Ser Val Ser Ser Asp
 170 175 180
 Leu Gln Pro Tyr Leu Gln Thr Leu Thr Val Thr Thr Glu Ile Asp Ser
 185 190 195
 Phe Ala Asp Ile Asp Tyr Ser Leu Val Glu Ala Pro Arg Ala Thr Ala
 200 205 210 215
 Gln Met Leu Glu Val Met Phe Lys Gly Glu Ile Phe His Arg Asn His
 220 225 230
 Arg Ser Pro Val Thr Leu Leu Ala Ala Val Met Ser Leu Pro Glu Glu
 235 240 245
 His Asn Lys Met Val Tyr Phe Ala Ile Ser Asp Tyr Val Phe Asn Thr

<212> PRT
<213> Homo sapiens

<400> 273
Met Ala Lys Tyr Gln Gly Glu Val Gln Ser Leu Lys Leu Asp Asp Asp
1 5 10 15
Ser Val Ile Glu Gly Val Ser Asp Gln Val Leu Val Ala Val Val Val
20 25 30
Ser Phe Ala Leu Ile Ala Thr Leu Val Tyr Ala Leu Phe Arg Asn Val
35 40 45
His Gln Asn Ile His Pro Glu Asn Gln Glu Leu Val Arg Val Leu Arg
50 55 60
Glu Gln Leu Gln Thr Glu Gln Asp Ala Pro Ala Asp Ser Thr Ala Val
65 70 75 80
Leu His

<210> 274
<211> 373
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27...-1

<400> 274
Met Ala Thr Gln Ala His Ser Leu Ser Tyr Ala Gly Cys Asn Phe Leu
-25 -20 -15
Cys Gln Arg Leu Val Leu Ser Thr Leu Ser Gly Arg Pro Val Lys Ile
-10 -5 1 5
Arg Lys Ile Arg Ala Arg Asp Asp Asn Pro Gly Leu Arg Asp Phe Glu
10 15 20
Ala Ser Phe Ile Arg Leu Leu Asp Lys Ile Thr Asn Gly Ser Arg Ile
25 30 35
Glu Ile Asn Gln Thr Gly Thr Thr Leu Tyr Tyr Gln Pro Gly Leu Leu
40 45 50
Tyr Gly Gly Ser Val Glu His Asp Cys Ser Val Leu Arg Gly Ile Gly
55 60 65
Tyr Tyr Leu Glu Ser Leu Leu Cys Leu Ala Pro Phe Met Lys His Pro
70 75 80 85
Leu Lys Ile Val Leu Arg Gly Val Thr Asn Asp Gln Ile Asp Pro Ser
90 95 100
Val Asp Val Leu Lys Ala Thr Ala Leu Pro Leu Leu Lys Gln Phe Gly
105 110 115
Ile Asp Gly Glu Ser Phe Glu Leu Lys Ile Val Arg Arg Gly Met Pro
120 125 130
Pro Gly Gly Gly Glu Val Phe Ser Cys Pro Val Arg Lys Val
135 140 145
Leu Lys Pro Ile Gln Leu Thr Asp Pro Gly Lys Ile Lys Arg Ile Arg
150 155 160 165
Gly Met Ala Tyr Ser Val Arg Val Ser Pro Gln Met Ala Asn Arg Ile
170 175 180
Val Asp Ser Ala Arg Ser Ile Leu Asn Lys Phe Ile Pro Asp Ile Tyr
185 190 195
Ile Tyr Thr Asp His Ile Lys Gly Val Asn Ser Gly Lys Ser Pro Gly
200 205 210
Phe Gly Leu Ser Leu Val Ala Glu Thr Thr Ser Gly Thr Phe Leu Ser
215 220 225

Ala Glu Leu Ala Ser Asn Pro Gln Gly Gln Gly Ala Ala Val Leu Pro
 230 235 240 245
 Glu Asp Leu Gly Arg Asn Cys Ala Arg Leu Leu Glu Glu Ile Tyr
 250 255 260
 Arg Gly Gly Cys Val Asp Ser Thr Asn Gln Ser Leu Ala Leu Leu Leu
 265 270 275
 Met Thr Leu Gly Gln Gln Asp Val Ser Lys Val Leu Leu Gly Pro Leu
 280 285 290
 Ser Pro Tyr Thr Ile Glu Phe Leu Arg His Leu Lys Ser Phe Phe Gln
 295 300 305
 Ile Met Phe Lys Ile Glu Thr Lys Pro Cys Gly Glu Glu Leu Lys Gly
 310 315 320 325
 Gly Asp Lys Val Leu Met Thr Cys Val Gly Ile Gly Phe Ser Asn Leu
 330 335 340
 Ser Arg Thr Leu Lys
 345

<210> 275
 <211> 94
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 275
 Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
 -25 -20 -15 -10
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
 -5 1 5
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
 10 15 20
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
 25 30 35
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
 40 45 50 55
 Val Ser Cys Ser Val Ala Ala Pro Leu Phe Pro Phe Leu Gly
 60 65

<210> 276
 <211> 197
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 276
 Met Thr Val Leu Glu Ile Thr Leu Ala Val Ile Leu Thr Leu Leu Gly
 -20 -15 -10 -5
 Leu Ala Ile Leu Ala Ile Leu Leu Thr Arg Trp Ala Arg Arg Lys Gln
 1 5 10
 Ser Glu Met Tyr Ile Ser Arg Tyr Ser Ser Glu Gln Ser Ala Arg Leu
 15 20 25
 Leu Asp Tyr Glu Asp Gly Arg Gly Ser Arg His Ala Tyr Ser Thr Gln
 30 35 40

Ser Glu Arg Ser Lys Arg Asp Tyr Thr Pro Ser Thr Asn Ser Leu Ala
 45 50 55 60
 Leu Ser Arg Ser Ser Ile Ala Leu Pro Gln Gly Ser Met Ser Ser Ile
 65 70 75
 Lys Cys Leu Gln Thr Thr Glu Glu Pro Pro Ser Arg Thr Ala Gly Ala
 80 85 90
 Met Met Gln Phe Thr Ala Pro Ile Pro Gly Ala Thr Gly Pro Ile Lys
 95 100 105
 Leu Ser Gln Lys Thr Ile Val Gln Thr Leu Gly Pro Ile Val Gln Tyr
 110 115 120
 Pro Gly Ser Asn Gly Arg Ile Asn Ile Ser Gln Leu Thr Ser Glu Asp
 125 130 135 140
 Leu Thr Gly Ala Lys Gly Arg Val Thr Ser Gly Pro Gln Phe Pro Asn
 145 150 155
 Ser His His Val Pro Glu Asn Leu His Gly Tyr Met Asn Ser Leu Ser
 160 165 170
 Leu Phe Ser Pro Ala
 175

<210> 277
 <211> 344
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 277
 Met Asp Phe Leu Val Leu Phe Leu Phe Tyr Leu Ala Ser Val Leu Met
 -25 -20 -15
 Gly Leu Val Leu Ile Cys Val Cys Ser Lys Thr His Ser Leu Lys Gly
 -10 -5 1
 Leu Ala Arg Gly Gly Ala Gln Ile Phe Ser Cys Ile Ile Pro Glu Cys
 5 10 15
 Leu Gln Arg Ala Val His Gly Leu Leu His Tyr Leu Phe His Thr Arg
 20 25 30 35
 Asn His Thr Phe Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr
 40 45 50
 Thr Glu Tyr Thr Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu
 55 60 65
 Ser Leu His Tyr Leu Leu Leu Pro Tyr Leu Leu Leu Gly Val Asn Leu
 70 75 80
 Phe Phe Phe Thr Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys
 85 90 95
 Ala Asn Glu Leu Leu Phe Leu His Val Tyr Glu Phe Asp Glu Val Met
 100 105 110 115
 Phe Pro Lys Asn Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala
 120 125 130
 Arg Ser Lys His Cys Ser Val Cys Asn Trp Cys Val His Arg Phe Asp
 135 140 145
 His His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg
 150 155 160
 Tyr Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val
 165 170 175
 Ala Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp
 180 185 190 195
 Leu Tyr Gln Glu Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met

Ala	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Lys
		75					80					85			
Lys	Met	Asp	Glu	Leu	Tyr	Pro	Met	Glu	Pro	Glu	Glu	Glu	Ala	Asn	Gly
	90					95					100				
Ser	Glu	Ile	Leu	Ala	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Lys	Lys	Asp	Ala
105					110					115					120
Glu	Glu	Asp	Asp	Ser	Leu	Ala	Asn	Ser	Ser	Asp	Leu	Leu	Lys	Glu	Leu
				125					130					135	
Leu	Glu	Thr	Gly	Asp	Asn	Arg	Glu	Arg	Ser	His	His	Gln	Asp	Gly	Ser
			140					145					150		
Asp	Asn	Glu	Glu	Glu	Val	Ser	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Arg	Gly
		155					160					165			
Leu	Lys	Arg	Ser	Pro	Gln	Leu	Glu	Asp	Glu	Ala	Lys	Glu	Leu	Gln	Lys
	170					175					180				
Arg	Tyr	Gly	Gly	Phe	Met	Arg	Arg	Val	Gly	Arg	Pro	Glu	Trp	Trp	Met
185					190					195					200
Asp	Tyr	Gln	Lys	Arg	Tyr	Gly	Gly	Phe	Leu	Lys	Arg	Phe	Ala	Glu	Ala
				205				210						215	
Leu	Pro	Ser	Asp	Glu	Glu	Gly	Glu	Ser	Tyr	Ser	Lys	Glu	Val	Pro	Glu
			220				225						230		
Met	Glu	Lys	Arg	Tyr	Gly	Gly	Phe	Met	Arg	Phe					
		235					240								

<210> 280
 <211> 362
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40...-1

<400> 280

Met	Pro	Phe	Ala	Tyr	Phe	Phe	Thr	Glu	Ser	Glu	Gly	Phe	Ala	Gly	Ser
-40					-35					-30					-25
Arg	Lys	Gly	Val	Leu	Gly	Arg	Val	Tyr	Glu	Thr	Val	Val	Met	Leu	Met
			-20						-15						-10
Leu	Leu	Thr	Leu	Leu	Val	Leu	Gly	Met	Val	Trp	Val	Ala	Ser	Ala	Ile
			-5					1				5			
Val	Asp	Lys	Asn	Lys	Ala	Asn	Arg	Glu	Ser	Leu	Tyr	Asp	Phe	Trp	Glu
	10				15						20				
Tyr	Tyr	Leu	Pro	Tyr	Leu	Tyr	Ser	Cys	Ile	Ser	Phe	Leu	Gly	Val	Leu
25					30					35					40
Leu	Leu	Leu	Val	Cys	Thr	Pro	Leu	Gly	Leu	Ala	Arg	Met	Phe	Ser	Val
			45					50						55	
Thr	Gly	Lys	Leu	Leu	Val	Lys	Pro	Arg	Leu	Leu	Glu	Asp	Leu	Glu	Glu
			60					65					70		
Gln	Leu	Tyr	Cys	Ser	Ala	Phe	Glu	Glu	Ala	Ala	Leu	Thr	Arg	Arg	Ile
		75					80					85			
Cys	Asn	Pro	Thr	Ser	Cys	Trp	Leu	Pro	Leu	Asp	Met	Glu	Leu	Leu	His
	90					95					100				
Arg	Gln	Val	Leu	Ala	Leu	Gln	Thr	Gln	Arg	Val	Leu	Leu	Glu	Lys	Arg
105					110					115					120
Arg	Lys	Ala	Ser	Ala	Trp	Gln	Arg	Asn	Leu	Gly	Tyr	Pro	Leu	Ala	Met
			125						130					135	
Leu	Cys	Leu	Leu	Val	Leu	Thr	Gly	Leu	Ser	Val	Leu	Ile	Val	Ala	Ile
			140					145					150		

His Ile Leu Glu Leu Leu Ile Asp Glu Ala Ala Met Pro Arg Gly Met
155 160 165
Gln Gly Thr Ser Leu Gly Gln Val Ser Phe Ser Lys Leu Gly Ser Phe
170 175 180
Gly Ala Val Ile Gln Val Val Leu Ile Phe Tyr Leu Met Val Ser Ser
185 190 195 200
Val Val Gly Phe Tyr Ser Ser Pro Leu Phe Arg Ser Leu Arg Pro Arg
205 210 215
Trp His Asp Thr Ala Met Thr Gln Ile Ile Gly Asn Cys Val Cys Leu
220 225 230
Leu Val Leu Ser Ser Ala Leu Pro Val Phe Ser Arg Thr Leu Gly Leu
235 240 245
Thr Arg Phe Asp Leu Leu Gly Asp Phe Gly Arg Phe Asn Trp Leu Gly
250 255 260
Asn Phe Tyr Ile Val Phe Leu Tyr Asn Ala Ala Phe Ala Gly Leu Thr
265 270 275 280
Thr Leu Tyr Leu Val Lys Thr Phe Thr Ala Val Arg Ala Glu Leu
285 290 295
Ile Arg Ala Phe Gly Leu Asp Arg Leu Pro Leu Pro Val Ser Gly Phe
300 305 310
Pro Gln Ala Ser Arg Lys Thr Gln His Gln
315 320

<210> 281
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21...-1

<400> 281
Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu Thr
-20 -15 -10
Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp Gln Gln
-5 1 5 10
Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln Ile Arg Lys
15 20 25
Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile Leu Thr Glu Gln
30 35 40
Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala Lys Gly Ser Gln Lys
45 50 55
Ser
60

<210> 282
<211> 541
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28...-1

<400> 282
Met Gly Ser Gln Glu Val Leu Gly His Ala Ala Arg Leu Ala Ser Ser
-25 -20 -15

09876997-060804

Gly	Leu	Leu	Leu	Gln	Val	Leu	Phe	Arg	Leu	Ile	Thr	Phe	Val	Leu	Asn
	-10						-5					1			
Ala	Phe	Ile	Leu	Arg	Phe	Leu	Ser	Lys	Glu	Ile	Val	Gly	Val	Val	Asn
5					10					15					20
Val	Arg	Leu	Thr	Leu	Leu	Tyr	Ser	Thr	Thr	Leu	Phe	Leu	Ala	Arg	Glu
				25					30					35	
Ala	Phe	Arg	Arg	Ala	Cys	Leu	Ser	Gly	Gly	Thr	Gln	Arg	Asp	Trp	Ser
			40					45					50		
Gln	Thr	Leu	Asn	Leu	Leu	Trp	Leu	Thr	Val	Pro	Leu	Gly	Val	Phe	Trp
	55						60					65			
Ser	Leu	Phe	Leu	Gly	Trp	Ile	Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp
	70					75					80				
Pro	Asn	Val	Val	Pro	His	Tyr	Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu
85					90				95						100
Ser	Ala	Val	Val	Glu	Leu	Leu	Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln
				105					110						115
Ala	His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val
			120					125					130		
Ile	Leu	Lys	Ser	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His
	135						140					145			
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val
	150					155					160				
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro
165					170					175					180
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu
				185					190					195	
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala
			200					205					210		
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu
	215						220					225			
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe
	230					235					240				
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val
245					250				255						260
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe
				265					270					275	
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu
			280					285					290		
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala
	295						300					305			
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln
	310					315					320				
Leu	Ala	Leu	Asp	Ile	Asn	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly
325					330				335						340
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile
				345					350					355	
Asn	Gly	Val	Thr	Glu	Cys	Phe	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu
			360					365					370		
Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu
	375						380					385			
Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile
	390					395					400				
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys
405					410				415						420
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly
				425					430					435	
Leu	His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly
				440				445					450		

Val Thr Ala Val Ser Glu Val Phe Leu Cys Cys Glu Gln Gly Trp Pro
 455 460 465
 Ala Arg Leu Ala His Ile Ala Val Gly Ala Phe Cys Leu Gly Ala Thr
 470 475 480
 Leu Gly Thr Ala Phe Leu Thr Glu Thr Lys Leu Ile His Phe Leu Arg
 485 490 495 500
 Thr Gln Leu Gly Val Pro Arg Arg Thr Asp Lys Met Thr
 505 510

<210> 283
 <211> 468
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 283
 Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser
 -20 -15 -10
 Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Trp Arg Ala
 -5 1 5 10
 Val Asp Val Val Leu Asp Cys Phe Leu Val Lys Asp Gly Ala His Arg
 15 20 25
 Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu
 30 35 40
 Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp
 45 50 55
 Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Ile Ile Phe Glu
 60 65 70 75
 Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His
 80 85 90
 Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe
 95 100 105
 Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala
 110 115 120
 Asn Val Gln Val Ser Gly Gly Gly Pro Ser Ile Ser Leu Val Met Lys
 125 130 135
 Thr Pro Arg Val Ala Lys Asn Glu Val Leu Trp His Pro Thr Leu Asn
 140 145 150 155
 Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln
 160 165 170
 Val Met Thr Gln Thr Gln Ser Leu Ser Phe Leu Leu Gly Ser Ser Ala
 175 180 185
 Ser Leu Asp Cys Gly Phe Ser Met Ala Pro Gly Leu Asp Leu Ile Ser
 190 195 200
 Val Glu Trp Arg Leu Gln His Lys Gly Arg Gly Gln Leu Val Tyr Ser
 205 210 215
 Trp Thr Ala Gly Gln Gly Gln Ala Val Arg Lys Gly Ala Thr Leu Glu
 220 225 230 235
 Pro Ala Gln Leu Gly Met Ala Arg Asp Ala Ser Leu Thr Leu Pro Gly
 240 245 250
 Leu Thr Ile Gln Asp Glu Gly Thr Tyr Ile Cys Gln Ile Thr Thr Ser
 255 260 265
 Leu Tyr Arg Ala Gln Gln Ile Ile Gln Leu Asn Ile Gln Ala Ser Pro
 270 275 280
 Lys Val Arg Leu Ser Leu Ala Asn Glu Ala Leu Leu Pro Thr Leu Ile

285		290		295
Cys Asp Ile Ala Gly Tyr Tyr Pro Leu Asp Val Val Val Thr Trp Thr				
300		305		310
Arg Glu Glu Leu Gly Gly Ser Pro Ala Gln Val Ser Gly Ala Ser Phe				315
	320		325	330
Ser Ser Leu Arg Gln Ser Val Ala Gly Thr Tyr Ser Ile Ser Ser Ser				
	335		340	345
Leu Thr Ala Glu Pro Gly Ser Ala Gly Ala Thr Tyr Thr Cys Gln Val				
	350		355	360
Thr His Ile Ser Leu Glu Glu Pro Leu Gly Ala Ser Thr Gln Val Val				
	365		370	375
Pro Pro Glu Arg Arg Thr Ala Leu Gly Val Ile Phe Ala Ser Ser Leu				
380		385		390
Phe Leu Leu Ala Leu Met Phe Leu Gly Leu Gln Arg Arg Gln Ala Pro				395
	400		405	410
Thr Gly Leu Gly Leu Leu Gln Ala Glu Arg Trp Glu Thr Thr Ser Cys				
	415		420	425
Ala Asp Thr Gln Ser Ser His Leu His Glu Asp Arg Thr Ala Arg Val				
	430		435	440
Ser Gln Pro Ser				
445				

<210> 284
 <211> 406
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -31...-1

<400> 284
Met Val Arg Ile Gln Arg Arg Lys Leu Leu Ala Ser Cys Leu Cys Val
-30 -25 -20
Thr Ala Thr Val Phe Leu Leu Val Thr Leu Gln Ala Leu Asp Thr Val
-15 -10 -5 1
Glu Asn Leu Met Lys Val Thr Gly Pro Pro Gln Gly Val Thr Asp Ser
5 10 15
Met Gln Cys Phe Asn Asp Gln Trp Pro Leu Ser Asn Thr Arg Ser Ser
20 25 30
Glu His Ile Lys Glu Val Met Val Glu Leu Gly Lys Phe Glu Arg Lys
35 40 45
Glu Phe Lys Ser Ser Ser Leu Gln Asp Gly His Thr Lys Met Glu Glu
50 55 60 65
Ala Pro Thr His Leu Asn Ser Phe Leu Lys Lys Glu Gly Leu Thr Phe
70 75 80
Asn Arg Lys Arg Lys Trp Glu Leu Asp Ser Tyr Pro Ile Met Leu Trp
85 90 95
Trp Ser Pro Leu Thr Gly Glu Thr Gly Arg Leu Gly Gln Cys Gly Ala
100 105 110
Asp Ala Cys Phe Phe Thr Ile Asn Arg Thr Tyr Leu His His His Met
115 120 125
Thr Lys Ala Phe Leu Phe Tyr Gly Thr Asp Phe Asn Ile Asp Ser Leu
130 135 140 145
Pro Leu Pro Arg Lys Ala His His Asp Trp Ala Val Phe His Glu Glu
150 155 160
Ser Pro Lys Asn Asn Tyr Lys Leu Phe His Lys Pro Val Ile Thr Leu
165 170 175

Phe Asn Tyr Thr Ala Thr Phe Ser Arg His Ser His Leu Pro Leu Thr
 180 185 190
 Thr Gln Tyr Leu Glu Ser Ile Glu Val Leu Lys Ser Leu Arg Tyr Leu
 195 200 205
 Val Pro Leu Gln Ser Lys Asn Lys Leu Arg Lys Arg Leu Ala Pro Leu
 210 215 220 225
 Val Tyr Val Gln Ser Tyr Cys Asp Pro Pro Ser Asp Arg Asp Ser Tyr
 230 235 240
 Val Arg Glu Leu Met Thr Tyr Ile Glu Val Asp Ser Tyr Gly Glu Cys
 245 250 255
 Leu Arg Asn Lys Asp Leu Pro Gln Gln Leu Lys Asn Pro Ala Ser Met
 260 265 270
 Asp Ala Asp Gly Phe Tyr Arg Ile Ile Ala Gln Tyr Lys Phe Ile Leu
 275 280 285
 Ala Phe Glu Asn Ala Val Cys Asp Asp Tyr Ile Thr Glu Lys Phe Trp
 290 295 300 305
 Arg Pro Leu Lys Leu Gly Val Val Pro Val Tyr Tyr Gly Ser Pro Ser
 310 315 320
 Ile Thr Asp Trp Leu Pro Ser Asn Lys Ser Ala Ile Leu Val Ser Glu
 325 330 335
 Phe Ser His Pro Arg Glu Leu Ala Ser Tyr Ile Arg Arg Leu Asp Ser
 340 345 350
 Asp Asp Arg Leu Tyr Glu Ala Tyr Val Glu Trp Lys Leu Lys Gly Arg
 355 360 365
 Ser Leu Thr Ser Asp Phe
 370 375

<210> 285

<211> 305

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 285

Met Gly Ile Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly
 -25 -20 -15
 Leu Val Thr Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg
 -10 -5 1 5
 Ser Arg Arg Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu
 10 15 20
 Leu Arg Leu Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe
 25 30 35
 Arg Phe Ala Leu Pro Thr Ala His His Thr Leu Gly Leu Pro Val Gly
 40 45 50
 Lys His Ile Tyr Leu Ser Thr Arg Ile Asp Gly Ser Leu Val Ile Arg
 55 60 65 70
 Pro Tyr Thr Pro Val Thr Ser Asp Glu Asp Gln Gly Tyr Val Asp Leu
 75 80 85
 Val Ile Lys Val Tyr Leu Lys Gly Val His Pro Lys Phe Pro Glu Gly
 90 95 100
 Gly Lys Met Ser Gln Tyr Leu Asp Ser Leu Lys Val Gly Asp Val Val
 105 110 115
 Glu Phe Arg Gly Pro Ser Gly Leu Leu Thr Tyr Thr Gly Lys Gly His
 120 125 130
 Phe Asn Ile Gln Pro Asn Lys Lys Ser Pro Pro Glu Pro Arg Val Ala

135 140 145 150
 Lys Lys Leu Gly Met Ile Ala Gly Gly Thr Gly Ile Thr Pro Met Leu
 155 160 165
 Gln Leu Ile Arg Ala Ile Leu Lys Val Pro Glu Asp Pro Thr Gln Cys
 170 175 180
 Phe Leu Leu Phe Ala Asn Gln Thr Glu Lys Asp Ile Ile Leu Arg Glu
 185 190 195
 Asp Leu Glu Glu Leu Gln Ala Arg Tyr Pro Asn Arg Phe Lys Leu Trp
 200 205 210
 Phe Thr Leu Asp His Pro Pro Lys Asp Trp Ala Tyr Ser Lys Gly Phe
 215 220 225 230
 Val Thr Ala Asp Met Ile Arg Glu His Leu Pro Ala Pro Gly Asp Asp
 235 240 245
 Val Leu Val Leu Leu Cys Gly Pro Pro Pro Met Val Gln Leu Ala Cys
 250 255 260
 His Pro Asn Leu Asp Lys Leu Gly Tyr Ser Gln Lys Met Arg Phe Thr
 265 270 275

Tyr

<210> 286
 <211> 442
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<220>
 <221> UNSURE
 <222> 132
 <223> Xaa = Pro,Arg

<400> 286
 Met Gly Thr Gln Glu Gly Trp Cys Leu Leu Leu Cys Leu Ala Leu Ser
 -20 -15 -10
 Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Leu Arg Ala
 -5 1 5 10
 Val Asp Val Val Leu Asp Cys Phe Leu Ala Lys Asp Gly Ala His Arg
 15 20 25
 Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg Ala Ser Leu Val Leu
 30 35 40
 Lys Gln Val Pro Val Leu Asp Asp Gly Ser Leu Glu Asp Phe Thr Asp
 45 50 55
 Phe Gln Gly Gly Thr Leu Ala Gln Asp Asp Pro Pro Ile Ile Phe Glu
 60 65 70 75
 Ala Ser Val Asp Leu Val Gln Ile Pro Gln Ala Glu Ala Leu Leu His
 80 85 90
 Ala Asp Cys Ser Gly Lys Glu Val Thr Cys Glu Ile Ser Arg Tyr Phe
 95 100 105
 Leu Gln Met Thr Glu Thr Thr Val Lys Thr Ala Ala Trp Phe Met Ala
 110 115 120
 Asn Met Gln Val Ser Gly Gly Gly Xaa Ser Ile Ser Leu Val Met Lys
 125 130 135
 Thr Pro Arg Val Thr Lys Asn Glu Ala Leu Trp His Pro Thr Leu Asn
 140 145 150 155
 Leu Pro Leu Ser Pro Gln Gly Thr Val Arg Thr Ala Val Glu Phe Gln
 160 165 170

Val	Met	Thr	Gln	Thr	Gln	Ser	Leu	Ser	Phe	Leu	Leu	Gly	Ser	Ser	Ala	
			175					180					185			
Ser	Leu	Asp	Cys	Gly	Phe	Ser	Met	Ala	Pro	Gly	Leu	Asp	Leu	Ile	Ser	
		190					195					200				
Val	Glu	Trp	Arg	Leu	Gln	His	Lys	Gly	Arg	Gly	Gln	Leu	Val	Tyr	Ser	
	205					210					215					
Trp	Thr	Ala	Gly	Gln	Gly	Gln	Ala	Val	Arg	Lys	Gly	Ala	Thr	Leu	Glu	
220					225					230					235	
Pro	Ala	Gln	Leu	Gly	Met	Ala	Arg	Asp	Ala	Ser	Leu	Thr	Leu	Pro	Gly	
				240				245						250		
Leu	Thr	Ile	Gln	Asp	Glu	Gly	Thr	Tyr	Ile	Cys	Gln	Ile	Thr	Thr	Ser	
			255					260					265			
Leu	Tyr	Arg	Ala	Gln	Gln	Ile	Ile	Gln	Leu	Asn	Ile	Gln	Ala	Ser	Pro	
		270					275					280				
Lys	Val	Arg	Leu	Ser	Leu	Ala	Asn	Glu	Ala	Leu	Leu	Pro	Thr	Leu	Ile	
	285					290					295					
Cys	Asp	Ile	Ala	Gly	Tyr	Tyr	Pro	Leu	Asp	Val	Val	Val	Thr	Trp	Thr	
300					305					310					315	
Arg	Glu	Glu	Leu	Gly	Gly	Ser	Pro	Ala	Gln	Val	Ser	Gly	Ala	Ser	Phe	
				320					325					330		
Ser	Ser	Leu	Arg	Gln	Ser	Val	Ala	Gly	Thr	Tyr	Ser	Ile	Ser	Ser	Ser	
			335					340					345			
Leu	Thr	Ala	Glu	Pro	Gly	Ser	Ala	Gly	Ala	Thr	Tyr	Thr	Cys	Gln	Val	
		350					355					360				
Thr	His	Ile	Ser	Leu	Glu	Glu	Pro	Leu	Gly	Ala	Ser	Thr	Gln	Val	Val	
	365					370					375					
Pro	Pro	Glu	Arg	Arg	Thr	Ala	Leu	Gly	Val	Ile	Phe	Ala	Ser	Ser	Leu	
380					385					390					395	
Phe	Leu	Leu	Ala	Leu	Met	Phe	Leu	Gly	Leu	Gln	Arg	Arg	Gln	Ala	Pro	
				400					405					410		
Thr	Gly	Leu	Gly	Leu	Leu	Gln	Ala	Glu	Arg							
			415					420								

<210> 287

<211> 286

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -48...-1

<400> 287

Met	Asn	Pro	Ala	Ser	Asp	Gly	Gly	Thr	Ser	Glu	Ser	Ile	Phe	Asp	Leu	
			-45					-40					-35			
Asp	Tyr	Ala	Ser	Trp	Gly	Ile	Arg	Ser	Thr	Leu	Met	Val	Ala	Gly	Phe	
		-30					-25					-20				
Val	Phe	Tyr	Leu	Gly	Val	Phe	Val	Val	Cys	His	Gln	Leu	Ser	Ser	Ser	
	-15				-10						-5					
Leu	Asn	Ala	Thr	Tyr	Arg	Ser	Leu	Val	Ala	Arg	Glu	Lys	Val	Phe	Trp	
1			5					10					15			
Asp	Leu	Ala	Ala	Thr	Arg	Ala	Val	Phe	Gly	Val	Gln	Ser	Thr	Ala	Ala	
		20						25					30			
Gly	Leu	Trp	Ala	Leu	Leu	Gly	Asp	Pro	Val	Leu	His	Ala	Asp	Lys	Ala	
		35				40					45					
Arg	Gly	Gln	Gln	Asn	Trp	Cys	Trp	Phe	His	Ile	Thr	Thr	Ala	Thr	Gly	
	50					55				60						
Phe	Phe	Cys	Phe	Glu	Asn	Val	Ala	Val	His	Leu	Ser	Asn	Leu	Ile	Phe	

65					70					75					80
Arg	Thr	Phe	Asp	Leu	Phe	Leu	Val	Ile	His	His	Leu	Phe	Ala	Phe	Leu
				85					90					95	
Gly	Phe	Leu	Gly	Cys	Leu	Val	Asn	Leu	Gln	Ala	Gly	His	Tyr	Leu	Ala
			100					105					110		
Met	Thr	Thr	Leu	Leu	Leu	Glu	Met	Ser	Thr	Pro	Phe	Thr	Cys	Val	Ser
		115					120					125			
Trp	Met	Leu	Leu	Lys	Ala	Gly	Trp	Ser	Glu	Ser	Leu	Phe	Trp	Lys	Leu
	130					135					140				
Asn	Gln	Trp	Leu	Met	Ile	His	Met	Phe	His	Cys	Arg	Met	Val	Leu	Thr
145					150					155				160	
Tyr	His	Met	Trp	Trp	Val	Cys	Phe	Trp	His	Trp	Asp	Gly	Leu	Val	Ser
			165					170					175		
Ser	Leu	Tyr	Leu	Pro	His	Leu	Thr	Leu	Phe	Leu	Val	Gly	Leu	Ala	Leu
			180					185					190		
Leu	Thr	Leu	Ile	Ile	Asn	Pro	Tyr	Trp	Thr	His	Lys	Lys	Thr	Gln	Gln
		195					200					205			
Leu	Leu	Asn	Pro	Val	Asp	Trp	Asn	Phe	Ala	Gln	Pro	Glu	Ala	Lys	Ser
	210					215					220				
Arg	Pro	Glu	Gly	Asn	Gly	Gln	Leu	Leu	Arg	Lys	Lys	Arg	Pro		
225					230					235					

<210> 288
 <211> 398
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 288

Met	Val	Asn	Asp	Pro	Pro	Val	Pro	Ala	Leu	Leu	Trp	Ala	Gln	Glu	Val
	-20					-15					-10				
Gly	Gln	Val	Leu	Ala	Gly	Arg	Ala	Arg	Arg	Leu	Leu	Leu	Gln	Phe	Gly
-5					1				5				10		
Val	Leu	Phe	Cys	Thr	Ile	Leu	Leu	Leu	Trp	Val	Ser	Val	Phe	Leu	
			15					20				25			
Tyr	Gly	Ser	Phe	Tyr	Tyr	Ser	Tyr	Met	Pro	Thr	Val	Ser	His	Leu	Ser
		30					35					40			
Pro	Val	His	Phe	Tyr	Tyr	Arg	Thr	Asp	Cys	Asp	Ser	Ser	Thr	Thr	Ser
	45					50				55					
Leu	Cys	Ser	Phe	Pro	Val	Ala	Asn	Val	Ser	Leu	Thr	Lys	Gly	Gly	Arg
60					65				70					75	
Asp	Arg	Val	Leu	Met	Tyr	Gly	Gln	Pro	Tyr	Arg	Val	Thr	Leu	Glu	Leu
				80					85				90		
Glu	Leu	Pro	Glu	Ser	Pro	Val	Asn	Gln	Asp	Leu	Gly	Met	Phe	Leu	Val
			95				100						105		
Thr	Ile	Ser	Cys	Tyr	Thr	Arg	Gly	Gly	Arg	Ile	Ile	Ser	Thr	Ser	Ser
	110						115					120			
Arg	Ser	Val	Met	Leu	His	Tyr	Arg	Ser	Asp	Leu	Leu	Gln	Met	Leu	Asp
	125					130					135				
Thr	Leu	Val	Phe	Ser	Ser	Leu	Leu	Leu	Phe	Gly	Phe	Ala	Glu	Gln	Lys
140					145				150						155
Gln	Leu	Leu	Glu	Val	Glu	Leu	Tyr	Ala	Asp	Tyr	Arg	Glu	Asn	Ser	Tyr
			160					165					170		
Val	Pro	Thr	Thr	Gly	Ala	Ile	Ile	Glu	Ile	His	Ser	Lys	Arg	Ile	Gln
			175					180					185		

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 290

Met	Ala	Val	Gly	Gly	Gly	Leu	Ala	Val	Ala	Gly	Leu	Pro	Ala	Leu	Gly
-20					-15					-10					-5
Phe	Thr	Gly	Ala	Gly	Ile	Ala	Ala	Asn	Ser	Val	Ala	Ala	Ser	Leu	Met
				1				5					10		
Ser	Trp	Ser	Ala	Ile	Leu	Asn	Gly	Gly	Gly	Val	Pro	Ala	Gly	Gly	Leu
		15					20					25			
Val	Ala	Thr	Leu	Gln	Ser	Leu	Gly	Ala	Gly	Gly	Ser	Ser	Val	Val	Ile
	30					35					40				
Gly	Asn	Ile	Gly	Ala	Leu	Met	Gly	Tyr	Ala	Thr	His	Lys	Tyr	Leu	Asp
45					50					55					60
Ser	Glu	Glu	Asp	Glu	Glu										
					65										

<210> 291
 <211> 207
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 291

Met	Ala	Pro	Phe	Glu	Pro	Leu	Ala	Ser	Gly	Ile	Leu	Leu	Leu	Leu	Trp
		-20						-15					-10		
Leu	Ile	Ala	Pro	Ser	Arg	Ala	Cys	Thr	Cys	Val	Pro	Pro	His	Pro	Gln
		-5					1				5				
Thr	Ala	Phe	Cys	Asn	Ser	Asp	Leu	Val	Ile	Arg	Ala	Lys	Phe	Val	Gly
10					15					20				25	
Thr	Pro	Glu	Val	Asn	Gln	Thr	Thr	Leu	Tyr	Gln	Arg	Tyr	Glu	Ile	Lys
				30				35						40	
Met	Thr	Lys	Met	Tyr	Lys	Gly	Phe	Gln	Ala	Leu	Gly	Asp	Ala	Ala	Asp
			45				50						55		
Ile	Arg	Phe	Val	Tyr	Thr	Pro	Ala	Met	Glu	Ser	Val	Cys	Gly	Tyr	Phe
		60					65					70			
His	Arg	Ser	His	Asn	Arg	Ser	Glu	Glu	Phe	Leu	Ile	Ala	Gly	Lys	Leu
		75				80					85				
Gln	Asp	Gly	Leu	Leu	His	Ile	Thr	Thr	Cys	Ser	Phe	Val	Ala	Pro	Trp
90					95					100					105
Asn	Ser	Leu	Ser	Leu	Ala	Gln	Arg	Arg	Gly	Phe	Thr	Lys	Thr	Tyr	Thr
				110					115					120	
Val	Gly	Cys	Glu	Glu	Cys	Thr	Val	Phe	Pro	Cys	Leu	Ser	Phe	Pro	Cys
			125					130					135		
Lys	Leu	Gln	Ser	Gly	Thr	His	Cys	Leu	Trp	Thr	Asp	Gln	Leu	Leu	Gln
		140					145					150			
Gly	Ser	Glu	Lys	Gly	Phe	Gln	Ser	Arg	His	Leu	Ala	Cys	Leu	Pro	Arg
		155				160					165				
Glu	Pro	Gly	Leu	Cys	Thr	Trp	Gln	Ser	Leu	Arg	Ser	Gln	Ile	Ala	
170						175					180				

<210> 292
 <211> 111

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24...-1

<400> 292
Met Lys Tyr Asp Cys Pro Phe Ser Gly Thr Ser Phe Val Val Phe Ser
 -20 -15 -10
Leu Phe Leu Ile Cys Ala Met Ala Gly Asp Val Val Tyr Ala Asp Ile
 -5 1 5
Lys Thr Val Arg Thr Ser Pro Leu Glu Leu Ala Phe Pro Leu Gln Arg
10 15 20
Ser Val Ser Phe Asn Phe Ser Thr Val His Lys Ser Cys Pro Ala Lys
25 30 35 40
Asp Trp Lys Val His Lys Gly Lys Cys Tyr Trp Ile Ala Glu Thr Lys
 45 50 55
Lys Ser Trp Asn Lys Ser Gln Asn Asp Cys Ala Ile Asn Asn Ser Tyr
60 65 70
Leu Met Val Ile Gln Asp Ile Thr Ala Met Val Arg Phe Asn Ile
75 80 85

<210> 293
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<400> 293
Met Glu Ala Val Val Phe Val Phe Ser Leu Leu Asp Cys Cys Ala Leu
-15 -10 -5 1
Ile Phe Leu Ser Val Tyr Phe Ile Ile Thr Leu Ser Asp Leu Glu Cys
5 10 15
Asp Tyr Ile Asn Ala Arg Ser Cys Cys Ser Lys Leu Asn Lys Trp Val
20 25 30
Ile Pro Glu Leu Ile Gly His Thr Ile Val Thr Val Leu Leu Leu Met
35 40 45
Ser Leu His Trp Phe Ile Phe Leu Leu Asn Leu Pro Val Ala Thr Trp
50 55 60 65
Asn Ile Tyr Arg Tyr Ile Met Val Pro Ser Gly Asn Met Gly Val Phe
70 75 80
Asp Pro Thr Glu Ile His Asn Arg Gly Gln Leu Lys Ser His Met Lys
85 90 95
Glu Ala Met Ile Lys Leu Gly Phe His Leu Leu Cys Phe Phe Met Tyr
100 105 110
Leu Tyr Ser Met Ile Leu Ala Leu Ile Asn Asp
115 120

<210> 294
<211> 160
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -27...-1

<400> 294

Met	Gln	Arg	Val	Ser	Gly	Leu	Leu	Ser	Trp	Thr	Leu	Ser	Arg	Val	Leu
	-25						-20					-15			
Trp	Leu	Ser	Gly	Leu	Ser	Glu	Pro	Gly	Ala	Ala	Arg	Gln	Pro	Arg	Ile
	-10					-5					1				5
Met	Glu	Glu	Lys	Ala	Leu	Glu	Val	Tyr	Asp	Leu	Ile	Arg	Thr	Ile	Arg
			10						15					20	
Asp	Pro	Glu	Lys	Pro	Asn	Thr	Leu	Glu	Glu	Leu	Glu	Val	Val	Ser	Glu
			25					30					35		
Ser	Cys	Val	Glu	Val	Gln	Glu	Ile	Asn	Glu	Glu	Glu	Tyr	Leu	Val	Ile
		40					45					50			
Ile	Arg	Phe	Thr	Pro	Thr	Val	Pro	His	Cys	Ser	Leu	Ala	Thr	Leu	Ile
	55					60					65				
Gly	Leu	Cys	Leu	Arg	Val	Lys	Leu	Gln	Arg	Cys	Leu	Pro	Phe	Lys	His
70					75					80					85
Lys	Leu	Glu	Ile	Tyr	Ile	Ser	Glu	Gly	Thr	His	Ser	Thr	Glu	Glu	Asp
				90					95					100	
Ile	Asn	Lys	Gln	Ile	Asn	Asp	Lys	Glu	Arg	Val	Ala	Ala	Ala	Met	Glu
			105					110					115		
Asn	Pro	Asn	Leu	Arg	Glu	Ile	Val	Glu	Gln	Cys	Val	Leu	Glu	Pro	Asp
		120					125						130		

<210> 295
<211> 181
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16...-1

<400> 295

Met	Pro	Pro	Phe	Leu	Leu	Leu	Thr	Cys	Leu	Phe	Ile	Thr	Gly	Thr	Ser
	-15					-10					-5				
Val	Ser	Pro	Val	Ala	Leu	Asp	Pro	Cys	Ser	Ala	Tyr	Ile	Ser	Leu	Asn
1			5					10						15	
Glu	Pro	Trp	Arg	Asn	Thr	Asp	His	Gln	Leu	Asp	Glu	Ser	Gln	Gly	Pro
			20					25					30		
Pro	Leu	Cys	Asp	Asn	His	Val	Asn	Gly	Glu	Trp	Tyr	His	Phe	Thr	Gly
		35					40					45			
Met	Ala	Gly	Asp	Ala	Met	Pro	Thr	Phe	Cys	Ile	Pro	Glu	Asn	His	Cys
	50					55					60				
Gly	Thr	His	Ala	Pro	Val	Trp	Leu	Asn	Gly	Ser	His	Pro	Leu	Glu	Gly
65					70					75					80
Asp	Gly	Ile	Val	Gln	Arg	Gln	Ala	Cys	Ala	Ser	Phe	Asn	Gly	Asn	Cys
				85					90					95	
Cys	Leu	Trp	Asn	Thr	Thr	Val	Glu	Val	Lys	Ala	Cys	Pro	Gly	Gly	Tyr
			100					105					110		
Tyr	Val	Tyr	Arg	Leu	Thr	Lys	Pro	Ser	Val	Cys	Phe	His	Val	Tyr	Cys
		115					120					125			
Gly	Arg	Glu	Tyr	Leu	Pro	Cys	Ala	Leu	Phe	Leu	His	Gln	Gln	Gly	His
	130					135					140				
Arg	Trp	Ser	Pro	Lys	Val	Pro	Asn	Tyr	Arg	Ile	Cys	Ser	Tyr	Ser	Gly
145					150					155					160
Asn	Tyr	Ile	Ser	Ile											

165

<210> 296
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18...-1

<400> 296

Met Gly Leu Pro Gly Leu Phe Cys Leu Ala Val Leu Ala Ala Ser Ser
-15 -10 -5
Phe Ser Lys Ala Arg Glu Glu Glu Ile Thr Pro Val Val Ser Ile Ala
1 5 10
Tyr Lys Val Leu Glu Val Phe Pro Lys Gly Arg Trp Val Leu Ile Thr
15 20 25 30
Cys Cys Ala Pro Gln Pro Pro Pro Pro Ile Thr Tyr Ser Leu Cys Gly
35 40 45
Thr Lys Asn Ile Lys Val Ala Lys Lys Val Val Lys Thr His Glu Pro
50 55 60
Ala Ser Phe Asn Leu Asn Val Thr Leu Lys Ser Ser Pro Asp Leu Leu
65 70 75
Thr Tyr Phe Cys Arg Ala Ser Ser Thr Ser Gly Ala His Val Asp Ser
80 85 90
Ala Arg Leu Gln Met His Trp Glu Leu Trp Ser Lys Pro Val Ser Glu
95 100 105 110
Leu Arg Ala Asn Phe Thr Leu Gln Asp Arg Gly Ala Gly Pro Arg Val
115 120 125
Glu Met Ile Cys Gln Ala Ser Ser Gly Ser Pro Pro Ile Thr Asn Ser
130 135 140
Leu Ile Gly Lys Asp Gly Gln Val His Leu Gln Gln Arg Pro Cys His
145 150 155
Arg Gln Pro Ala Asn Phe Ser Phe Leu Pro Ser Gln Thr Ser Asp Trp
160 165 170
Phe Trp Cys Gln Ala Ala Asn Asn Ala Asn Val Gln His Ser Ala Leu
175 180 185 190
Thr Val Val Pro Pro Gly Gly Leu Pro Arg Ala Pro Thr Ile Val Leu
195 200 205
Val Gly Ser Leu Ala Ser Thr Ala Ala Ile Thr Ser Arg Met Leu Gly
210 215 220
Trp Thr Thr Trp Ala Arg Trp
225

<210> 297
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41...-1

<400> 297

Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys Ala Gly Gly Ala Phe Asp
-40 -35 -30
Pro Tyr Thr Leu Val Arg Gln Pro His Thr Ile Leu Arg Val Val Ser

<210> 299
 <211> 137
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -22...-1

<400> 299

Met	Leu	Ser	Gly	Arg	Leu	Val	Leu	Gly	Leu	Val	Ser	Met	Ala	Gly	Arg
		-20					-15				-10				
Val	Cys	Leu	Cys	Gln	Gly	Ser	Ala	Gly	Ser	Gly	Ala	Ile	Gly	Pro	Val
	-5				1				5					10	
Glu	Ala	Ala	Ile	Arg	Thr	Lys	Leu	Glu	Glu	Ala	Leu	Ser	Pro	Glu	Val
			15					20						25	
Leu	Glu	Leu	Arg	Asn	Glu	Ser	Gly	Gly	His	Ala	Val	Pro	Pro	Gly	Ser
			30				35					40			
Glu	Thr	His	Phe	Arg	Val	Ala	Val	Val	Ser	Ser	Arg	Phe	Glu	Gly	Leu
	45					50					55				
Ser	Pro	Leu	Gln	Arg	His	Arg	Leu	Val	His	Ala	Ala	Leu	Ala	Glu	Glu
	60				65					70					
Leu	Gly	Gly	Pro	Val	His	Ala	Leu	Ala	Ile	Gln	Ala	Arg	Thr	Pro	Ala
75				80					85					90	
Gln	Trp	Arg	Glu	Asn	Ser	Gln	Leu	Asp	Thr	Ser	Pro	Pro	Cys	Leu	Gly
			95					100						105	
Gly	Asn	Lys	Lys	Thr	Leu	Gly	Thr	Pro							
			110					115							

<210> 300
 <211> 541
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 300

Met	Gly	Ser	Gln	Glu	Val	Leu	Gly	His	Ala	Ala	Arg	Leu	Ala	Ser	Ser
		-25					-20				-15				
Gly	Leu	Leu	Leu	Gln	Val	Leu	Phe	Arg	Leu	Ile	Thr	Phe	Val	Leu	Asn
	-10					-5					1				
Ala	Phe	Ile	Leu	Arg	Phe	Leu	Ser	Lys	Glu	Ile	Val	Gly	Val	Val	Asn
5				10					15					20	
Val	Arg	Leu	Thr	Leu	Leu	Tyr	Ser	Thr	Thr	Leu	Phe	Leu	Ala	Arg	Glu
			25					30						35	
Ala	Phe	Arg	Arg	Ala	Cys	Leu	Ser	Gly	Gly	Thr	Gln	Arg	Asp	Trp	Ser
		40					45				50				
Gln	Thr	Leu	Asn	Leu	Leu	Trp	Leu	Thr	Val	Pro	Leu	Gly	Val	Phe	Trp
	55					60					65				
Ser	Leu	Phe	Leu	Gly	Trp	Ile	Trp	Leu	Gln	Leu	Leu	Glu	Val	Pro	Asp
	70				75				80						
Pro	Asn	Val	Val	Pro	His	Tyr	Ala	Thr	Gly	Val	Val	Leu	Phe	Gly	Leu
85				90					95					100	
Ser	Ala	Val	Val	Glu	Leu	Leu	Gly	Glu	Pro	Phe	Trp	Val	Leu	Ala	Gln
			105					110						115	

Ala	His	Met	Phe	Val	Lys	Leu	Lys	Val	Ile	Ala	Glu	Ser	Leu	Ser	Val
			120					125					130		
Ile	Leu	Lys	Ser	Val	Leu	Thr	Ala	Phe	Leu	Val	Leu	Trp	Leu	Pro	His
		135					140					145			
Trp	Gly	Leu	Tyr	Ile	Phe	Ser	Leu	Ala	Gln	Leu	Phe	Tyr	Thr	Thr	Val
	150					155					160				
Leu	Val	Leu	Cys	Tyr	Val	Ile	Tyr	Phe	Thr	Lys	Leu	Leu	Gly	Ser	Pro
165					170					175					180
Glu	Ser	Thr	Lys	Leu	Gln	Thr	Leu	Pro	Val	Ser	Arg	Ile	Thr	Asp	Leu
			185						190					195	
Leu	Pro	Asn	Ile	Thr	Arg	Asn	Gly	Ala	Phe	Ile	Asn	Trp	Lys	Glu	Ala
		200						205					210		
Lys	Leu	Thr	Trp	Ser	Phe	Phe	Lys	Gln	Ser	Phe	Leu	Lys	Gln	Ile	Leu
		215					220					225			
Thr	Glu	Gly	Glu	Arg	Tyr	Val	Met	Thr	Phe	Leu	Asn	Val	Leu	Asn	Phe
	230					235						240			
Gly	Asp	Gln	Gly	Val	Tyr	Asp	Ile	Val	Asn	Asn	Leu	Gly	Ser	Leu	Val
245					250					255					260
Ala	Arg	Leu	Ile	Phe	Gln	Pro	Ile	Glu	Glu	Ser	Phe	Tyr	Ile	Phe	Phe
				265					270					275	
Ala	Lys	Val	Leu	Glu	Arg	Gly	Lys	Asp	Ala	Thr	Leu	Gln	Lys	Gln	Glu
		280						285					290		
Asp	Val	Ala	Val	Ala	Ala	Ala	Val	Leu	Glu	Ser	Leu	Leu	Lys	Leu	Ala
		295					300					305			
Leu	Leu	Ala	Gly	Leu	Thr	Ile	Thr	Val	Phe	Gly	Phe	Ala	Tyr	Ser	Gln
	310					315					320				
Leu	Ala	Leu	Asp	Ile	Tyr	Gly	Gly	Thr	Met	Leu	Ser	Ser	Gly	Ser	Gly
325					330					335					340
Pro	Val	Leu	Leu	Arg	Ser	Tyr	Cys	Leu	Tyr	Val	Leu	Leu	Leu	Ala	Ile
				345					350					355	
Asn	Gly	Val	Thr	Glu	Cys	Leu	Thr	Phe	Ala	Ala	Met	Ser	Lys	Glu	Glu
		360						365					370		
Val	Asp	Arg	Tyr	Asn	Phe	Val	Met	Leu	Ala	Leu	Ser	Ser	Ser	Phe	Leu
		375					380					385			
Val	Leu	Ser	Tyr	Leu	Leu	Thr	Arg	Trp	Cys	Gly	Ser	Val	Gly	Phe	Ile
	390					395					400				
Leu	Ala	Asn	Cys	Phe	Asn	Met	Gly	Ile	Arg	Ile	Thr	Gln	Ser	Leu	Cys
405					410					415					420
Phe	Ile	His	Arg	Tyr	Tyr	Arg	Arg	Ser	Pro	His	Arg	Pro	Leu	Ala	Gly
				425					430					435	
Leu	His	Leu	Ser	Pro	Val	Leu	Leu	Gly	Thr	Phe	Ala	Leu	Ser	Gly	Gly
			440					445					450		
Val	Thr	Ala	Val	Ser	Glu	Val	Phe	Leu	Cys	Cys	Asp	Gln	Gly	Trp	Pro
	455						460					465			
Ala	Arg	Leu	Ala	His	Ile	Ala	Val	Gly	Ala	Phe	Cys	Leu	Gly	Ala	Thr
	470					475					480				
Leu	Gly	Thr	Ala	Phe	Leu	Thr	Glu	Thr	Lys	Leu	Ile	His	Phe	Leu	Arg
485					490					495					500
Thr	Gln	Leu	Gly	Val	Pro	Arg	Arg	Thr	Asp	Lys	Met	Thr			
				505					510						

<210> 301
 <211> 287
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -17...-1

<400> 301

Met	Glu	Leu	Glu	Arg	Ile	Val	Ser	Ala	Ala	Leu	Leu	Ala	Phe	Val	Gln
	-15						-10					-5			
Thr	His	Leu	Pro	Glu	Ala	Asp	Leu	Ser	Gly	Leu	Asp	Glu	Val	Ile	Phe
1				5					10					15	
Ser	Tyr	Val	Leu	Gly	Val	Leu	Glu	Asp	Leu	Gly	Pro	Ser	Gly	Pro	Ser
			20						25					30	
Glu	Glu	Asn	Phe	Asp	Met	Glu	Ala	Phe	Thr	Glu	Met	Met	Glu	Ala	Tyr
		35						40					45		
Val	Pro	Gly	Phe	Ala	His	Ile	Pro	Arg	Gly	Thr	Ile	Gly	Asp	Met	Met
	50						55					60			
Gln	Lys	Leu	Ser	Gly	Gln	Leu	Ser	Asp	Ala	Arg	Asn	Lys	Glu	Asn	Leu
65						70					75				
Gln	Pro	Gln	Ser	Ser	Gly	Val	Gln	Gly	Gln	Val	Pro	Ile	Ser	Pro	Glu
80					85					90					95
Pro	Leu	Gln	Arg	Pro	Glu	Met	Leu	Lys	Glu	Glu	Thr	Arg	Ser	Ser	Ala
				100					105					110	
Ala	Ala	Ala	Ala	Asp	Thr	Gln	Asp	Glu	Ala	Thr	Gly	Ala	Glu	Glu	Glu
			115					120					125		
Leu	Leu	Pro	Gly	Val	Asp	Val	Leu	Leu	Glu	Val	Phe	Pro	Thr	Cys	Ser
		130					135					140			
Val	Glu	Gln	Ala	Gln	Trp	Val	Leu	Ala	Lys	Ala	Arg	Gly	Asp	Leu	Glu
	145					150					155				
Glu	Ala	Val	Gln	Met	Leu	Val	Glu	Gly	Lys	Glu	Glu	Gly	Pro	Ala	Ala
160					165					170					175
Trp	Glu	Gly	Pro	Asn	Gln	Asp	Leu	Pro	Arg	Arg	Leu	Arg	Gly	Pro	Gln
				180					185					190	
Lys	Asp	Glu	Leu	Lys	Ser	Phe	Ile	Leu	Gln	Lys	Tyr	Met	Met	Val	Asp
		195						200					205		
Ser	Ala	Glu	Asp	Gln	Lys	Ile	His	Arg	Pro	Met	Ala	Pro	Lys	Glu	Ala
	210						215					220			
Pro	Lys	Lys	Leu	Ile	Arg	Tyr	Ile	Asp	Asn	Gln	Val	Val	Ser	Thr	Lys
	225					230					235				
Gly	Glu	Arg	Phe	Lys	Asp	Val	Arg	Asn	Pro	Glu	Ala	Glu	Glu	Met	Lys
240					245					250					255
Ala	Thr	Tyr	Ile	Asn	Leu	Lys	Pro	Ala	Arg	Lys	Tyr	Arg	Phe	His	
				260					265					270	

<210> 302

<211> 165

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -35...-1

<400> 302

Met	Met	Arg	Cys	Cys	Arg	Arg	Arg	Cys	Cys	Cys	Arg	Gln	Pro	Pro	His
-35					-30					-25					-20
Ala	Leu	Arg	Pro	Leu	Leu	Leu	Pro	Leu	Val	Leu	Leu	Pro	Pro	Leu	
				-15				-10					-5		
Ala	Ala	Ala	Ala	Ala	Gly	Pro	Asn	Arg	Cys	Asp	Thr	Ile	Tyr	Gln	Gly
			1			5					10				
Phe	Ala	Glu	Cys	Leu	Ile	Arg	Leu	Gly	Asp	Ser	Met	Gly	Arg	Gly	Gly
15						20					25				

09876997-060801

Glu Leu Glu Thr Ile Cys Arg Ser Trp Asn Tyr Phe His Ala Cys Ala
 30 35 40 45
 Ser Gln Val Leu Ser Gly Cys Pro Glu Glu Ala Ala Ala Val Trp Glu
 50 55 60
 Ser Leu Gln Gln Glu Ala Arg Gln Ala Pro Arg Pro Asn Asn Leu His
 65 70 75
 Thr Leu Cys Gly Ala Pro Val His Val Arg Glu Arg Gly Thr Gly Ser
 80 85 90
 Glu Thr Asn Gln Glu Thr Leu Arg Ala Thr Ala Pro Ala Leu Pro Met
 95 100 105
 Ala Pro Ala Pro Pro Leu Leu Ala Ala Ala Leu Ala Leu Ala Tyr Leu
 110 115 120 125
 Leu Arg Pro Leu Ala
 130

<210> 303
 <211> 148
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -25...-1

<400> 303
 Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg Thr Ala Val Thr Ser
 -25 -20 -15 -10
 Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser
 -5 1 5
 Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly
 10 15 20
 Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His Tyr Val His Ala Gly
 25 30 35
 Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp His Pro Gly Ala His
 40 45 50 55
 Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile
 60 65 70
 Val Arg Tyr Thr Lys Glu Val Tyr Val Pro His Pro Arg Asn Thr Glu
 75 80 85
 Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly Ala Val Leu Tyr Lys
 90 95 100
 Thr Phe Val His Val Val Pro Ala Lys Pro Glu Gly Thr Phe Lys Leu
 105 110 115
 Val Ala Met Leu
 120

<210> 304
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 304
 Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu
 -30 -25 -20

Lys Arg Ile Ala Tyr Phe Leu Cys Leu Leu Ser Ala Leu Leu Leu Thr
 -15 -10 -5
 Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys
 1 5 10
 Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr
 15 20 25 30
 Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Gly Phe Thr
 35 40 45
 Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu
 50 55 60
 Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile
 65 70 75
 Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys
 80 85 90
 Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu
 95 100 105 110
 Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys
 115 120 125
 Gly Leu Asp Ser Leu Thr Asn Val Asp Leu Arg Gly Asn Ser Phe Asn
 130 135 140
 Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn
 145 150 155
 Ala Thr Val Glu Asp Ile Tyr Cys Glu Gly Pro Pro Glu Tyr Lys Lys
 160 165 170
 Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr
 175 180 185 190
 Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp
 195 200 205
 Thr Phe Ser Tyr Leu Asn Asp Glu Tyr Val Val Ile Ala Gln Pro Phe
 210 215 220
 Thr Gly Lys Cys Ile Phe Leu Glu Trp Asp His Val Glu Lys Thr Phe
 225 230 235
 Arg Asn Tyr Asp Asn Ile Thr Val Leu Arg Glu Ile His Arg Phe Thr
 240 245 250
 Asn Met Ser
 255

<210> 305
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -49...-1

<400> 305
 Met Glu Gly Ala Gly Ala Gly Ser Gly Phe Arg Lys Glu Leu Val Ser
 -45 -40 -35
 Arg Leu Leu His Leu His Phe Lys Asp Asp Lys Thr Lys Val Ser Gly
 -30 -25 -20
 Asp Ala Leu Gln Leu Met Val Glu Leu Lys Val Phe Val Val Glu
 -15 -10 -5
 Ala Ala Val Arg Gly Val Arg Gln Ala Gln Ala Glu Asp Ala Leu Arg
 1 5 10 15
 Val Asp Val Asp Gln Leu Glu Lys Val Leu Pro Gln Leu Leu Leu Asp
 20 25 30
 Phe

<210> 306
 <211> 233
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -30...-1

<400> 306
 Met Ala Ala Thr Ser Gly Thr Asp Glu Pro Val Ser Gly Glu Leu Val
 -30 -25 -20 -15
 Ser Val Ala His Ala Leu Ser Leu Pro Ala Glu Ser Tyr Gly Asn Asp
 -10 -5 1
 Pro Asp Ile Glu Met Ala Trp Ala Met Arg Ala Met Gln His Ala Glu
 5 10 15
 Val Tyr Tyr Lys Leu Ile Ser Ser Val Asp Pro Gln Phe Leu Lys Leu
 20 25 30
 Thr Lys Val Asp Asp Gln Ile Tyr Ser Glu Phe Arg Lys Asn Phe Glu
 35 40 45 50
 Thr Leu Arg Ile Asp Val Leu Asp Pro Glu Glu Leu Lys Ser Glu Ser
 55 60 65
 Ala Lys Glu Lys Trp Arg Pro Phe Cys Leu Lys Phe Asn Gly Ile Val
 70 75 80
 Glu Asp Phe Asn Tyr Gly Thr Leu Leu Arg Leu Asp Cys Ser Gln Gly
 85 90 95
 Tyr Thr Glu Glu Asn Thr Ile Phe Ala Pro Arg Ile Gln Phe Phe Ala
 100 105 110
 Ile Glu Ile Ala Arg Asn Arg Glu Gly Tyr Asn Lys Ala Val Tyr Ile
 115 120 125 130
 Ser Val Gln Asp Lys Glu Gly Glu Lys Gly Val Asn Asn Gly Gly Glu
 135 140 145
 Lys Arg Ala Asp Ser Gly Glu Glu Glu Asn Thr Lys Asn Gly Gly Glu
 150 155 160
 Lys Gly Ala Asp Ser Gly Glu Glu Lys Glu Glu Gly Ile Asn Arg Glu
 165 170 175
 Asp Lys Thr Asp Lys Gly Gly Glu Lys Gly Lys Glu Ala Asp Lys Glu
 180 185 190
 Ile Asn Lys Ser Gly Glu Lys Ala Met
 195 200

<210> 307
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 307
 Met Arg Gln Lys Ala Val Ser Leu Phe Leu Cys Tyr Leu Leu Leu Phe
 -20 -15 -10 -5
 Thr Cys Ser Gly Val Glu Ala Gly Lys Lys Lys Cys Ser Glu Ser Ser
 1 5 10
 Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu Thr Phe Met Ala Val Gly
 15 20 25

Gly Gly Leu Ala Val Ala Gly Leu Pro Ala Leu Gly Phe Thr Gly Ala
 30 35 40
 Gly Ile Ala Ala Asn Ser Val Ala Ala Ser Leu Met Ser Trp Ser Ala
 45 50 55 60
 Ile Leu Asn Gly Gly
 65

<210> 308
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -43...-1

<400> 308
 Met Gly Phe Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys
 -40 -35 -30
 Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly
 -25 -20 -15
 Ser Leu Val Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr
 -10 -5 1 5
 Ser Ser Asn Ile Leu Leu Ala Ser Val Gly Ser Val Leu Gly Ala Cys
 10 15 20
 Leu Gly Asn Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys
 25 30 35
 Glu Asp Glu Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro
 40 45 50
 Pro Leu Lys Ser Glu Lys His Glu Glu
 55 60

<210> 309
 <211> 291
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 309
 Met Glu Ser Glu Arg Ser Lys Arg Met Gly Asn Ala Cys Ile Pro Leu
 -30 -25 -20
 Lys Arg Ile Ala Tyr Phe Leu Cys Leu Ser Ala Leu Leu Leu Thr
 -15 -10 -5
 Glu Gly Lys Lys Pro Ala Lys Pro Lys Cys Pro Ala Val Cys Thr Cys
 1 5 10
 Thr Lys Asp Asn Ala Leu Cys Glu Asn Ala Arg Ser Ile Pro Arg Thr
 15 20 25 30
 Val Pro Pro Asp Val Ile Ser Leu Ser Phe Val Arg Ser Val Phe Thr
 35 40 45
 Glu Ile Ser Glu Gly Ser Phe Leu Phe Thr Pro Ser Leu Gln Leu Leu
 50 55 60
 Leu Phe Thr Ser Asn Ser Phe Asp Val Ile Ser Asp Asp Ala Phe Ile
 65 70 75
 Gly Leu Pro His Leu Glu Tyr Leu Phe Ile Glu Asn Asn Asn Ile Lys
 80 85 90

09876997 050804

Ser Ile Ser Arg His Thr Phe Arg Gly Leu Lys Ser Leu Ile His Leu
 95 100 105 110
 Ser Leu Ala Asn Asn Asn Leu Gln Thr Leu Pro Lys Asp Ile Phe Lys
 115 120 125
 Gly Leu Asp Ser Leu Thr Asn Val Asp Leu Arg Gly Asn Ser Phe Asn
 130 135 140
 Cys Asp Cys Lys Leu Lys Trp Leu Val Glu Trp Leu Gly His Thr Asn
 145 150 155
 Ala Thr Val Glu Asp Ile Tyr Cys Glu Gly Pro Pro Glu Tyr Lys Lys
 160 165 170
 Arg Lys Ile Asn Ser Leu Ser Ser Lys Asp Phe Asp Cys Ile Ile Thr
 175 180 185 190
 Glu Phe Ala Lys Ser Gln Asp Leu Pro Tyr Gln Ser Leu Ser Ile Asp
 195 200 205
 Thr Phe Ser Tyr Leu Asn Asp Glu Tyr Val Val Ile Ala Gln Pro Phe
 210 215 220
 Thr Gly Lys Cys Ile Phe Leu Glu Trp Asp His Val Glu Lys Thr Phe
 225 230 235
 Arg Asn Tyr Asp Asn Ile Thr Val Leu Arg Glu Ile His Arg Phe Thr
 240 245 250
 Asn Met Ser
 255

<210> 310
 <211> 426
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 310
 Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
 -25 -20 -15
 Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val
 -10 -5 1
 Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu
 5 10 15 20
 His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro
 25 30 35
 Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg
 40 45 50
 Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val
 55 60 65
 Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg
 70 75 80
 Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro
 85 90 95 100
 Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His
 105 110 115
 Lys Leu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr
 120 125 130
 Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr
 135 140 145
 Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys
 150 155 160
 Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn

165 170 175 180
 Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly
 185 190 195
 Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln
 200 205 210
 Ile Arg Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Arg Val
 215 220 225
 Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met
 230 235 240
 Asn Lys Tyr His Gly Arg Lys Leu Ser Met Gln Gly Phe Lys Glu Ala
 245 250 255 260
 Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu
 265 270 275
 Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg
 280 285 290
 Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Leu Leu Val Ile Tyr Asp
 295 300 305
 Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu
 310 315 320
 Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala
 325 330 335 340
 Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe
 345 350 355
 Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu
 360 365 370
 Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile
 375 380 385
 Val Thr Glu Ile Ser Glu Glu Ser Gly Glu
 390 395

<210> 311
 <211> 466
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 311
 Met Gly Leu Tyr Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser
 -15 -10 -5
 Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn
 1 5 10 15
 Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala
 20 25 30
 Val Leu Asp Ala Val Ile Ala Ser Ala Gly Leu Leu Arg Ala Glu Lys
 35 40 45
 Lys Leu Arg Pro His Leu Ala Lys Val Leu Val Tyr Glu Leu Leu Leu
 50 55 60
 Gly Lys Gly Phe Arg Gly Gly Gly Arg Trp Lys Ala Leu Leu Gly
 65 70 75 80
 Arg His Gln Ala Arg Leu Lys Ala Glu Leu Ala Arg Leu Lys Val His
 85 90 95
 Arg Gly Val Ser Arg Asn Glu Asp Leu Leu Glu Val Gly Ser Arg Pro
 100 105 110
 Gly Pro Ala Ser Gln Leu Pro Arg Phe Val Arg Val Asn Thr Leu Lys
 115 120 125

Thr Cys Ser Asp Asp Val Val Asp Tyr Phe Lys Arg Gln Gly Phe Ser
 130 135 140
 Tyr Gln Gly Arg Ala Ser Ser Leu Asp Asp Leu Arg Ala Leu Lys Gly
 145 150 155 160
 Lys His Phe Leu Leu Asp Pro Leu Met Pro Glu Leu Leu Val Phe Pro
 165 170 175
 Ala Gln Thr Asp Leu His Glu His Pro Leu Tyr Arg Ala Gly His Leu
 180 185 190
 Ile Leu Gln Asp Arg Ala Ser Cys Leu Pro Ala Met Leu Leu Asp Pro
 195 200 205
 Pro Pro Gly Ser His Val Ile Asp Ala Cys Ala Ala Pro Gly Asn Lys
 210 215 220
 Thr Ser His Leu Ala Ala Leu Leu Lys Asn Gln Gly Lys Ile Phe Ala
 225 230 235 240
 Phe Asp Leu Asp Ala Lys Arg Leu Ala Ser Met Ala Thr Leu Leu Ala
 245 250 255
 Arg Ala Gly Val Ser Cys Cys Glu Leu Ala Glu Glu Asp Phe Leu Ala
 260 265 270
 Val Ser Pro Ser Asp Pro Arg Tyr His Glu Val His Tyr Ile Leu Leu
 275 280 285
 Asp Pro Ser Cys Ser Gly Ser Gly Met Pro Ser Arg Gln Leu Glu Glu
 290 295 300
 Pro Gly Ala Gly Thr Pro Ser Pro Val Arg Leu His Ala Leu Ala Gly
 305 310 315 320
 Phe Gln Gln Arg Ala Leu Cys His Ala Leu Thr Phe Pro Ser Leu Gln
 325 330 335
 Arg Leu Val Tyr Ser Thr Cys Ser Leu Cys Gln Glu Glu Asn Glu Asp
 340 345 350
 Val Val Arg Asp Ala Leu Gln Gln Asn Pro Gly Ala Phe Arg Leu Ala
 355 360 365
 Pro Ala Leu Pro Ala Trp Pro His Arg Gly Leu Ser Thr Phe Pro Gly
 370 375 380
 Ala Glu His Cys Leu Arg Ala Ser Pro Glu Thr Thr Leu Ser Ser Gly
 385 390 395 400
 Phe Phe Val Ala Val Ile Glu Arg Val Glu Val Pro Ser Ser Ala Ser
 405 410 415
 Gln Ala Lys Ala Ser Ala Pro Glu Arg Thr Pro Ser Pro Ala Pro Lys
 420 425 430
 Arg Lys Lys Arg Gln Gln Arg Ala Ala Ala Gly Ala Cys Thr Pro Pro
 435 440 445
 Cys Thr
 450

<210> 312
 <211> 382
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 312
 Met Gly Leu Tyr Ala Ala Ala Ala Gly Val Leu Ala Gly Val Glu Ser
 -15 -10 -5
 Arg Gln Gly Ser Ile Lys Gly Leu Val Tyr Ser Ser Asn Phe Gln Asn
 1 5 10 15
 Val Lys Gln Leu Tyr Ala Leu Val Cys Glu Thr Gln Arg Tyr Ser Ala

20					25					30						
Val	Leu	Asp	Ala	Val	Ile	Ala	Ser	Ala	Gly	Leu	Leu	Arg	Ala	Glu	Lys	
35						40						45				
Lys	Leu	Arg	Pro	His	Leu	Ala	Lys	Val	Leu	Val	Tyr	Glu	Leu	Leu	Leu	
50						55			60							
Gly	Lys	Gly	Phe	Arg	Gly	Gly	Gly	Gly	Arg	Trp	Lys	Ala	Leu	Leu	Gly	
65					70					75					80	
Arg	His	Gln	Ala	Arg	Leu	Lys	Ala	Glu	Leu	Ala	Arg	Leu	Lys	Val	His	
				85					90					95		
Arg	Gly	Val	Ser	Arg	Asn	Glu	Asp	Leu	Leu	Glu	Val	Gly	Ser	Arg	Pro	
			100				105						110			
Gly	Pro	Ala	Ser	Gln	Leu	Pro	Arg	Phe	Val	Arg	Val	Asn	Thr	Leu	Lys	
			115				120						125			
Thr	Cys	Ser	Asp	Asp	Val	Val	Asp	Tyr	Phe	Lys	Arg	Gln	Gly	Phe	Ser	
			130				135			140						
Tyr	Gln	Gly	Arg	Ala	Ser	Ser	Leu	Asp	Asp	Leu	Arg	Ala	Leu	Lys	Gly	
145					150					155					160	
Lys	His	Phe	Leu	Leu	Asp	Pro	Leu	Met	Pro	Glu	Leu	Leu	Val	Phe	Pro	
				165					170						175	
Ala	Gln	Thr	Asp	Leu	His	Glu	His	Pro	Leu	Tyr	Arg	Ala	Gly	His	Leu	
			180				185						190			
Ile	Leu	Gln	Asp	Arg	Ala	Ser	Cys	Leu	Pro	Ala	Met	Leu	Leu	Asp	Pro	
			195				200						205			
Pro	Pro	Gly	Ser	His	Val	Ile	Asp	Ala	Cys	Ala	Ala	Pro	Gly	Asn	Lys	
			210				215			220						
Thr	Ser	His	Leu	Ala	Ala	Leu	Leu	Lys	Asn	Gln	Gly	Lys	Ile	Phe	Ala	
225					230					235						240
Phe	Asp	Leu	Asp	Ala	Lys	Arg	Leu	Ala	Ser	Met	Ala	Thr	Leu	Leu	Ala	
			245				250						255			
Arg	Ala	Gly	Val	Ser	Cys	Cys	Glu	Leu	Ala	Glu	Glu	Asp	Phe	Leu	Ala	
			260				265						270			
Val	Ser	Pro	Ser	Asp	Pro	Arg	Tyr	His	Glu	Val	His	Tyr	Ile	Leu	Leu	
			275				280						285			
Asp	Pro	Ser	Cys	Ser	Gly	Ser	Gly	Met	Pro	Ser	Arg	Gln	Leu	Glu	Glu	
			290				295			300						
Pro	Gly	Ala	Gly	Thr	Pro	Ser	Pro	Val	Arg	Leu	His	Ala	Leu	Ala	Ala	
305					310					315						320
Ser	Ser	Ser	Glu	Pro	Cys	Ala	Thr	Arg	Ser	Leu	Ser	Leu	Pro	Cys	Ser	
			325				330						335			
Gly	Ser	Ser	Thr	Pro	Arg	Ala	Pro	Ser	Ala	Arg	Arg	Arg	Met	Lys	Thr	
			340				345						350			
Trp	Cys	Glu	Met	Arg	Cys	Ser	Arg	Thr	Arg	Ala	Pro	Ser	Gly			
			355				360						365			

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<210> 313
<211> 258
<212> PRT
<213> Homo sapiens
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<220>
<221> SIGNAL
<222> -36.,.-1
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<400> 313
Met  Glu  Glu  Leu  Gln  Glu  Pro  Leu  Arg  Gly  Glu  Leu  Arg  Leu  Cys  Phe
    -35                -30                -25
Thr  Glu  Ala  Ala  Arg  Thr  Ser  Leu  Leu  Leu  Leu  Arg  Leu  Asn  Asp  Ala
    -20                -15                -10                -5

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Ala Leu Arg Ala Leu Gln Glu Cys Gln Arg Gln Gln Val Arg Pro Val
 1 5 10
 Ile Ala Phe Gln Gly His Arg Gly Tyr Leu Arg Leu Pro Gly Pro Gly
 15 20 25
 Trp Ser Cys Leu Phe Ser Phe Ile Val Ser Gln Cys Cys Gln Glu Gly
 30 35 40
 Ala Gly Gly Ser Leu Asp Leu Val Cys Gln Arg Phe Leu Arg Ser Gly
 45 50 55 60
 Pro Asn Ser Leu His Cys Leu Gly Ser Leu Arg Glu Arg Leu Ile Ile
 65 70 75
 Trp Ala Ala Met Asp Ser Ile Pro Ala Pro Ser Ser Val Gln Gly His
 80 85 90
 Asn Leu Thr Glu Asp Ala Arg His Pro Glu Ser Trp Gln Asn Thr Gly
 95 100 105
 Gly Tyr Ser Glu Gly Asp Ala Val Ser Gln Pro Gln Met Ala Leu Glu
 110 115 120
 Glu Val Ser Val Ser Asp Pro Leu Ala Ser Asn Gln Gly Gln Ser Leu
 125 130 135 140
 Pro Gly Ser Ser Arg Glu His Met Ala Gln Trp Glu Val Arg Ser Gln
 145 150 155
 Thr His Val Pro Asn Arg Glu Pro Val Gln Ala Leu Pro Ser Ser Ala
 160 165 170
 Ser Arg Lys Arg Leu Asp Lys Lys Arg Ser Val Pro Val Ala Thr Val
 175 180 185
 Glu Leu Glu Glu Lys Arg Phe Arg Thr Leu Pro Leu Val Pro Pro Pro
 190 195 200
 Thr Arg Pro Asp Gln Ser Gly Phe Thr Arg Gly Arg Arg Leu Gly Ala
 205 210 215 220
 Arg Arg

<210> 314
 <211> 280
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 314
 Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu Pro
 -30 -25 -20
 Ala Ala Trp Val Leu Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu
 -15 -10 -5
 Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val Val
 1 5 10 15
 His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu Tyr
 20 25 30
 Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu Phe
 35 40 45
 Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly Phe
 50 55 60
 Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val His
 65 70 75
 Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu Ser
 80 85 90 95
 Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser Pro
 100 105 110

Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe Pro
 115 120 125
 Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro Leu Ile
 130 135 140
 Asn Gly Glu Arg Asp His Pro Asn Ala Thr Val Trp Arg Lys Asn Phe
 145 150 155
 Leu Arg Val Gly His Leu Val Leu Ile Gly Gly Pro Asp Asp Gly Val
 160 165 170 175
 Ile Thr Pro Trp Gln Ser Ser Phe Phe Gly Phe Tyr Asp Ala Asn Glu
 180 185 190
 Thr Val Leu Glu Met Glu Glu Gln Leu Val Tyr Leu Arg Asp Ser Phe
 195 200 205
 Gly Leu Lys Thr Leu Leu Ala Arg Gly Ala Ile Val Arg Cys Pro Met
 210 215 220
 Ala Gly Ile Ser His Thr Ala Trp His Ser Asn Arg Thr Leu Tyr Glu
 225 230 235
 Thr Cys Ile Glu Pro Trp Leu Ser
 240 245

<210> 315
 <211> 174
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -33...-1

<400> 315
 Met Lys Ser Cys Gly Ser Met Leu Gly Leu Trp Gly Gln Arg Leu Pro
 -30 -25 -20
 Ala Ala Trp Val Leu Leu Leu Leu Pro Phe Leu Pro Leu Leu Leu Leu
 -15 -10 -5
 Ala Ala Pro Ala Pro His Arg Ala Ser Tyr Lys Pro Val Ile Val Val
 1 5 10 15
 His Gly Leu Phe Asp Ser Ser Tyr Ser Phe Arg His Leu Leu Glu Tyr
 20 25 30
 Ile Asn Glu Thr His Pro Gly Thr Val Val Thr Val Leu Asp Leu Phe
 35 40 45
 Asp Gly Arg Glu Ser Leu Arg Pro Leu Trp Glu Gln Val Gln Gly Phe
 50 55 60
 Arg Glu Ala Val Val Pro Ile Met Ala Lys Ala Pro Gln Gly Val His
 65 70 75
 Leu Ile Cys Tyr Ser Gln Gly Gly Leu Val Cys Arg Ala Leu Leu Ser
 80 85 90 95
 Val Met Asp Asp His Asn Val Asp Ser Phe Ile Ser Leu Ser Ser Pro
 100 105 110
 Gln Met Gly Gln Tyr Gly Asp Thr Asp Tyr Leu Lys Trp Leu Phe Pro
 115 120 125
 Thr Ser Met Arg Ser Asn Leu Tyr Arg Ile Cys Tyr Ser Pro
 130 135 140

<210> 316
 <211> 160
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> -17...-1

<400> 316
Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ser Leu Val Leu
-15 -10 -5
Cys Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala Phe Asp
1 5 10 15
Glu Leu Arg Thr Asp Phe Lys Ser Pro Ile Asp Gln Cys Asn Pro Val
20 25 30
His Ala Arg Glu Arg Leu Arg Asn Ile Glu Arg Ile Cys Phe Leu Leu
35 40 45
Arg Lys Leu Val Leu Pro Glu Tyr Ser Ile His Ser Leu Phe Cys Ile
50 55 60
Met Phe Leu Cys Ala Gln Glu Trp Leu Thr Leu Gly Leu Asn Val Pro
65 70 75
Leu Leu Phe Tyr His Phe Trp Arg Tyr Phe His Cys Pro Ala Asp Ser
80 85 90 95
Ser Glu Leu Ala Tyr Asp Pro Pro Val Val Met Asn Pro Asp Thr Leu
100 105 110
Ser Tyr Cys Gln Lys Glu Ala Trp Cys Lys Leu Ala Phe Tyr Leu Leu
115 120 125
Ser Phe Phe Tyr Tyr Leu Tyr Cys Met Ile Tyr Thr Leu Val Ser Ser
130 135 140

<210> 317
<211> 426
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28...-1

<400> 317
Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
-25 -20 -15
Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val
-10 -5 1
Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu
5 10 15 20
His Gln Phe Tyr Glu Thr Leu Pro Ser Glu Met Arg Lys Phe Thr Pro
25 30 35
Gln Tyr Lys Gly Val Val Ser Val Arg Phe Glu Glu Asp Glu Asp Arg
40 45 50
Asn Leu Cys Leu Ile Ala Tyr Pro Leu Lys Gly Asp His Gly Ile Val
55 60 65
Asp Ile Val Asp Asn Ser Asp Cys Glu Pro Lys Ser Lys Leu Leu Arg
70 75 80
Trp Thr Thr Asn Lys Lys His His Val Leu Glu Thr Glu Lys Thr Pro
85 90 95 100
Lys Asp Trp Val Arg Gln His Arg Lys Glu Glu Lys Met Lys Ser His
105 110 115
Lys Leu Glu Glu Glu Phe Glu Trp Leu Lys Lys Ser Glu Val Leu Tyr
120 125 130
Tyr Thr Val Glu Lys Lys Gly Asn Ile Ser Ser Gln Leu Lys His Tyr
135 140 145
Asn Pro Trp Ser Met Lys Cys His Gln Gln Gln Leu Gln Arg Met Lys

150		155		160
Glu Asn Ala Lys His Arg Asn Gln Tyr Lys Phe Ile Leu Leu Glu Asn				
165		170		175
Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu Asp Leu Lys Met Gly				180
	185		190	195
Thr Arg Gln His Gly Asp Asp Ala Ser Glu Glu Lys Ala Ala Asn Gln				
	200		205	210
Ile Arg Lys Cys Gln Gln Ser Thr Ser Ala Val Ile Gly Val Arg Val				
	215		220	225
Cys Gly Met Gln Val Tyr Gln Ala Gly Ser Gly Gln Leu Met Phe Met				
	230		235	240
Asn Lys Tyr His Gly Arg Lys Leu Ser Val Gln Gly Phe Lys Glu Ala				
245		250		255
Leu Phe Gln Phe Phe His Asn Gly Arg Tyr Leu Arg Arg Glu Leu Leu				260
	265		270	275
Gly Pro Val Leu Lys Lys Leu Thr Glu Leu Lys Ala Val Leu Glu Arg				
	280		285	290
Gln Glu Ser Tyr Arg Phe Tyr Ser Ser Ser Leu Leu Val Ile Tyr Asp				
	295		300	305
Gly Lys Glu Arg Pro Glu Val Val Leu Asp Ser Asp Ala Glu Asp Leu				
	310		315	320
Glu Asp Leu Ser Glu Glu Ser Ala Asp Glu Ser Ala Gly Ala Tyr Ala				
325		330		335
Tyr Lys Pro Ile Gly Ala Ser Ser Val Asp Val Arg Met Ile Asp Phe				
	345		350	355
Ala His Thr Thr Cys Arg Leu Tyr Gly Glu Asp Thr Val Val His Glu				
	360		365	370
Gly Gln Asp Ala Gly Tyr Ile Phe Gly Leu Gln Ser Leu Ile Asp Ile				
	375		380	385
Val Thr Glu Ile Ser Glu Glu Ser Gly Glu				
390		395		

<210> 318
 <211> 301
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 318
 Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val
 -20 -15 -10 -5
 Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln
 1 5 10
 Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg
 15 20 25
 Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile
 30 35 40
 Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu
 45 50 55 60
 Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Leu Ser Phe Val Phe
 65 70 75
 Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met
 80 85 90
 Lys Ser Val Leu Trp Trp Leu Pro Val Glu Lys Ala Phe Trp Arg Gln
 95 100 105

Pro Ala Gly Pro Gly Ser Gly Ile Arg Glu Arg Leu Glu His Pro Val
 110 115 120
 Leu His Val Ser Trp Asn Asp Ala Arg Ala Tyr Cys Ala Trp Arg Gly
 125 130 135 140
 Lys Arg Leu Pro Thr Glu Glu Glu Trp Glu Phe Ala Ala Arg Gly Gly
 145 150 155
 Leu Lys Gly Gln Val Tyr Pro Trp Gly Asn Trp Phe Gln Pro Asn Arg
 160 165 170
 Thr Asn Leu Trp Gln Gly Lys Phe Pro Lys Gly Asp Lys Ala Glu Asp
 175 180 185
 Gly Phe His Gly Val Ser Pro Val Asn Ala Phe Pro Ala Gln Asn Asn
 190 195 200
 Tyr Gly Leu Tyr Asp Leu Leu Gly Asn Val Trp Glu Trp Thr Ala Ser
 205 210 215 220
 Pro Tyr Gln Ala Ala Glu Gln Asp Met Arg Val Leu Arg Gly Ala Ser
 225 230 235
 Trp Ile Asp Thr Ala Asp Gly Ser Ala Asn His Arg Ala Arg Val Thr
 240 245 250
 Thr Arg Met Gly Asn Thr Pro Asp Ser Ala Ser Asp Asn Leu Gly Phe
 255 260 265
 Arg Cys Ala Ala Asp Ala Gly Arg Pro Pro Gly Glu Leu
 270 275 280

<210> 319
 <211> 119
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -17...-1

<400> 319
 Met Gly Ser Gly Trp Leu Thr Ala Val Ala Ser Leu Leu Pro Ser Pro
 -15 -10 -5
 Gly Asn Ser Glu Leu Pro Val Gln Ala Leu Gly Arg Arg Gly Gly Arg
 1 5 10 15
 Asp Trp Ala Arg Asn Glu Ala Gly Arg Asp Leu Glu Lys Pro Pro Arg
 20 25 30
 Leu His Cys Ser Gly Arg Gly Arg Leu Glu Glu Pro Val Pro Pro Asn
 35 40 45
 His Leu Pro Val Gly Leu Ser Val Arg Gly Ser Gln Val Leu Ser Ser
 50 55 60
 Ala Gly Pro Arg Arg Cys Arg Leu Thr Gly Thr Arg Asn Pro Val Arg
 65 70 75
 Gly Pro Arg Arg Val Glu Gln Ile Ala Arg Gly Gly Pro Glu Ala Arg
 80 85 90 95
 Arg Gln Ala Gly Asp Ser Cys
 100

<210> 320
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -39...-1

<400> 320

Met Asp Tyr Ser Arg Val Phe Gln Gly Val Phe Phe Thr Phe Lys His
 -35 -30 -25
 Ala Phe Ala Asp Gly Ala Trp Asp Leu Ser Phe Leu Cys Ala Leu Cys
 -20 -15 -10
 Ser Phe Cys Pro Ile Ser Ala Ala Ser Gly Arg Pro Tyr Arg Tyr Leu
 -5 1 5
 Glu Phe Trp Arg Leu Tyr Leu Ser Pro Ser Ser Met Glu Asn Gly Val
 10 15 20 25
 Gln Lys Phe His Glu Thr Phe Phe Ile Val Phe Leu Leu Leu Phe Asp
 30 35 40
 Ile Glu Arg Lys Gly Lys Ser Ser Val Cys Pro Phe Cys Tyr Arg
 45 50 55

<210> 321

<211> 191

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -39...-1

<400> 321

Met Met Thr Ile Thr Phe Leu Pro Tyr Thr Phe Ser Leu Met Val Thr
 -35 -30 -25
 Phe Pro Asp Val Pro Leu Gly Ile Phe Leu Phe Cys Val Cys Val Ile
 -20 -15 -10
 Ala Ile Gly Val Val Gln Ala Leu Ile Val Gly Tyr Ala Phe His Phe
 -5 1 5
 Pro His Leu Leu Ser Pro Gln Ile Gln Arg Ser Ala His Arg Ala Leu
 10 15 20 25
 Tyr Arg Arg His Val Leu Gly Ile Val Leu Gln Gly Pro Ala Leu Cys
 30 35 40
 Phe Ala Ala Ala Ile Phe Ser Leu Phe Phe Val Pro Leu Ser Tyr Leu
 45 50 55
 Leu Met Val Thr Val Ile Leu Leu Pro Tyr Val Ser Lys Val Thr Gly
 60 65 70
 Trp Cys Arg Asp Arg Leu Leu Gly His Arg Glu Pro Ser Ala His Pro
 75 80 85
 Val Glu Val Phe Ser Phe Asp Leu His Glu Pro Leu Ser Lys Glu Arg
 90 95 100 105
 Val Glu Ala Phe Ser Asp Gly Val Tyr Ala Ile Val Ala Thr Leu Leu
 110 115 120
 Ile Leu Asp Ile Cys Pro Ser Cys Ser Leu Trp Leu Ala Val Ala Ser
 125 130 135
 Phe Gln Arg Leu Leu Leu Arg Gly Leu Ile Cys Leu Phe Val Cys
 140 145 150

<210> 322

<211> 89

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -41...-1

Asp Leu Val Val Ala Met Leu Ile Ala Pro Val Ala Gly Leu Ile Ala
75 80 85
Ala Pro Ala Ile Ala Thr Ser Val Leu Gly Pro Val Ala Val Pro Ala
90 95 100
Thr Ala Met Pro Pro Ala Val Leu Ala Ala Pro Pro Ser Ala Ala Pro
105 110 115
Gly Val Leu Val Asp Gly Glu Ala Ala Leu Ala Val Pro Trp Glu Ala
120 125 130 135
Cys Trp Ile Pro Ser Pro Pro Ala
140

<210> 325
<211> 166
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<400> 325
Met Leu Pro Leu Leu Ile Ile Cys Leu Leu Pro Ala Ile Glu Gly Lys
-15 -10 -5 1
Asn Cys Leu Arg Cys Trp Pro Glu Leu Ser Ala Leu Ile Asp Tyr Asp
5 10 15
Leu Gln Ile Leu Trp Val Thr Pro Gly Pro Pro Thr Glu Leu Ser Gln
20 25 30
Asn Arg Asp His Leu Glu Glu Glu Thr Ala Lys Phe Phe Thr Gln Val
35 40 45
His Gln Ala Ile Lys Thr Leu Arg Asp Asp Lys Thr Val Leu Leu Glu
50 55 60 65
Glu Ile Tyr Thr His Lys Asn Leu Phe Thr Glu Arg Leu Asn Lys Ile
70 75 80
Ser Asp Gly Leu Lys Glu Lys Asp Ile Gln Ser Thr Leu Lys Val Thr
85 90 95
Ser Cys Ala Asp Cys Arg Thr His Phe Leu Ser Cys Asn Asp Pro Thr
100 105 110
Phe Cys Pro Ala Arg Asn Arg Arg Thr Ser Leu Trp Ala Val Ser Leu
115 120 125
Ser Ser Ala Leu Leu Leu Ala Ile Ala Gly Asp Val Ser Phe Thr Gly
130 135 140 145
Lys Gly Arg Arg Arg Gln
150

<210> 326
<211> 156
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15...-1

<400> 326
Met Asn Ile Leu Met Leu Thr Phe Ile Ile Cys Gly Leu Leu Thr Arg
-15 -10 -5 1
Val Thr Lys Gly Ser Phe Glu Pro Gln Lys Cys Trp Lys Asn Asn Val
5 10 15

Gly His Cys Arg Arg Arg Cys Leu Asp Thr Glu Arg Tyr Ile Leu Leu
 20 25 30
 Cys Arg Asn Lys Leu Ser Cys Cys Ile Ser Ile Ile Ser His Glu Tyr
 35 40 45
 Thr Arg Arg Pro Ala Phe Pro Val Ile His Leu Glu Asp Ile Thr Leu
 50 55 60 65
 Asp Tyr Ser Asp Val Asp Ser Phe Thr Gly Ser Pro Val Ser Met Leu
 70 75 80
 Asn Asp Leu Ile Thr Phe Asp Thr Thr Lys Phe Gly Glu Thr Met Thr
 85 90 95
 Pro Glu Thr Asn Thr Pro Glu Thr Thr Met Pro Pro Ser Glu Ala Thr
 100 105 110
 Thr Pro Glu Thr Thr Met Pro Pro Ser Glu Thr Ala Thr Ser Glu Thr
 115 120 125
 Met Pro Pro Pro Ser Gln Thr Ala Leu Thr His Asn
 130 135 140

<210> 327
 <211> 105
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 327
 Met Ala Lys Met Phe Asp Leu Arg Thr Lys Ile Met Ile Gly Ile Glu
 -30 -25 -20
 Ser Ser Leu Leu Val Ala Ala Met Val Leu Leu Ser Val Val Phe Cys
 -15 -10 -5
 Leu Tyr Phe Lys Val Ala Lys Ala Leu Lys Ala Ala Lys Asp Pro Asp
 1 5 10 15
 Ala Val Ala Val Lys Asn His Asn Pro Asp Lys Val Cys Trp Ala Thr
 20 25 30
 Asn Ser Gln Ala Lys Ala Thr Thr Met Glu Ser Cys Pro Ser Leu Gln
 35 40 45
 Cys Cys Glu Gly Cys Arg Met His Ala Ser Ser Asp Ser Leu Pro Pro
 50 55 60
 Cys Cys Cys Asp Ile Asn Glu Gly Leu
 65 70

<210> 328
 <211> 81
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 328
 Met Ser Asp Glu Asp Glu Ser Ser Asp Tyr Leu Cys Leu Ser Ile Leu
 -25 -20 -15
 Gly Leu Phe Cys Cys Leu Pro Leu Ala Ile Pro Ala Val Ile Phe Ser
 -10 -5 1 5
 Cys Leu Thr Lys Asn Tyr Asn Lys Ser Ser Asp Tyr Glu Leu Ala Ala
 10 15 20

Lys Thr Ser Lys Gln Ala Tyr Tyr Trp Ala Ile Ala Ser Ile Thr Val
 25 30 35
 Gly Ile Leu Gly Thr Ile Leu Tyr Thr Tyr Leu Ile Tyr Leu Leu Arg
 40 45 50
 Leu

<210> 329
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<400> 329
 Met Thr Asp Gln Asp Arg Ile Ile Asn Leu Val Val Gly Ser Leu Thr
 -25 -20 -15
 Ser Leu Leu Ile Leu Val Thr Leu Ile Ser Ala Phe Val Phe Pro Gln
 -10 -5 1 5
 Leu Pro Pro Lys Pro Leu Asn Ile Phe Phe Ala Val Cys Ile Ser Leu
 10 15 20
 Ser Ser Ile Thr Ala Cys Ile Ile Tyr Trp Tyr Arg Gln Gly Asp Leu
 25 30 35
 Glu Pro Lys Phe Arg Lys Leu Ile Tyr Tyr Ile Ile Phe Ser Ile Ile
 40 45 50
 Met Leu Cys Ile Cys Ala Asn Leu Tyr Phe His Asp Val Gly Arg
 55 60 65

<210> 330
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 330
 Met Ala Ala Ala Val Pro Ser Leu Leu Leu Ser Leu Pro Pro His
 -20 -15 -10 -5
 Gln Gly Leu Thr Phe Ser Asn Lys Ile Gln Pro Phe Gly Ala Gln Gly
 1 5 10
 Val Leu His Pro Glu Pro Gly Leu Arg Asp Trp Leu Leu Pro Thr Cys
 15 20 25
 Ser Arg Gln Leu Arg Val Ala Leu Pro Glu Lys Gly Ser Glu Gly Ser
 30 35 40
 Leu Cys Gln Thr Gln Leu Pro Ala Thr Pro Cys Phe Leu Pro Ser Asn
 45 50 55 60
 Thr Val Arg Thr

<210> 331
 <211> 124
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL

<222> -32...-1

<400> 331

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Met Val Val Val Glu Pro Gly Ala Ser Leu Phe Pro Asn Gly Val Pro
    -30          -25          -20
Trp Leu Tyr Ala Val Phe Ala Val Leu Phe Val Phe Phe Leu Phe Ala
    -15          -10          -5
Met Leu Ser Pro Phe Leu Leu Glu Ile Asp Gln His Ile Lys Lys Phe
1      5      10      15
Leu Ile Arg Cys Arg Tyr Ser Leu His Asn Thr Val His Lys Asp Lys
    20      25      30
Lys Asn Ser Glu Ile Lys Met Asp His Leu Glu Arg Pro Gly Cys Pro
    35      40      45
Leu Glu Ser Pro Arg Arg Gly Val Leu Gly Gly Lys Lys Asn Gly Met
    50      55      60
Gly Asn Asp Pro Leu Leu Phe Val Lys Val Thr Lys Glu Pro Arg Asp
65      70      75      80
Ser Glu Ala Glu Ile Tyr Thr Pro Gly Pro Ser Val
    85          90

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<210> 332

<211> 62

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -46...-1

<400> 332

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Met Asp Gln Leu Val Phe Lys Glu Thr Ile Trp Asn Asp Ala Phe Trp
    -45          -40          -35
Gln Asn Pro Trp Asp Gln Gly Gly Leu Ala Val Ile Ile Leu Phe Ile
    -30          -25          -20          -15
Thr Ala Val Leu Leu Ile Leu Phe Ala Ile Val Phe Gly Leu Leu
    -10          -5      1
Thr Ser Thr Glu Asn Thr Gln Cys Glu Ala Gly Glu Glu Glu
    5      10      15

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<210> 333

<211> 150

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -23...-1

<400> 333

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Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys
    -20          -15          -10
Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys
    -5      1      5
Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Gly Cys
10      15      20      25
Leu Tyr Leu Ile Tyr Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe
    30      35      40
Val Leu Ser Val His Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys

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[illegible]

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<220>  
<221> SIGNAL  
<222> -13...-1
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<210> 335
<211> 88
<212> PRT
<213> Homo sapiens
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320

<400> 335

Met Val Pro Leu Pro Lys Gln Ser Leu Lys Phe Phe Cys Ala Leu Glu
 -20 -15 -10
 Val Val Leu Pro Ser Cys Asp Cys Arg Ser Pro Gly Ile Gly Leu Val
 -5 1 5
 Glu Glu Pro Met Asp Lys Val Glu Glu Gly Pro Leu Ser Phe Leu Met
 10 15 20
 Lys Arg Lys Thr Ala Gln Lys Leu Ala Ile Gln Lys Ala Leu Ser Asp
 25 30 35 40
 Ala Phe Gln Lys Leu Leu Ile Val Val Leu Gly Lys Thr Val Leu Ile
 45 50 55
 Ile Leu Glu Val Leu Gln Phe Gln
 60

<210> 336

<211> 150

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -45...-1

<400> 336

Met Val Leu Met Trp Thr Ser Gly Asp Ala Phe Lys Thr Ala Tyr Phe
 -45 -40 -35 -30
 Leu Leu Lys Gly Ala Pro Leu Gln Phe Ser Val Cys Gly Leu Leu Gln
 -25 -20 -15
 Val Leu Val Asp Leu Ala Ile Leu Gly Gln Ala Tyr Ala Phe Ala Pro
 -10 -5 1
 Pro Pro Glu Ala Gly Ala Pro Arg Arg Ala Pro His Trp His Gln Gly
 5 10 15
 Pro Leu Thr Val Gly Arg Thr Arg Met Trp Asp Arg Gln Pro Arg Ala
 20 25 30 35
 Leu Val Gly Pro Asp Leu Pro Ala Gly Arg Val Gly Ala Val Ala Pro
 40 45 50
 Ala Gly Val Ala Glu Met Gly His Gly His Trp Gly Leu His Gln Pro
 55 60 65
 Leu Trp Gly Val Ser Gly Trp Ala Val Gly Val Gly Leu Gly Arg Cys
 70 75 80
 Leu Cys Ser Ala Gly Thr Ala Arg Val Asp Leu Ala Pro Arg Val Leu
 85 90 95
 Asp Val Phe Arg Met Thr
 100 105

<210> 337

<211> 142

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<400> 337

Met Ala Thr Ala Ser Pro Ser Val Phe Leu Leu Met Val Asn Gly Gln
 -15 -10 -5
 Val Glu Ser Ala Gln Phe Pro Glu Tyr Asp Asp Phe Tyr Cys Lys Tyr

		1				5				10					
Cys	Phe	Val	Tyr	Gly	Gln	Asp	Trp	Ala	Pro	Thr	Ala	Gly	Leu	Glu	Glu
15						20					25				
Gly	Ile	Ser	Gln	Ile	Thr	Ser	Lys	Ser	Gln	Asp	Val	Arg	Gln	Ala	Leu
30					35					40					45
Val	Trp	Asn	Phe	Pro	Ile	Asp	Val	Thr	Phe	Lys	Ser	Thr	Asn	Pro	Tyr
				50					55					60	
Gly	Trp	Pro	Gln	Ile	Val	Leu	Ser	Val	Tyr	Gly	Pro	Asp	Val	Phe	Gly
			65					70					75		
Asn	Asp	Val	Val	Arg	Gly	Tyr	Gly	Ala	Val	His	Val	Pro	Phe	Ser	Pro
		80					85					90			
Gly	Arg	His	Lys	Arg	Thr	Ile	Pro	Met	Phe	Val	Pro	Glu	Ser	Thr	Ser
	95					100					105				
Lys	Leu	Gln	Lys	Phe	Thr	Arg	Ser	Ala	Ser	Cys	Ser	Thr	His		
110					115					120					

<210> 338
 <211> 112
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -27...-1

<220>
 <221> UNSURE
 <222> 21
 <223> Xaa = Ala,Pro

<400>	338														
Thr	Ser	Glu	Glu	Arg	Thr	Ala	Met	Lys	Arg	Glu	Gly	Gly	Ala	Ala	His
		-25					-20					-15			
Leu	Cys	Ser	Asp	Ser	Leu	Pro	Glu	Ser	Gln	Gln	Gln	Asp	Gly	Asn	His
	-10					-5					1				5
Ala	Pro	Asn	Phe	Ser	Ser	His	Gly	Ser	Cys	Arg	Arg	Arg	Gln	Arg	Xaa
				10					15					20	
Asp	Met	Thr	Arg	Arg	Cys	Met	Pro	Ala	Arg	Pro	Gly	Phe	Pro	Ser	Ser
		25						30					35		
Pro	Ala	Pro	Gly	Ser	Ser	Pro	Pro	Arg	Cys	His	Leu	Arg	Pro	Gly	Ser
		40					45					50			
Thr	Ala	His	Ala	Ala	Ala	Gly	Lys	Arg	Thr	Glu	Ser	Pro	Gly	Asp	Arg
	55					60					65				
Tyr	Arg	Ala	Glu	Gly	Leu	Arg	Arg	Gly	Arg	Val	Ala	Gly	Ala	Arg	Val
70					75					80					85

<210> 339
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 339
 Met Pro Cys Leu Asp Gln Gln Leu Thr Val His Ala Leu Pro Cys Pro
 -30 -25 -20

Ala Cys Lys
115

<210> 342
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39...-1

<400> 342
Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
 -35 -30 -25
Ile Phe Gly Tyr Lys Arg Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
 -20 -15 -10
Leu Phe Val Gly Cys Leu Ala Gly Tyr Gly Ala Tyr Arg Val Ser Asn
 -5 1 5
Asp Lys Arg Asp Val Lys Val Ser Leu Phe Thr Ala Phe Phe Leu Ala
10 15 20 25
Thr Ile Met Gly Val Arg Phe Lys Arg Ser Lys Lys Ile Met Pro Ala
 30 35 40
Gly Leu Val Ala Gly Leu Ser Leu Met Met Ile Leu Arg Leu Val Leu
 45 50 55
Leu Leu Leu
 60

<210> 343
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -43...-1

<400> 343
Met Cys Glu Thr Leu Leu Thr Ser Lys Trp Ala Ser Val Ser Pro Ile
 -40 -35 -30
Pro Ala Leu Leu Gln Glu Gly Glu Asn Arg Asp Ser Arg Arg Leu Gly
 -25 -20 -15
Asp Ala Leu Leu Phe Leu Arg Pro Ala Gly Ser Cys Ala Leu Gln Val
 -10 -5 1 5
Ser Trp Pro Ala Ala Leu Ala Gly Pro Arg Ser His Thr Gly Gln Leu
 10 15 20
Thr Gln His Phe Cys His Leu Lys Asn Asp Thr Cys Ile Pro Pro Ser
 25 30 35
Leu Gly Pro Pro Arg Asn Ser Gly Ser Leu Glu Ser Leu Arg Ser Lys
 40 45 50
Arg Tyr
 55

<210> 344
<211> 217
<212> PRT
<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -19...-1

<220>
 <221> UNSURE
 <222> 185
 <223> Xaa = Phe,Val

<400> 344
 Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser Leu
 -15 -10 -5
 Cys Cys Ser Ser Tyr Val Pro Ser Val Ala Pro Thr Ala Ala His Ser
 1 5 10
 Val Arg Val Pro His Ser Ala Gly His Cys Gly Gln Arg Val Leu Ala
 15 20 25
 Cys Ser Leu Pro Gln Val Phe Leu Lys Pro Trp Ile Phe Val Glu His
 30 35 40 45
 Phe Ser Ser Trp Leu Ser Leu Glu Leu Phe Ser Phe Leu Arg Tyr Leu
 50 55 60
 Gly Thr Leu Leu Cys Ala Cys Gly His Arg Leu Arg Glu Gly Arg Leu
 65 70 75
 Leu Pro Cys Leu Leu Gly Val Gly Ser Trp Leu Leu Phe Asn Asn Trp
 80 85 90
 Thr Gly Gly Ser Trp Phe Ser Leu His Leu Gln Gln Val Ser Leu Ser
 95 100 105
 Gln Gly Ser His Val Ala Ala Phe Leu Pro Glu Ala Ile Gly Pro Gly
 110 115 120 125
 Val Pro Val Pro Val Ser Gly Glu Ser Thr Ser Ala Gln Gln Ser His
 130 135 140
 Ala Gly Trp Gln Leu Ser Ala Glu Ala Asp Ala Cys Pro Ser Val Leu
 145 150 155
 Tyr Ser Glu Val Leu Glu Trp Asn Lys Asn Ile Asn Thr Tyr Thr Ser
 160 165 170
 Phe His Asp Phe Cys Leu Ile Leu Gly Ile Phe Xaa Val Leu Phe Cys
 175 180 185
 Phe Gly Gly Asp Arg Leu Thr Leu His
 190 195

<210> 345
 <211> 183
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 345
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 -20 -15 -10 -5
 Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
 1 5 10
 Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
 15 20 25
 Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
 30 35 40
 Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

45 50 55 60
 Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
 65 70 75
 Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
 80 85 90
 Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
 95 100 105
 Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
 110 115 120
 Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
 125 130 135 140
 Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
 145 150 155
 Asp Arg His Lys Met Leu Ser
 160

<210> 346
 <211> 247
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -13...-1

<400> 346
 Met Leu Val Leu Arg Ser Ala Leu Thr Arg Ala Leu Ala Ser Arg Thr
 -10 -5 1
 Leu Ala Pro Gln Met Cys Ser Ser Phe Ala Thr Gly Pro Arg Gln Tyr
 5 10 15
 Asp Gly Ile Phe Tyr Glu Phe Arg Ser Tyr Tyr Leu Lys Pro Ser Lys
 20 25 30 35
 Met Asn Glu Phe Leu Glu Asn Phe Glu Lys Asn Ala His Leu Arg Thr
 40 45 50
 Ala His Ser Glu Leu Val Gly Tyr Trp Ser Val Glu Phe Gly Gly Arg
 55 60 65
 Met Asn Thr Val Phe His Ile Trp Lys Tyr Asp Asn Phe Ala His Arg
 70 75 80
 Thr Glu Val Gln Lys Ala Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln
 85 90 95
 Phe Leu Ile Pro Asn Leu Ala Leu Ile Asp Lys Gln Glu Ser Glu Ile
 100 105 110 115
 Thr Tyr Leu Val Pro Trp Cys Lys Leu Glu Lys Pro Pro Lys Glu Gly
 120 125 130
 Val Tyr Glu Leu Ala Thr Phe Gln Met Lys Pro Gly Gly Pro Ala Leu
 135 140 145
 Trp Gly Asp Ala Phe Lys Arg Ala Val His Ala His Val Asn Leu Gly
 150 155 160
 Tyr Thr Lys Leu Val Gly Val Phe His Thr Glu Tyr Gly Ala Leu Asn
 165 170 175
 Arg Val His Val Leu Trp Trp Asn Glu Ser Ala Asp Ser Arg Ala Ala
 180 185 190 195
 Gly Arg His Lys Ser His Glu Asp Pro Arg Val Val Ala Ala Val Arg
 200 205 210
 Glu Ser Val Asn Tyr Leu Val Ser Gln Asn Met Leu Leu Ile Pro
 215 220 225
 Thr Ser Phe Ser Pro Leu Lys
 230

<210> 347
 <211> 104
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL .
 <222> -47...-1

<400> 347
 Met Phe Ser Pro Arg Gln Ala Leu Thr Pro Asp Pro Leu His Ser Pro
 -45 -40 -35
 Ala Tyr Ser Pro Val Leu Gly Gly Trp Ser Arg Phe Arg Ser Val Asp
 -30 -25 -20
 Phe Arg Phe Leu Tyr Leu Thr Leu Asn Gln Ser Cys Ile Phe Ala Asn
 -15 -10 -5 1
 Tyr Lys Glu Ala His Ala Asn Arg Tyr Cys Thr Glu Gly Arg Tyr Thr
 5 10 15
 Arg Glu Ile Gln Arg Leu Thr Ser Pro Ala Ala Trp Pro Thr Arg Asp
 20 25 30
 Lys Asn Arg Met Ile Ser Asn Gly Met Ala Leu Asn Ser Pro Ala Glu
 35 40 45
 Gly Leu Ala Phe Gln Cys Arg Phe
 50 55

<210> 348
 <211> 125
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -21...-1

<400> 348
 Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met Gly Val Gln Val Val
 -20 -15 -10
 Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu Phe Ala Ala Ser Arg
 -5 1 5 10
 Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala Ala
 15 20 25
 Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu Asn
 30 35 40
 Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys Asn Tyr Glu His Leu
 45 50 55
 Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln Ser
 60 65 70 75
 Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile Gln
 80 85 90
 Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His Thr
 95 100

<210> 349
 <211> 302
 <212> PRT
 <213> Homo sapiens

09876997.060001

[illegible]

Met	Ala	Pro	Asn -15	Ser	Ile	Thr	Leu	Leu -10	Gly	Leu	Ala	Val	Asn -5	Val	Val
Thr	Thr	Leu 1	Val	Leu	Ile 5	Ser	Tyr	Cys	Pro	Thr	Ala 10	Thr	Glu	Glu	Ala
Pro 15	Tyr	Trp	Thr	Tyr	Leu 20	Leu	Cys	Ala	Leu	Gly 25	Leu	Phe	Ile	Tyr	Gln 30
Ser	Leu	Asp	Ala	Ile 35	Asp	Gly	Lys	Gln	Ala 40	Arg	Arg	Thr	Asn	Ser	Cys
Ser	Pro	Leu	Gly 50	Glu	Leu	Phe	Asp 55	His	Gly	Cys	Asp	Ser	Leu 60	Ser	Thr
Val	Phe 65	Met	Ala	Val	Gly	Ala	Ser 70	Ile	Ala	Ala	Arg	Leu 75	Gly	Thr	Tyr
Pro	Asp 80	Trp	Phe	Phe	Phe	Cys 85	Ser	Phe	Ile	Gly	Met 90	Phe	Val	Phe	Tyr
Cys 95	Ala	His	Trp	Gln	Thr 100	Tyr	Val	Ser	Gly	Met 105	Leu	Arg	Phe	Gly	Lys 110
Val	Asp	Val	Thr	Glu 115	Ile	Gln	Ile	Ala	Leu 120	Val	Ile	Val	Phe	Val	Leu
Ser	Ala	Phe	Gly 130	Gly	Ala	Thr	Met	Trp 135	Asp	Tyr	Thr	Gly	Thr 140	Ser	Val
Leu	Ser 145	Pro	Gly	Leu	His	Ile	Gly 150	Leu	Ile	Ile	Ile	Leu 155	Ala	Ile	Met
Ile	Tyr 160	Lys	Lys	Ser	Ala	Thr 165	Asp	Val	Phe	Glu	Lys 170	His	Pro	Cys	Leu
Tyr 175	Ile	Leu	Met	Phe	Gly 180	Cys	Val	Phe	Ala	Lys 185	Val	Ser	Gln	Lys	Leu 190
Val	Val	Ala	His 195	Met	Thr	Lys	Ser	Glu	Leu 200	Tyr	Leu	Gln	Asp 205	Thr	Val
Phe	Leu	Gly	Pro 210	Gly	Leu	Leu	Phe	Leu 215	Asp	Gln	Tyr	Phe	Asn 220	Asn	Phe
Ile	Asp 225	Glu	Tyr	Val	Val	Leu	Trp 230	Met	Ala	Met	Val	Ile 235	Ser	Ser	Phe
Asp	Met 240	Val	Ile	Tyr	Phe	Ser	Ala 245	Leu	Cys	Leu	Gln 250	Ile	Ser	Arg	His
Leu 255	His	Leu	Asn	Ile	Phe 260	Lys	Thr	Ala	Cys	His 265	Gln	Ala	Pro	Glu	Gln 270
Val	Gln	Val	Leu 275	Ser	Ser	Lys	Ser	His 280	Gln	Asn	Asn	Met	Asp		

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<220>
<221> SIGNAL
<222> -14..-1
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Met Ile Leu Val Thr Val Pro Gly Val Cys Pro Ala Gln Cys Cys Trp
-10 -5 1
Ala Glu Gln Arg Gly Arg Gly Ser Gly Met Tyr Phe Ile Asp Lys Trp
5 10 15

Ala Arg Pro Ser Trp Val Pro His Trp Leu Asn Asp Leu Phe Ile Val
 20 25 30
 Lys Ser Gly Tyr Leu Val Cys Ile Arg Thr Thr Val Ile Arg Gln Gly
 35 40 45 50
 Ile Val Arg Ile Gly Arg Asn Lys Ile Ser Glu Ser Gly Arg Ser Ala
 55 60 65
 Leu Tyr Thr Ile Ala Lys Asn Lys Met Val Ile Phe Lys Val Pro Asp
 70 75 80
 Cys Met His Leu Asn Ala Asp Tyr Phe Gly Val
 85 90

<210> 351
 <211> 229
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -34...-1

<400> 351
 Met Ser Phe Leu Gln Asp Pro Ser Phe Phe Thr Met Gly Met Trp Ser
 -30 -25 -20
 Ile Gly Ala Gly Ala Leu Gly Ala Ala Ala Leu Ala Leu Leu Ala
 -15 -10 -5
 Asn Thr Asp Val Phe Leu Ser Lys Pro Gln Lys Ala Ala Leu Glu Tyr
 1 5 10
 Leu Glu Asp Ile Asp Leu Lys Thr Leu Glu Lys Glu Pro Arg Thr Phe
 15 20 25 30
 Lys Ala Lys Glu Leu Trp Glu Lys Asn Gly Ala Val Ile Met Ala Val
 35 40 45
 Arg Arg Pro Gly Cys Phe Leu Cys Arg Glu Glu Ala Ala Asp Leu Ser
 50 55 60
 Ser Leu Lys Ser Met Leu Asp Gln Leu Gly Val Pro Leu Tyr Ala Val
 65 70 75
 Val Lys Glu His Ile Arg Thr Glu Val Lys Asp Phe Gln Pro Tyr Phe
 80 85 90
 Lys Gly Glu Ile Phe Leu Asp Glu Lys Lys Lys Phe Tyr Gly Pro Gln
 95 100 105 110
 Arg Arg Lys Met Met Phe Met Gly Phe Ile Arg Leu Gly Val Trp Tyr
 115 120 125
 Asn Phe Phe Arg Ala Trp Asn Gly Gly Phe Ser Gly Asn Leu Glu Gly
 130 135 140
 Glu Gly Phe Ile Leu Gly Gly Val Phe Val Val Gly Ser Gly Lys Gln
 145 150 155
 Gly Ile Leu Leu Glu His Arg Glu Lys Glu Phe Gly Asp Lys Val Asn
 160 165 170
 Leu Leu Ser Val Leu Glu Ala Ala Lys Met Ile Lys Pro Gln Thr Leu
 175 180 185 190
 Ala Ser Glu Lys Lys
 195

<210> 352
 <211> 206
 <212> PRT
 <213> Homo sapiens

<220>

<221> SIGNAL
<222> -34...-1

<400> 352

Met	Ser	Phe	Leu	Gln	Asp	Pro	Ser	Phe	Phe	Thr	Met	Gly	Met	Trp	Ser
			-30						-25					-20	
Ile	Gly	Ala	Gly	Ala	Leu	Gly	Ala	Ala	Ala	Leu	Ala	Leu	Leu	Leu	Ala
		-15					-10					-5			
Asn	Thr	Asp	Val	Phe	Leu	Ser	Lys	Pro	Gln	Lys	Ala	Ala	Leu	Glu	Tyr
	1				5					10					
Leu	Glu	Asp	Ile	Asp	Leu	Lys	Thr	Leu	Glu	Lys	Glu	Pro	Arg	Thr	Phe
15					20				25					30	
Lys	Ala	Lys	Glu	Leu	Trp	Glu	Lys	Asn	Gly	Ala	Val	Ile	Met	Ala	Val
			35					40					45		
Arg	Arg	Pro	Gly	Cys	Phe	Leu	Cys	Arg	Glu	Glu	Ala	Ala	Asp	Leu	Ser
		50					55						60		
Ser	Leu	Lys	Ser	Met	Leu	Asp	Gln	Leu	Gly	Val	Pro	Leu	Tyr	Ala	Val
	65					70					75				
Val	Lys	Glu	His	Ile	Arg	Thr	Glu	Val	Lys	Asp	Phe	Gln	Pro	Tyr	Phe
	80				85					90					
Lys	Gly	Glu	Ile	Phe	Leu	Asp	Glu	Lys	Lys	Lys	Phe	Tyr	Gly	Pro	Gln
95					100					105				110	
Arg	Arg	Lys	Met	Met	Phe	Met	Gly	Phe	Ile	Arg	Leu	Gly	Val	Trp	Tyr
			115					120						125	
Asn	Phe	Phe	Arg	Ala	Trp	Asn	Gly	Gly	Phe	Ser	Gly	Asn	Leu	Glu	Gly
			130				135					140			
Glu	Gly	Phe	Ile	Leu	Gly	Gly	Val	Phe	Val	Val	Gly	Ser	Gly	Ser	Arg
		145				150					155				
Ala	Phe	Phe	Leu	Ser	Thr	Glu	Lys	Lys	Asn	Leu	Glu	Thr	Lys		
	160					165					170				

<210> 353
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -44...-1

<400> 353

Met	Ala	Ala	Glu	Gly	Trp	Ile	Trp	Arg	Trp	Gly	Trp	Gly	Arg	Arg	Cys
			-40						-35					-30	
Leu	Gly	Arg	Pro	Gly	Leu	Leu	Gly	Pro	Gly	Pro	Gly	Pro	Thr	Thr	Pro
		-25						-20					-15		
Leu	Phe	Leu	Leu	Leu	Leu	Leu	Gly	Ser	Val	Thr	Ala	Asp	Ile	Thr	Asp
		-10					-5					1			
Gly	Asn	Ile	Glu	His	Leu	Lys	Arg	Glu	His	Ser	Leu	Ile	Lys	Pro	Tyr
5					10					15				20	
Gln	Gly	Val	Gly	Ser	Ser	Ser	Pro	Ser	Gly	Thr	Ser	Arg	Ala	Ala	Leu
			25					30					35		
Cys	Ser	Arg	Ala	Ser	Thr	Tyr	Val								
			40												

<210> 354
<211> 151
<212> PRT
<213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -32...-1

<400> 354
 Met Asp Ser Ala Ser Asn Pro Thr Asn Leu Val Ser Thr Ser Gln Arg
 -30 -25 -20
 His Arg Pro Leu Leu Ser Ser Cys Gly Leu Pro Pro Ser Thr Ala Ser
 -15 -10 -5
 Ala Val Arg Arg Leu Cys Ser Arg Gly Val Leu Lys Gly Ser Asn Glu
 1 5 10 15
 Arg Arg Asp Met Glu Ser Phe Trp Lys Leu Asn Arg Ser Pro Gly Ser
 20 25 30
 Asp Arg Tyr Leu Glu Ser Arg Asp Ala Ser Arg Leu Ser Gly Arg Asp
 35 40 45
 Pro Ser Ser Trp Thr Val Glu Asp Val Met Gln Phe Val Arg Glu Ala
 50 55 60
 Asp Pro Gln Leu Gly Pro His Ala Asp Leu Phe Arg Lys His Glu Ile
 65 70 75 80
 Asp Gly Lys Ala Leu Leu Leu Leu Arg Ser Asp Met Met Met Lys Tyr
 85 90 95
 Met Gly Leu Lys Leu Gly Pro Ala Leu Lys Leu Ser Tyr His Ile Asp
 100 105 110
 Arg Leu Lys Gln Gly Lys Phe
 115

<210> 355
 <211> 65
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -16...-1

<400> 355
 Met Ala Glu Leu Ala Cys Val Arg Glu Ser Thr Ser Val Ala Trp Ala
 -15 -10 -5
 Cys Lys Val Arg Gly Gly Thr Ala Pro Ser Pro Ser Gly Ala Glu Gly
 1 5 10 15
 His Val Met Leu Asn Lys Ser Arg Glu Val Glu Ser Pro Val Ser Ser
 20 25 30
 Arg Pro Arg Cys Gly Met Pro Thr Val Pro Pro Gly Ser Leu Lys Thr
 35 40 45
 Leu

<210> 356
 <211> 189
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -24...-1

<220>
 <221> UNSURE

<222> 41

<223> Xaa = Ala,Gly

<400> 356

Met	Glu	Glu	Gly	Gly	Asn	Leu	Gly	Gly	Leu	Ile	Lys	Met	Val	His	Leu
			-20					-15						-10	
Leu	Val	Leu	Ser	Gly	Ala	Trp	Gly	Met	Gln	Met	Trp	Val	Thr	Phe	Val
		-5					1				5				
Ser	Gly	Phe	Leu	Leu	Phe	Arg	Ser	Leu	Pro	Arg	His	Thr	Phe	Gly	Leu
10					15					20					
Val	Gln	Ser	Lys	Leu	Phe	Pro	Phe	Tyr	Phe	His	Ile	Ser	Met	Gly	Cys
25				30					35						40
Xaa	Phe	Ile	Asn	Leu	Cys	Ile	Leu	Ala	Ser	Gln	His	Ala	Trp	Ala	Gln
			45					50					55		
Leu	Thr	Phe	Trp	Glu	Ala	Ser	Gln	Leu	Tyr	Leu	Leu	Phe	Leu	Ser	Leu
		60					65					70			
Thr	Leu	Ala	Thr	Val	Asn	Ala	Arg	Trp	Leu	Glu	Pro	Arg	Thr	Thr	Ala
	75					80					85				
Ala	Met	Trp	Ala	Leu	Gln	Thr	Val	Glu	Lys	Glu	Arg	Gly	Leu	Gly	Gly
90					95					100					
Glu	Val	Pro	Gly	Ser	His	Gln	Gly	Pro	Asp	Pro	Tyr	Arg	Gln	Leu	Arg
105					110					115					120
Glu	Lys	Asp	Pro	Lys	Tyr	Ser	Ala	Leu	Arg	Gln	Asn	Phe	Phe	Arg	Tyr
				125				130					135		
His	Gly	Leu	Ser	Ser	Leu	Cys	Asn	Leu	Gly	Cys	Val	Leu	Ser	Asn	Gly
		140					145					150			
Leu	Cys	Leu	Ala	Gly	Leu	Ala	Leu	Glu	Ile	Arg	Ser	Leu			
	155						160					165			

<210> 357

<211> 183

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -47...-1

<400> 357

Met	Thr	Glu	Cys	Thr	Ser	Leu	Gln	Phe	Val	Ser	Pro	Phe	Ala	Phe	Glu
	-45					-40					-35				
Ala	Met	Gln	Lys	Val	Asp	Val	Val	Cys	Leu	Ala	Ser	Leu	Ser	Asp	Pro
-30				-25					-20						
Glu	Leu	Arg	Leu	Leu	Leu	Pro	Cys	Leu	Val	Arg	Met	Ala	Leu	Cys	Ala
-15				-10					-5					1	
Pro	Ala	Asp	Gln	Ser	Gln	Ser	Trp	Ala	Gln	Asp	Lys	Lys	Leu	Ile	Leu
	5					10						15			
Arg	Leu	Leu	Ser	Gly	Val	Glu	Ala	Val	Asn	Ser	Ile	Val	Ala	Leu	Leu
	20				25						30				
Ser	Val	Asp	Phe	His	Ala	Leu	Glu	Gln	Asp	Ala	Ser	Lys	Glu	Gln	Gln
35				40					45						
Leu	Arg	Pro	Ser	Leu	Ala	Leu	Leu	Pro	Arg	Leu	Glu	Cys	Gly	Gly	Val
50				55				60						65	
Ile	Ser	Ala	His	Cys	Asn	Leu	His	Leu	Leu	Gly	Ser	Ser	Asp	Ser	Ser
		70					75						80		
Ala	Ser	Val	Ser	Arg	Val	Asp	Gly	Thr	Gly	Thr	Arg	His	His	Ala	
	85					90					95				
Arg	Leu	Phe	Cys	Ile	Ile	Ser	Arg	Asp	Glu	Val	Ser	Pro	Tyr	Trp	Pro

100 105 110
 Gly Trp Ser Arg Thr Pro Asn Leu Val Ile His Leu Pro Gln Pro Pro
 115 120 125
 Lys Val Leu Gly Leu Pro Ala
 130 135

<210> 358
 <211> 102
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -14...-1

<400> 358
 Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
 -10 -5 1
 Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
 5 10 15
 Gln Asn Met Ile Arg Arg Leu Glu Ile Glu Ala Glu Asn His Tyr Trp
 20 25 30
 Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Ala
 35 40 45 50
 Val Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Thr Ser
 55 60 65
 Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
 70 75 80
 Val Thr Lys Lys Trp Ser
 85

<210> 359
 <211> 244
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -29...-1

<400> 359
 Met Glu Leu Thr Ile Phe Ile Leu Arg Leu Ala Ile Tyr Ile Leu Thr
 -25 -20 -15
 Phe Pro Leu Tyr Leu Leu Asn Phe Leu Gly Leu Trp Ser Trp Ile Cys
 -10 -5 1
 Lys Lys Trp Phe Pro Tyr Phe Leu Val Arg Phe Thr Val Ile Tyr Asn
 5 10 15
 Glu Gln Met Ala Ser Lys Lys Arg Glu Leu Phe Ser Asn Leu Gln Glu
 20 25 30 35
 Phe Ala Gly Pro Ser Gly Lys Leu Ser Leu Leu Glu Val Gly Cys Gly
 40 45 50
 Thr Gly Ala Asn Phe Lys Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys
 55 60 65
 Ile Asp Pro Asn Pro Asn Phe Glu Lys Phe Leu Ile Lys Ser Ile Ala
 70 75 80
 Glu Asn Arg His Leu Gln Phe Glu Arg Phe Val Val Ala Ala Gly Glu
 85 90 95
 Asn Met His Gln Val Ala Asp Gly Ser Val Asp Val Val Val Cys Thr

100 105 110 115
 Leu Val Leu Cys Ser Val Lys Asn Gln Glu Arg Ile Leu Arg Glu Val
 120 125 130
 Cys Arg Val Leu Arg Pro Gly Gly Ala Phe Tyr Phe Met Glu His Val
 135 140 145
 Ala Ala Glu Cys Ser Thr Trp Asn Tyr Phe Trp Gln Gln Val Leu Asp
 150 155 160
 Pro Ala Trp His Leu Leu Phe Asp Gly Cys Asn Leu Thr Arg Glu Ser
 165 170 175
 Trp Lys Ala Leu Glu Arg Ala Ser Phe Ser Lys Leu Lys Leu Gln His
 180 185 190 195
 Ile Gln Ala Pro Leu Ser Trp Glu Leu Val Arg Pro His Ile Tyr Gly
 200 205 210
 Tyr Ala Val Lys
 215

<210> 360
 <211> 177
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -23...-1

<400> 360
 Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile Cys
 -20 -15 -10
 Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr Lys
 -5 1 5
 Val Gly Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val Lys
 10 15 20 25
 Gly Ser Pro Ser His Cys Leu Pro Tyr Leu Leu Asp Lys Leu Cys Cys
 30 35 40
 Asp Phe Ala Asn Met Asp Ile Phe Gln Gly Cys Leu Tyr Leu Ile Tyr
 45 50 55
 Asn Leu Leu Gln Ala Val Phe Phe Val Leu Phe Val Leu Ser Val His
 60 65 70
 Tyr Leu Trp Lys Lys Trp Lys Lys His Gln Lys Lys Leu Lys Lys Gln
 75 80 85
 Ala Ser Leu Glu Lys Pro Gly Asn Asp Leu Glu Ser Pro Leu Ile Asn
 90 95 100 105
 Asn Ile Asp Gln Thr Leu His Arg Val Ala Thr Thr Ala Ser Val Ile
 110 115 120
 Tyr Lys Ile Trp Glu His Arg Ser His His Pro Ser Ser Lys Lys Ile
 125 130 135
 Lys His Cys Lys Leu Lys Lys Lys Ser Lys Glu Glu Gly Ala Arg Arg
 140 145 150
 Tyr

<210> 361
 <211> 158
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> -21...-1

<400> 361

Met	Ala	Leu	Cys	Ala	Leu	Thr	Arg	Ala	Leu	Pro	Ser	Leu	Asn	Leu	Ala
-20						-15					-10				
Pro	Pro	Thr	Val	Ala	Ala	Pro	Ala	Pro	Ser	Leu	Phe	Pro	Ala	Ala	Gln
-5					1				5					10	
Met	Met	Asn	Asn	Gly	Leu	Leu	Gln	Gln	Pro	Ser	Ala	Leu	Met	Leu	Leu
		15					20					25			
Pro	Cys	Arg	Pro	Val	Leu	Thr	Ser	Val	Ala	Leu	Asn	Ala	Asn	Phe	Val
	30						35				40				
Ser	Trp	Lys	Ser	Arg	Thr	Lys	Tyr	Thr	Ile	Thr	Pro	Val	Lys	Met	Arg
	45					50					55				
Lys	Ser	Gly	Gly	Arg	Asp	His	Thr	Gly	Ala	Gly	Asn	Val	Arg	Arg	Thr
60					65					70					75
Val	Gly	Arg	Val	Ser	Asn	Val	Asp	His	Asn	Lys	Arg	Val	Ile	Gly	Lys
				80					85					90	
Ala	Gly	Arg	Asn	Arg	Trp	Leu	Gly	Lys	Arg	Pro	Asn	Ser	Gly	Arg	Trp
			95					100					105		
His	Arg	Lys	Gly	Gly	Trp	Ala	Gly	Arg	Lys	Ile	Arg	Pro	Leu	Pro	Pro
		110					115					120			
Met	Lys	Ser	Tyr	Val	Lys	Leu	Pro	Ser	Ala	Ser	Ala	Gln	Ser		
	125					130					135				

<210> 362

<211> 186

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -19...-1

<400> 362

Met	Ala	Thr	Ala	Ser	Pro	Ser	Val	Phe	Leu	Leu	Met	Val	Asn	Gly	Gln
				-15					-10					-5	
Val	Glu	Ser	Ala	Gln	Phe	Pro	Glu	Tyr	Asp	Asp	Leu	Tyr	Cys	Lys	Tyr
			1				5					10			
Cys	Phe	Val	Tyr	Gly	Gln	Asp	Trp	Ala	Pro	Thr	Ala	Gly	Leu	Glu	Glu
	15				20						25				
Gly	Ile	Ser	Gln	Ile	Thr	Ser	Lys	Ser	Gln	Asp	Val	Arg	Gln	Ala	Leu
30					35					40					45
Val	Trp	Asn	Phe	Pro	Ile	Asp	Val	Thr	Phe	Lys	Ser	Thr	Asn	Pro	Tyr
				50					55					60	
Gly	Trp	Pro	Gln	Ile	Val	Leu	Ser	Val	Tyr	Gly	Pro	Asp	Val	Phe	Gly
			65					70					75		
Asn	Asp	Val	Val	Arg	Gly	Tyr	Gly	Ala	Val	His	Val	Pro	Phe	Ser	Pro
		80					85					90			
Gly	Arg	His	Lys	Arg	Thr	Ile	Pro	Met	Phe	Val	Pro	Glu	Ser	Thr	Ser
		95				100					105				
Lys	Leu	Gln	Lys	Phe	Thr	Ser	Trp	Phe	Met	Gly	Arg	Arg	Pro	Glu	Tyr
110					115					120					125
Thr	Asp	Pro	Lys	Val	Val	Ala	Gln	Gly	Glu	Gly	Arg	Glu	Ala	Ile	Thr
				130					135					140	
Ala	Pro	Arg	Lys	Ala	Val	Phe	Ser	Val	His	Gly	Leu	Thr	Ser	Pro	Arg
			145					150					155		
Ala	Leu	Ala	Leu	Val	His	Ile	Lys	Gly	Thr						
	160						165								

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<220>
 <221> SIGNAL
 <222> -26...-1

<400> 365
 Met Ala Ala Ile Glu Ile Glu Val Lys Pro Asn Gln Gly Phe Cys Gly
 -25 -20 -15
 Ser Ala Cys Leu Leu Ala Val Ile Arg Ala Phe Phe Phe Lys Lys Asn
 -10 -5 1 5
 Ala Cys Leu Leu Arg Glu Ile Leu Gln Ser Lys Leu Gly Gly Met Gly
 10 15 20
 Pro Val Val Phe Ser Tyr Arg Gly Leu Pro Leu Trp Leu Phe Ala Trp
 25 30 35
 Leu Phe Pro Arg Cys Thr Val Pro Leu Thr Phe Gly Phe Glu Asn Met
 40 45 50
 Arg Gly Leu Gly Val Val Ala Tyr Ala Cys Asn Pro Ser Thr
 55 60 65

<210> 366
 <211> 140
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40...-1

<400> 366
 Met Thr Ser Met Thr Gln Ser Leu Arg Glu Val Ile Lys Ala Met Thr
 -40 -35 -30 -25
 Lys Ala Arg Asn Phe Glu Arg Val Leu Gly Lys Ile Thr Leu Val Ser
 -20 -15 -10
 Ala Ala Pro Gly Lys Val Ile Cys Glu Met Lys Val Glu Glu Glu His
 -5 1 5
 Thr Asn Ala Ile Gly Thr Leu His Gly Gly Leu Thr Ala Thr Leu Val
 10 15 20
 Asp Asn Ile Ser Thr Met Ala Leu Leu Cys Thr Glu Arg Gly Ala Pro
 25 30 35 40
 Gly Val Ser Val Asp Met Asn Ile Thr Tyr Met Ser Pro Ala Lys Leu
 45 50 55
 Gly Glu Asp Ile Val Ile Thr Ala His Val Leu Lys Gln Gly Lys Thr
 60 65 70
 Leu Ala Phe Thr Ser Val Asp Leu Thr Asn Lys Ala Thr Gly Lys Leu
 75 80 85
 Ile Ala Gln Gly Arg His Thr Lys His Leu Gly Asn
 90 95 100

<210> 367
 <211> 39
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -35...-1

<400> 367

Met Asp Pro Gly Trp Pro His Phe Lys Leu Thr His Ser Arg Cys Met
 -35 -30 -25 -20
 Ala Val Leu Phe Leu Gly Thr Leu Pro Leu Cys Pro Val Thr Ser Pro
 -15 -10 -5
 Val Trp Gly Trp Ser Pro Gly
 1

<210> 368
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -41...-1

<400> 368
 Met Ser Ala Ser Val Val Ser Val Ile Ser Arg Phe Leu Glu Glu Tyr
 -40 -35 -30
 Leu Ser Ser Thr Pro Gln Arg Leu Lys Leu Leu Asp Ala Tyr Leu Leu
 -25 -20 -15 -10
 Tyr Ile Leu Leu Thr Gly Ala Leu Gln Phe Gly Tyr Cys Leu Leu Val
 -5 1 5
 Gly Thr Phe Pro Phe Asn Ser Phe Leu Ser Gly Phe Ile Ser Cys Val
 10 15 20
 Gly Ser Phe Ile Leu Ala Gly Ser Leu Phe Glu Phe Pro Gly
 25 30 35

<210> 369
 <211> 83
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -40...-1

<400> 369
 Met Gly Leu Thr Ser Thr Trp Arg Tyr Gly Arg Gly Pro Gly Ile Gly
 -40 -35 -30 -25
 Thr Val Thr Met Val Ser Trp Gly Arg Phe Ile Cys Leu Val Val Val
 -20 -15 -10
 Thr Met Ala Thr Leu Ser Leu Ala Arg Pro Ser Phe Ser Leu Val Glu
 -5 1 5
 Asp Thr Thr Leu Glu Pro Glu Asp Ala Ile Ser Ser Gly Asp Asp Glu
 10 15 20
 Asp Asp Thr Asp Gly Ala Glu Asp Phe Val Ser Glu Asn Ser Asn Asn
 25 30 35 40
 Lys Ser Lys

<210> 370
 <211> 92
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -15...-1

<400> 370

Met	Ala	Val	Leu	Ala	Gly	Ser	Leu	Leu	Gly	Pro	Thr	Ser	Arg	Ser	Ala
-15					-10					-5					1
Ala	Leu	Leu	Gly	Gly	Arg	Trp	Leu	Gln	Pro	Arg	Ala	Trp	Leu	Gly	Phe
		5						10					15		
Pro	Asp	Ala	Trp	Gly	Leu	Pro	Thr	Pro	Gln	Gln	Ala	Arg	Gly	Lys	Ala
	20					25						30			
Arg	Gly	Asn	Glu	Tyr	Gln	Pro	Ser	Asn	Ile	Lys	Arg	Lys	Asn	Lys	His
	35				40						45				
Gly	Trp	Val	Arg	Arg	Leu	Ser	Thr	Pro	Ala	Gly	Val	Gln	Val	Ile	Leu
50					55					60					65
Arg	Arg	Met	Leu	Lys	Gly	Arg	Lys	Ser	Leu	Ser	His				
			70						75						

<210> 371

<211> 279

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -42...-1

<400> 371

Met	Ala	Ala	Pro	Val	Arg	Arg	Thr	Leu	Leu	Gly	Val	Ala	Gly	Gly	Trp
	-40						-35					-30			
Arg	Arg	Phe	Glu	Arg	Leu	Trp	Ala	Gly	Ser	Leu	Ser	Ser	Arg	Ser	Leu
	-25					-20					-15				
Ala	Leu	Ala	Ala	Ala	Pro	Ser	Ser	Asn	Gly	Ser	Pro	Trp	Arg	Leu	Leu
-10					-5					1				5	
Gly	Ala	Leu	Cys	Leu	Gln	Arg	Pro	Pro	Val	Val	Ser	Lys	Pro	Leu	Thr
		10					15						20		
Pro	Leu	Gln	Glu	Glu	Met	Ala	Ser	Leu	Leu	Gln	Gln	Ile	Glu	Ile	Glu
	25					30						35			
Arg	Ser	Leu	Tyr	Ser	Asp	His	Glu	Leu	Arg	Ala	Leu	Asp	Glu	Asn	Gln
	40				45						50				
Arg	Leu	Ala	Lys	Lys	Lys	Ala	Asp	Leu	His	Asp	Glu	Glu	Asp	Glu	Gln
55					60					65				70	
Asp	Ile	Leu	Leu	Ala	Gln	Asp	Leu	Glu	Asp	Met	Trp	Glu	Gln	Lys	Phe
			75					80						85	
Leu	Gln	Phe	Lys	Leu	Gly	Ala	Arg	Ile	Thr	Glu	Ala	Asp	Glu	Lys	Asn
		90					95					100			
Asp	Arg	Thr	Ser	Leu	Asn	Arg	Asn	Leu	Asp	Arg	Asn	Leu	Val	Leu	Leu
	105					110					115				
Val	Arg	Glu	Lys	Phe	Gly	Asp	Gln	Asp	Val	Trp	Ile	Leu	Pro	Gln	Ala
	120				125						130				
Glu	Trp	Gln	Pro	Gly	Glu	Thr	Leu	Arg	Gly	Thr	Ala	Glu	Arg	Thr	Leu
135					140					145					150
Ala	Thr	Leu	Ser	Glu	Asn	Asn	Met	Glu	Ala	Lys	Phe	Leu	Gly	Asn	Ala
			155					160						165	
Pro	Cys	Gly	His	Tyr	Thr	Phe	Lys	Phe	Pro	Gln	Ala	Met	Arg	Thr	Glu
			170				175					180			
Ser	Asn	Leu	Gly	Ala	Lys	Val	Phe	Phe	Phe	Lys	Ala	Leu	Leu	Leu	Thr
	185					190						195			
Gly	Asp	Phe	Ser	Gln	Ala	Gly	Asn	Lys	Gly	His	His	Val	Trp	Val	Ile
	200				205					210					
Lys	Asp	Glu	Leu	Gly	Asp	Tyr	Leu	Lys	Pro	Lys	Tyr	Leu	Ala	Gln	Val

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<220>
<221> SIGNAL
<222> -31...-1

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<210> 373
<211> 101
<212> PRT
<213> Homo sapiens
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<220>  
<221> SIGNAL  
<222> -42..-1
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340

25 30 35
 Ile Ile Val Ala Arg Lys Met Glu Tyr Thr Lys Trp Thr Gly Leu Ala
 40 45 50
 Cys Thr His Arg Asp
 55

<210> 374
 <211> 85
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 374
 Met Gly Pro Asn Thr Lys Asn Leu Leu Leu Val Thr Leu Val Ala Ser
 -20 -15 -10 -5
 Thr Val Pro Gly Asn Ser Leu Gly Gln Asp Phe Thr Phe Ala His Leu
 1 5 10
 Glu Arg Ser Cys Thr Arg Glu Asn Arg Ser Pro Gly Glu Val Phe Gln
 15 20 25
 Gln Pro Cys Lys Ser Gly Gly Gly Val Gly Glu Pro Asn Ala Gln
 30 35 40
 Gly Gln Leu Leu Ser Gln His Pro Leu Pro Ala Phe Ile Asn Cys Ser
 45 50 55 60
 His Gly Gln Ala Phe
 65

<210> 375
 <211> 90
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -28...-1

<400> 375
 Met Ala Phe Pro Gly Gln Ser Asp Thr Lys Met Gln Trp Pro Glu Val
 -25 -20 -15
 Pro Ala Leu Pro Leu Leu Ser Ser Leu Cys Met Ala Met Val Arg Lys
 -10 -5 1
 Ser Ser Ala Leu Gly Lys Glu Val Gly Arg Arg Val Lys Glu Met Val
 5 10 15 20
 Met Leu Val Ala Pro Phe Arg Gln Ser Ser Leu Ser Arg Thr Phe
 25 30 35
 Ser Ser Arg Lys Val Val Lys Ala His Ala Ser Leu His Gly Ala Arg
 40 45 50
 Leu Ser Pro Leu Ser Arg Asn Ile Arg Gly
 55 60

<210> 376
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>

<222> -14...-1

<220>

<221> UNSURE

<222> 50

<223> Xaa = Ala,Gly

<220>

<221> UNSURE

<222> 51

<223> Xaa = Leu,Met,Val

<400> 378

Met Phe Leu Thr Ala Leu Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln
 -10 -5 1
Trp Ile Gly Lys His Arg Arg Pro Arg Phe Val Ser Leu Arg Ala Lys
 5 10 15
Gln Asn Met Ile Arg Arg Leu Glu Ile Asp Ala Glu Asn His Tyr Trp
 20 25 30
Leu Ser Met Pro Tyr Met Thr Arg Glu Gln Glu Arg Gly His Ala Xaa
35 40 45 50
Xaa Arg Arg Arg Glu Ala Phe Glu Ala Ile Lys Ala Ala Ala Thr Ser
 55 60 65
Lys Phe Pro Pro His Arg Phe Ile Ala Asp Gln Leu Asp His Leu Asn
 70 75 80
Val Thr Lys Lys Trp Ser
 85

<210> 379

<211> 504

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -24...-1

<400> 379

Met Gly Ile Lys Thr Ala Leu Pro Ala Ala Glu Leu Gly Leu Tyr Ser
 -20 -15 -10
Leu Val Leu Ser Gly Ala Leu Ala Tyr Ala Gly Arg Gly Leu Leu Glu
 -5 1 5
Ala Ser Gln Asp Gly Ala His Arg Lys Ala Phe Arg Glu Ser Val Arg
 10 15 20
Pro Gly Trp Glu Tyr Ile Gly Arg Lys Met Asp Val Ala Asp Phe Glu
25 30 35 40
Trp Val Met Trp Phe Thr Ser Phe Arg Asn Val Ile Ile Phe Ala Leu
 45 50 55
Ser Gly His Val Leu Phe Ala Lys Leu Cys Thr Met Val Ala Pro Lys
 60 65 70
Leu Arg Ser Trp Met Tyr Ala Val Tyr Gly Ala Leu Ala Val Met Gly
 75 80 85
Thr Met Gly Pro Trp Tyr Leu Leu Leu Leu Gly His Cys Val Gly
 90 95 100
Leu Tyr Val Ala Ser Leu Leu Gly Gln Pro Trp Leu Cys Leu Gly Leu
105 110 115 120
Gly Leu Ala Ser Leu Ala Ser Phe Lys Met Asp Pro Leu Ile Ser Trp
 125 130 135

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Gln	Ser	Gly	Phe	Val	Thr	Gly	Thr	Phe	Asp	Leu	Gln	Glu	Val	Leu	Phe
			140					145					150		
His	Gly	Gly	Ser	Ser	Phe	Thr	Val	Leu	Arg	Cys	Thr	Ser	Phe	Ala	Leu
		155					160					165			
Glu	Ser	Cys	Ala	His	Pro	Asp	Arg	His	Tyr	Ser	Leu	Ala	Asp	Leu	Leu
	170					175					180				
Lys	Tyr	Ser	Phe	Tyr	Leu	Pro	Phe	Phe	Phe	Phe	Gly	Pro	Ile	Met	Thr
185					190					195					200
Phe	Asp	Arg	Phe	His	Ala	Gln	Val	Ser	Gln	Val	Glu	Pro	Val	Arg	Arg
			205						210					215	
Glu	Gly	Glu	Leu	Trp	His	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Ser	Val	Val
			220					225					230		
Ala	Ile	Met	Ala	Val	Asp	Ile	Phe	His	Phe	Phe	Tyr	Ile	Leu	Thr	
		235					240				245				
Ile	Pro	Ser	Asp	Leu	Lys	Phe	Ala	Asn	Arg	Leu	Pro	Asp	Ile	Ala	Leu
	250					255					260				
Ala	Gly	Leu	Ala	Tyr	Ser	Asn	Leu	Val	Tyr	Asp	Trp	Val	Lys	Ala	Ala
265					270					275					280
Val	Leu	Phe	Gly	Val	Val	Asn	Thr	Val	Ala	Cys	Leu	Asp	His	Leu	Asp
			285						290					295	
Pro	Pro	Gln	Pro	Pro	Lys	Cys	Ile	Thr	Ala	Leu	Tyr	Val	Phe	Ala	Glu
			300					305					310		
Thr	His	Phe	Asp	Arg	Gly	Ile	Asn	Asp	Trp	Leu	Cys	Lys	Tyr	Val	Tyr
		315					320					325			
Asn	His	Ile	Gly	Gly	Glu	His	Ser	Ala	Val	Ile	Pro	Glu	Leu	Ala	Ala
	330					335					340				
Thr	Val	Ala	Thr	Phe	Ala	Ile	Thr	Thr	Leu	Trp	Leu	Gly	Pro	Cys	Asp
345					350					355					360
Ile	Val	Tyr	Leu	Trp	Ser	Phe	Leu	Asn	Cys	Phe	Gly	Leu	Asn	Phe	Glu
			365						370					375	
Leu	Trp	Met	Gln	Lys	Leu	Ala	Glu	Trp	Gly	Pro	Leu	Ala	Arg	Ile	Glu
		380						385					390		
Ala	Ser	Leu	Ser	Val	Gln	Met	Ser	Arg	Arg	Val	Arg	Ala	Leu	Phe	Gly
		395					400					405			
Ala	Met	Asn	Phe	Trp	Ala	Ile	Ile	Met	Tyr	Asn	Leu	Val	Ser	Leu	Asn
	410					415					420				
Ser	Leu	Lys	Phe	Thr	Glu	Leu	Val	Ala	Arg	Arg	Leu	Leu	Leu	Thr	Gly
425					430					435					440
Phe	Pro	Gln	Thr	Thr	Leu	Ser	Ile	Leu	Phe	Val	Thr	Tyr	Cys	Gly	Val
			445						450					455	
Gln	Leu	Val	Lys	Glu	Arg	Glu	Arg	Thr	Leu	Ala	Leu	Glu	Glu	Glu	Gln
		460						465					470		
Lys	Gln	Asp	Lys	Glu	Lys	Pro	Glu								
	475						480								

<210> 380

<211> 152

<212> PRT

<213> Homo sapiens

<220>

<221> SIGNAL

<222> -26...-1

<400> 380

Met	Val	Thr	Phe	Pro	Asp	Val	Pro	Leu	Gly	Ile	Phe	Leu	Phe	Cys	Val
-25						-20					-15				

Cys	Val	Ile	Ala	Ile	Gly	Val	Val	Gln	Ala	Leu	Ile	Val	Gly	Tyr	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

<210> 383
 <211> 95
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -48...-1

<400> 383
 Met Ala Ser Ser His Trp Asn Glu Thr Thr Thr Ser Val Tyr Gln Tyr
 -45 -40 -35
 Leu Gly Phe Gln Val Gln Lys Ile Tyr Pro Phe His Asp Asn Trp Asn
 -30 -25 -20
 Thr Ala Cys Phe Val Ile Leu Leu Leu Phe Ile Phe Thr Val Val Ser
 -15 -10 -5
 Leu Val Val Leu Ala Phe Leu Tyr Glu Val Leu Asp Cys Cys Cys Cys
 1 5 10 15
 Val Lys Asn Lys Thr Val Lys Asp Leu Lys Ser Glu Pro Asn Pro Leu
 20 25 30
 Arg Ser Met Met Asp Asn Ile Arg Lys Arg Glu Thr Glu Val Val
 35 40 45

<210> 384
 <211> 150
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SIGNAL
 <222> -20...-1

<400> 384
 Met Ala Arg His Gly Leu Pro Leu Leu Pro Leu Leu Ser Leu Leu Val
 -20 -15 -10 -5
 Gly Ala Trp Leu Lys Leu Gly Asn Gly Gln Ala Thr Ser Met Val Gln
 1 5 10
 Leu Gln Gly Gly Arg Phe Leu Met Gly Thr Asn Ser Pro Asp Ser Arg
 15 20 25
 Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala Ile
 30 35 40
 Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg Glu
 45 50 55 60
 Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val Phe
 65 70 75
 Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro Met
 80 85 90
 Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala Pro
 95 100 105
 Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met Ala
 110 115 120
 Ser Met Glu Ser Pro Gln
 125 130

<210> 385
 <211> 354
 <212> PRT
 <213> Homo sapiens

<400> 385
 Met Ser Ala Gly Gly Gly Arg Ala Phe Ala Trp Gln Val Phe Pro Pro
 1 5 10 15
 Met Pro Thr Cys Arg Val Tyr Gly Thr Val Ala His Gln Asp Gly His
 20 25 30
 Leu Leu Val Leu Gly Gly Cys Gly Arg Ala Gly Leu Pro Leu Asp Thr
 35 40 45
 Ala Glu Thr Leu Asp Met Ala Ser His Thr Trp Leu Ala Leu Ala Pro
 50 55 60
 Leu Pro Thr Ala Arg Ala Gly Ala Ala Ala Val Val Leu Gly Lys Gln
 65 70 75 80
 Val Leu Val Val Cys Gly Val Asp Glu Val Gln Ser Pro Val Ala Ala
 85 90 95
 Val Glu Ala Phe Leu Met Asp Glu Gly Arg Trp Glu Arg Arg Ala Thr
 100 105 110
 Leu Pro Gln Ala Ala Met Gly Val Ala Thr Val Glu Arg Asp Gly Met
 115 120 125
 Val Tyr Ala Leu Gly Gly Met Gly Pro Asp Thr Ala Pro Gln Ala Gln
 130 135 140
 Val Arg Val Tyr Asp Pro Arg Arg Asp Cys Trp Leu Ser Leu Pro Ser
 145 150 155 160
 Met Pro Thr Pro Cys Tyr Gly Ala Ser Thr Phe Leu His Gly Asn Lys
 165 170 175
 Ile Tyr Val Leu Gly Gly Arg Gln Gly Lys Leu Pro Val Thr Ala Phe
 180 185 190
 Glu Ala Phe Asp Leu Glu Ala Arg Thr Trp Thr Arg His Pro Ser Leu
 195 200 205
 Pro Ser Arg Arg Ala Phe Ala Gly Cys Ala Met Ala Glu Gly Ser Val
 210 215 220
 Phe Ser Leu Gly Gly Leu Gln Gln Pro Gly Pro His Asn Phe Tyr Ser
 225 230 235 240
 Arg Pro His Phe Val Asn Thr Val Glu Met Phe Asp Leu Glu His Gly
 245 250 255
 Ser Trp Thr Lys Leu Pro Arg Ser Leu Arg Met Arg Asp Lys Arg Ala
 260 265 270
 Asp Phe Val Val Gly Ser Leu Gly Gly His Ile Val Ala Ile Gly Gly
 275 280 285
 Leu Gly Asn Gln Pro Cys Pro Leu Gly Ser Val Glu Ser Phe Ser Leu
 290 295 300
 Ala Arg Arg Arg Trp Glu Ala Leu Pro Ala Met Pro Thr Ala Arg Cys
 305 310 315 320
 Ser Cys Ser Ser Leu Gln Ala Gly Pro Arg Leu Phe Val Ile Gly Gly
 325 330 335
 Val Ala Gln Gly Pro Ser Gln Ala Val Glu Ala Leu Cys Leu Arg Asp
 340 345 350
 Gly Val

<210> 386
 <211> 207
 <212> PRT
 <213> Homo sapiens

<400> 386
 Met Ala Leu Leu Phe Ala Arg Ser Leu Arg Leu Cys Arg Trp Gly Ala
 1 5 10 15
 Lys Arg Leu Gly Val Ala Ser Thr Glu Ala Gln Arg Gly Val Ser Phe
 20 25 30

Lys Leu Glu Glu Lys Thr Ala His Ser Ser Leu Ala Leu Phe Arg Asp
 35 40 45
 Asp Thr Gly Val Lys Tyr Gly Leu Val Gly Leu Glu Pro Thr Lys Val
 50 55 60
 Ala Leu Asn Val Glu Arg Phe Arg Glu Trp Ala Val Val Leu Ala Asp
 65 70 75 80
 Thr Ala Val Thr Ser Gly Arg His Tyr Trp Glu Val Thr Val Lys Arg
 85 90 95
 Ser Gln Gln Phe Arg Ile Gly Val Ala Asp Val Asp Met Ser Arg Asp
 100 105 110
 Ser Cys Ile Gly Val Asp Asp Arg Ser Trp Val Phe Thr Tyr Ala Gln
 115 120 125
 Arg Lys Trp Tyr Thr Met Leu Ala Asn Glu Lys Ala Pro Val Glu Gly
 130 135 140
 Ile Gly Gln Pro Glu Lys Val Gly Leu Leu Leu Glu Tyr Glu Ala Gln
 145 150 155 160
 Lys Leu Ser Leu Val Asp Val Ser Gln Val Ser Val Val His Thr Leu
 165 170 175
 Gln Thr Asp Phe Arg Gly Pro Val Val Pro Ala Phe Ala Leu Trp Asp
 180 185 190
 Gly Glu Leu Leu Thr His Ser Gly Leu Glu Val Pro Glu Gly Leu
 195 200 205

<210> 387
 <211> 210
 <212> PRT
 <213> Homo sapiens

<400> 387
 Met Ala Ala Ser Val Glu Gln Arg Glu Gly Thr Ile Gln Val Gln Gly
 1 5 10 15
 Gln Ala Leu Phe Phe Arg Glu Ala Leu Pro Gly Ser Gly Gln Ala Arg
 20 25 30
 Phe Ser Val Leu Leu Leu His Gly Ile Arg Phe Ser Ser Glu Thr Trp
 35 40 45
 Gln Asn Leu Gly Thr Leu His Arg Leu Ala Gln Ala Gly Tyr Arg Ala
 50 55 60
 Val Ala Ile Asp Leu Pro Gly Leu Gly His Ser Lys Glu Ala Ala Ala
 65 70 75 80
 Pro Ala Pro Ile Gly Glu Leu Ala Pro Gly Ser Phe Leu Ala Ala Val
 85 90 95
 Val Asp Ala Leu Glu Leu Gly Pro Pro Val Val Ile Ser Pro Ser Leu
 100 105 110
 Ser Gly Met Tyr Ser Leu Pro Phe Leu Thr Ala Pro Gly Ser Gln Leu
 115 120 125
 Pro Gly Phe Val Pro Val Ala Pro Ile Cys Thr Asp Lys Ile Asn Ala
 130 135 140
 Ala Asn Tyr Ala Ser Val Lys Thr Pro Ala Leu Ile Val Tyr Gly Asp
 145 150 155 160
 Gln Asp Pro Met Gly Gln Thr Ser Phe Glu His Leu Lys Gln Leu Pro
 165 170 175
 Asn His Arg Val Leu Ile Met Lys Gly Ala Gly His Pro Cys Tyr Leu
 180 185 190
 Asp Lys Pro Glu Glu Trp His Thr Gly Leu Leu Asp Phe Leu Gln Gly
 195 200 205
 Leu Gln
 210

<210> 388
 <211> 375
 <212> PRT
 <213> Homo sapiens

<400> 388
 Met Ala Val Thr Glu Ala Ser Leu Leu Arg Gln Cys Pro Leu Leu Leu
 1 5 10 15
 Pro Gln Asn Arg Ser Lys Thr Val Tyr Glu Gly Phe Ile Ser Ala Gln
 20 25 30
 Gly Arg Asp Phe His Leu Arg Ile Val Leu Pro Glu Asp Leu Gln Leu
 35 40 45
 Lys Asn Ala Arg Leu Leu Cys Ile Trp Gln Leu Arg Thr Ile Leu Ser
 50 55 60
 Gly Tyr His Arg Ile Val Gln Gln Arg Met Gln His Ser Pro Asp Leu
 65 70 75 80
 Met Ser Phe Met Met Glu Leu Lys Met Leu Leu Glu Val Ala Leu Lys
 85 90 95
 Asn Arg Gln Glu Leu Tyr Ala Leu Pro Pro Pro Gln Phe Tyr Ser
 100 105 110
 Ser Leu Ile Glu Glu Ile Gly Thr Leu Gly Trp Asp Lys Leu Val Tyr
 115 120 125
 Ala Asp Thr Cys Phe Ser Thr Ile Lys Leu Lys Ala Glu Asp Ala Ser
 130 135 140
 Gly Arg Glu His Leu Ile Thr Leu Lys Leu Lys Ala Lys Tyr Pro Ala
 145 150 155 160
 Glu Ser Pro Asp Tyr Phe Val Asp Phe Pro Val Pro Phe Cys Ala Ser
 165 170 175
 Trp Thr Pro Gln Ser Ser Leu Ile Ser Ile Tyr Ser Gln Phe Leu Ala
 180 185 190
 Ala Ile Glu Ser Leu Lys Ala Phe Trp Asp Val Met Asp Glu Ile Asp
 195 200 205
 Glu Lys Thr Trp Val Leu Glu Pro Glu Lys Pro Pro Arg Ser Ala Thr
 210 215 220
 Ala Arg Arg Ile Ala Leu Gly Asn Asn Val Ser Ile Asn Ile Glu Val
 225 230 235 240
 Asp Pro Arg His Pro Thr Met Leu Pro Glu Cys Phe Phe Leu Gly Ala
 245 250 255
 Asp His Val Val Lys Pro Leu Gly Ile Lys Leu Ser Arg Asn Ile His
 260 265 270
 Leu Trp Asp Pro Glu Asn Ser Val Leu Gln Asn Leu Lys Asp Val Leu
 275 280 285
 Glu Ile Asp Phe Pro Ala Arg Ala Ile Leu Glu Lys Ser Asp Phe Thr
 290 295 300
 Met Asp Cys Gly Ile Cys Tyr Ala Tyr Gln Leu Asp Gly Thr Ile Pro
 305 310 315 320
 Asp Gln Val Cys Asp Asn Ser Gln Cys Gly Gln Pro Phe His Gln Ile
 325 330 335
 Cys Leu Tyr Glu Trp Leu Arg Gly Leu Leu Thr Ser Arg Gln Ser Phe
 340 345 350
 Asn Ile Ile Phe Gly Glu Cys Pro Tyr Cys Ser Lys Pro Ile Thr Leu
 355 360 365
 Lys Met Ser Gly Arg Lys His
 370 375

<210> 389
 <211> 509
 <212> PRT

<213> Homo sapiens

<400> 389

Met	Ala	Ala	Ile	Gly	Val	His	Leu	Gly	Cys	Thr	Ser	Ala	Cys	Val	Ala	1	5	10	15
Val	Tyr	Lys	Asp	Gly	Arg	Ala	Gly	Val	Val	Ala	Asn	Asp	Ala	Gly	Asp	20	25	30	
Arg	Val	Thr	Pro	Ala	Val	Val	Ala	Tyr	Ser	Glu	Asn	Glu	Glu	Ile	Val	35	40	45	
Gly	Leu	Ala	Ala	Lys	Gln	Ser	Arg	Ile	Arg	Asn	Ile	Ser	Asn	Thr	Val	50	55	60	
Met	Lys	Val	Lys	Gln	Ile	Leu	Gly	Arg	Ser	Ser	Ser	Asp	Pro	Gln	Ala	65	70	75	80
Gln	Lys	Tyr	Ile	Ala	Glu	Ser	Lys	Cys	Leu	Val	Ile	Glu	Lys	Asn	Gly	85	90	95	
Lys	Leu	Arg	Tyr	Glu	Ile	Asp	Thr	Gly	Glu	Glu	Thr	Lys	Phe	Val	Asn	100	105	110	
Pro	Glu	Asp	Val	Ala	Arg	Leu	Ile	Phe	Ser	Lys	Met	Lys	Glu	Thr	Ala	115	120	125	
His	Ser	Val	Leu	Gly	Ser	Asp	Ala	Asn	Asp	Val	Val	Ile	Thr	Val	Pro	130	135	140	
Phe	Asp	Phe	Gly	Glu	Lys	Gln	Lys	Asn	Ala	Leu	Gly	Glu	Ala	Ala	Arg	145	150	155	160
Ala	Ala	Gly	Phe	Asn	Val	Leu	Arg	Leu	Ile	His	Glu	Pro	Ser	Ala	Ala	165	170	175	
Leu	Leu	Ala	Tyr	Gly	Ile	Gly	Gln	Asp	Ser	Pro	Thr	Gly	Lys	Ser	Asn	180	185	190	
Ile	Leu	Val	Phe	Lys	Leu	Gly	Gly	Thr	Ser	Leu	Ser	Leu	Ser	Val	Met	195	200	205	
Glu	Val	Asn	Ser	Gly	Ile	Tyr	Arg	Val	Leu	Ser	Thr	Asn	Thr	Asp	Asp	210	215	220	
Asn	Ile	Gly	Gly	Ala	His	Phe	Thr	Glu	Thr	Leu	Ala	Gln	Tyr	Leu	Ala	225	230	235	240
Ser	Glu	Phe	Gln	Arg	Ser	Phe	Lys	His	Asp	Val	Arg	Gly	Asn	Ala	Arg	245	250	255	
Ala	Met	Met	Lys	Leu	Thr	Asn	Ser	Ala	Glu	Val	Ala	Lys	His	Ser	Leu	260	265	270	
Ser	Thr	Leu	Gly	Ser	Ala	Asn	Cys	Phe	Leu	Asp	Ser	Leu	Tyr	Glu	Gly	275	280	285	
Gln	Asp	Phe	Asp	Cys	Asn	Val	Ser	Arg	Ala	Arg	Phe	Glu	Leu	Leu	Cys	290	295	300	
Ser	Pro	Leu	Phe	Asn	Lys	Cys	Ile	Glu	Ala	Ile	Arg	Gly	Leu	Leu	Asp	305	310	315	320
Gln	Asn	Gly	Phe	Thr	Thr	Asp	Asp	Ile	Asn	Lys	Val	Val	Leu	Cys	Gly	325	330	335	
Gly	Ser	Ser	Arg	Ile	Pro	Lys	Leu	Gln	Gln	Leu	Ile	Lys	Asp	Leu	Phe	340	345	350	
Pro	Ala	Val	Glu	Leu	Leu	Asn	Ser	Ile	Pro	Pro	Asp	Glu	Val	Ile	Pro	355	360	365	
Ile	Gly	Ala	Ala	Ile	Glu	Ala	Gly	Ile	Leu	Ile	Gly	Lys	Glu	Asn	Leu	370	375	380	
Leu	Val	Glu	Asp	Ser	Leu	Met	Ile	Glu	Cys	Ser	Ala	Arg	Asp	Ile	Leu	385	390	395	400
Val	Lys	Gly	Val	Asp	Glu	Ser	Gly	Ala	Ser	Arg	Phe	Thr	Val	Leu	Phe	405	410	415	
Pro	Ser	Gly	Thr	Pro	Leu	Pro	Ala	Arg	Gln	His	Thr	Leu	Gln	Ala		420	425	430	
Pro	Gly	Ser	Ile	Ser	Ser	Val	Cys	Leu	Glu	Leu	Tyr	Glu	Ser	Asp	Gly				

435 440 445
 Lys Asn Ser Ala Lys Glu Glu Thr Lys Phe Ala Gln Val Val Leu Gln
 450 455 460
 Asp Leu Asp Lys Lys Glu Asn Gly Leu Arg Asp Ile Leu Ala Val Leu
 465 470 475 480
 Thr Met Lys Arg Asp Gly Ser Leu His Val Thr Cys Thr Asp Gln Glu
 485 490 495
 Thr Gly Lys Cys Glu Ala Ile Ser Ile Glu Ile Ala Ser
 500 505

<210> 390
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 390
 Met Tyr Asn Thr Gly Arg His Val Ser Leu Arg Leu Asp Lys Glu His
 1 5 10 15
 Leu Val Asn Ile Ser Gly Gly Pro Met Thr Tyr Ser His Arg Leu Glu
 20 25 30
 Glu Ile Arg Leu His Phe Gly Ser Glu Asp Ser Gln Gly Ser Glu His
 35 40 45
 Leu Leu Asn Gly Gln Ala Phe Ser Gly Glu Leu Gln Glu Arg Asp Leu
 50 55 60
 Phe Ile Leu Leu Thr Ser Val Ser Gly His Leu Pro Asp Thr
 65 70 75

<210> 391
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 391
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Ile Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
 65 70 75 80
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
 85 90 95
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
 100 105 110
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
 115 120 125
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
 130 135 140
 Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
 145 150 155 160
 Leu Gly

<210> 392
 <211> 146
 <212> PRT

<213> Homo sapiens

<400> 392

Met Asn Ser Leu Leu His Phe Gly Ile Leu Leu Glu Leu Ser Leu Leu
1 5 10 15
Lys Gln Phe Lys Ser Val Tyr Val Pro Gly Asn His Thr His Gln Ala
20 25 30
Ser Tyr Lys Pro Leu Leu Lys Gln Val Val Glu Glu Ile Phe His Pro
35 40 45
Glu Arg Pro Asp Ser Val Asp Ile Glu His Met Ser Ser Gly Leu Thr
50 55 60
Asp Leu Leu Lys Thr Gly Phe Ser Met Phe Met Lys Val Ser Arg Pro
65 70 75 80
His Pro Ser Asp Tyr Pro Leu Leu Ile Leu Phe Val Val Gly Gly Val
85 90 95
Thr Val Ser Glu Val Lys Met Val Lys Asp Leu Val Ala Ser Leu Lys
100 105 110
Pro Gly Thr Gln Val Ile Val Leu Ser Thr Arg Leu Leu Lys Pro Leu
115 120 125
Asn Ile Pro Glu Leu Leu Phe Ala Thr Asp Arg Leu His Pro Asp Leu
130 135 140
Gly Phe
145

<210> 393

<211> 225

<212> PRT

<213> Homo sapiens

<400> 393

Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
1 5 10 15
Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
20 25 30
Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
35 40 45
Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
50 55 60
Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
65 70 75 80
Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
85 90 95
Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
100 105 110
Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
115 120 125
Ala Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
130 135 140
Ile Arg Asp Phe Tyr Asn Pro Ile Val Asn Val Ala Gln Lys Arg Glu
145 150 155 160
Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile
165 170 175
Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser
180 185 190
Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser
195 200 205
Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr
210 215 220

Val
225

<210> 394
<211> 114
<212> PRT
<213> Homo sapiens

<400> 394
Met Arg Leu Gln Asp Arg Ile Ala Thr Phe Phe Phe Pro Lys Gly Met
1 5 10 15
Met Leu Thr Thr Ala Ala Leu Met Leu Phe Phe Leu His Leu Gly Ile
20 25 30
Phe Ile Arg Asp Val His Asn Phe Cys Ile Thr Tyr His Tyr Asp His
35 40 45
Met Ser Phe His Tyr Thr Val Leu Met Phe Ser Gln Val Ile Ser
50 55 60
Ile Cys Trp Ala Ala Met Gly Ser Leu Tyr Ala Glu Met Thr Glu Asn
65 70 75 80
Asn Ala Gln Arg Ser His Val Leu Gln Pro Pro Val Leu Gly Val Ser
85 90 95
Gly His Arg Val Pro Gly Gly Ala Pro Leu Arg Pro Gly Glu Ser Glu
100 105 110
Gln Gly

<210> 395
<211> 367
<212> PRT
<213> Homo sapiens

<400> 395
Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro
1 5 10 15
Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp
20 25 30
Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val
35 40 45
Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Val Arg Leu Val
50 55 60
Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg Asp Val Ser Leu Pro
65 70 75 80
Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg Leu Asn Leu Gly Glu
85 90 95
Glu Val Pro Val Ile Ile His Arg Asp Asn Ile Ile Ser Asp Tyr Asp
100 105 110
Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr Gly Glu His Val Val
115 120 125
Ala Leu Met Pro Glu Val Gly Ser Leu Gln His Ala Arg Val Leu Gln
130 135 140
Tyr Arg Glu Leu Leu Asp Ala Leu Pro Met Asp Ala Tyr Thr His Gly
145 150 155 160
Cys Ile Leu His Pro Glu Leu Thr Thr Asp Ser Met Ile Pro Lys Tyr
165 170 175
Ala Thr Ala Glu Ile Arg Arg His Leu Ala Asn Ala Thr Thr Asp Leu
180 185 190
Met Lys Leu Asp His Glu Glu Glu Pro Gln Leu Ser Glu Pro Tyr Leu
195 200 205
Ser Lys Gln Lys Lys Leu Met Val Lys Ile Leu Glu His Asp Asp Val

210		215		220
Ser Tyr Leu Lys Lys Ile	Leu Gly Glu Leu Ala Met Val Leu Asp Gln			
225		230		235
Ile Glu Ala Glu Leu Glu Lys Arg Lys	Leu Glu Asn Glu Gly Gln Lys			240
		245		250
Cys Glu Leu Trp Leu Cys Gly Cys Ala Phe Thr Leu Ala Asp Val Leu				255
		260		265
Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu Gly Leu Ser Lys Lys				270
		275		280
Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln Ser Phe Phe Glu Arg				285
		290		295
Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu Gly Asp Ile His Thr				300
305		310		315
Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe Arg Leu Val Lys Arg				320
		325		330
Lys Pro Pro Ser Phe Phe Gly Ala Ser Phe Leu Met Gly Ser Leu Gly				335
		340		345
Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys Lys Lys Tyr Ile				350
		355		360
				365

<210> 396

<211> 279

<212> PRT

<213> Homo sapiens

<400> 396

Met Pro Val Cys Ala Pro Val Leu Trp Arg Ala Arg Arg Leu Cys Gly				
1	5	10	15	
Met Pro Val Cys Ala Pro Val Pro Trp Arg Ala Arg Arg Leu Cys Thr				
	20	25	30	
Arg Ala Val Val Cys Pro Ser Ser Val Pro Phe Ile Ala Gly Gln Gly				
	35	40	45	
Cys Thr His Met Cys Lys Pro Ala Thr Asp Pro Arg Phe Thr Arg Ser				
	50	55	60	
Pro Leu Ala Gly Gly Val Ile Leu Gly Val Ala Leu Trp Leu Arg His				
65	70	75	80	
Asp Pro Gln Thr Thr Asn Leu Leu Tyr Leu Glu Leu Gly Asp Lys Pro				
	85	90	95	
Ala Pro Asn Thr Phe Tyr Val Gly Ile Tyr Ile Leu Ile Ala Val Gly				
	100	105	110	
Ala Val Met Met Phe Val Gly Phe Leu Gly Cys Tyr Gly Ala Ile Gln				
	115	120	125	
Glu Ser Gln Cys Leu Leu Gly Thr Phe Phe Thr Cys Leu Val Ile Leu				
	130	135	140	
Phe Ala Cys Glu Val Ala Ala Gly Ile Trp Gly Phe Val Asn Lys Asp				
145	150	155	160	
Gln Ile Ala Lys Asp Val Lys Gln Phe Tyr Asp Gln Ala Leu Gln Gln				
	165	170	175	
Ala Val Val Asp Asp Ala Asn Asn Ala Lys Ala Val Val Lys Thr				
	180	185	190	
Phe His Glu Thr Leu Asp Cys Cys Gly Ser Ser Thr Leu Thr Ala Leu				
	195	200	205	
Thr Thr Ser Val Leu Lys Asn Asn Leu Cys Pro Ser Gly Ser Asn Ile				
	210	215	220	
Ile Ser Asn Leu Phe Lys Glu Asp Cys His Gln Lys Ile Asp Asp Leu				
225	230	235	240	
Phe Ser Gly Lys Leu Tyr Leu Ile Gly Ile Ala Ala Ile Val Val Ala				
	245	250	255	

Thr Ser Ser Leu Thr Asp Thr Asp Val Gln Val Ser Pro Met Leu Val
 100 105 110
 Ala Gly Val Asn His Ser Ser Ser Leu Leu Asp Asn Ile Pro Phe Thr
 115 120 125
 Gly Cys Leu Pro Phe His Leu Ser Ser Ser Leu Pro Tyr Leu Cys Leu
 130 135 140
 Leu Gly Ser Pro Phe Lys
 145 150

<210> 401

<211> 170

<212> PRT

<213> Homo sapiens

<400> 401

Met Glu Asp Pro Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro
 1 5 10 15
 Lys Glu Arg Ser Pro Gln Ser Pro Gly Gly Asn Ile Cys His Leu Gly
 20 25 30
 Ala Pro Lys Cys Thr Arg Cys Leu Ile Thr Phe Ala Asp Ser Lys Phe
 35 40 45
 Gln Glu Arg His Met Lys Arg Glu His Pro Ala Asp Phe Val Ala Gln
 50 55 60
 Lys Leu Gln Gly Val Leu Phe Ile Cys Phe Thr Cys Ala Arg Ser Phe
 65 70 75 80
 Pro Ser Ser Lys Ala Leu Ile Thr His Gln Arg Ser His Gly Pro Ala
 85 90 95
 Ala Lys Pro Thr Leu Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe
 100 105 110
 Pro Cys Pro Asp Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg
 115 120 125
 Arg His Arg Gln Met His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala
 130 135 140
 Cys Thr Glu Cys Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln
 145 150 155 160
 His Tyr Ile Arg His Ala Arg Gly Glu Leu
 165 170

<210> 402

<211> 169

<212> PRT

<213> Homo sapiens

<400> 402

Met Glu Asp Pro Asn Pro Glu Glu Asn Met Lys Gln Gln Asp Ser Pro
 1 5 10 15
 Lys Glu Arg Ser Pro Gln Pro Arg Arg Gln His Leu Pro Pro Gly Gly
 20 25 30
 Pro Glu Val His Pro Leu Pro His His Leu Arg Arg Phe Gln Val Pro
 35 40 45
 Gly Ala Ser His Glu Ala Gly Ala Pro Ser Gly Leu Arg Gly Pro Glu
 50 55 60
 Ala Ala Gly Gly Pro Leu His Leu Leu His Leu Arg Pro Leu Leu Pro
 65 70 75 80
 Leu Leu Gln Ser Pro Asn His Pro Pro Ala Gln His Gly Pro Ala Ala
 85 90 95
 Lys Pro Thr Leu Pro Val Ala Thr Thr Thr Ala Gln Pro Thr Phe Pro
 100 105 110

Cys Pro Asp Cys Gly Lys Thr Phe Gly Gln Ala Val Ser Leu Arg Arg
 115 120 125
 His Arg Gln Met His Glu Val Arg Ala Pro Pro Gly Thr Phe Ala Cys
 130 135 140
 Thr Glu Cys Gly Gln Asp Phe Ala Gln Glu Ala Gly Leu His Gln His
 145 150 155 160
 Tyr Ile Arg His Ala Arg Gly Glu Leu
 165

<210> 403

<211> 367

<212> PRT

<213> Homo sapiens

<400> 403

Met Ala Thr Pro Asn Asn Leu Thr Pro Thr Asn Cys Ser Trp Trp Pro
 1 5 10 15
 Ile Ser Ala Leu Glu Ser Asp Ala Ala Lys Pro Ala Glu Ala Pro Asp
 20 25 30
 Ala Pro Glu Ala Ala Ser Pro Ala His Trp Pro Arg Glu Ser Leu Val
 35 40 45
 Leu Tyr His Trp Thr Gln Ser Phe Ser Ser Gln Lys Val Arg Leu Val
 50 55 60
 Ile Ala Glu Lys Gly Leu Val Cys Glu Glu Arg Asp Val Ser Leu Pro
 65 70 75 80
 Gln Ser Glu His Lys Glu Pro Trp Phe Met Arg Leu Asn Leu Gly Glu
 85 90 95
 Glu Val Pro Val Ile Ile His Arg Asp Asn Ile Ile Ser Asp Tyr Asp
 100 105 110
 Gln Ile Ile Asp Tyr Val Glu Arg Thr Phe Thr Gly Glu His Val Val
 115 120 125
 Ala Leu Met Pro Glu Val Gly Ser Leu Gln His Ala Arg Val Leu Gln
 130 135 140
 Tyr Arg Glu Leu Leu Asp Ala Leu Pro Met Asp Ala Tyr Thr His Gly
 145 150 155 160
 Cys Ile Leu His Leu Glu Leu Thr Thr Asp Ser Met Ile Pro Lys Tyr
 165 170 175
 Ala Thr Ala Glu Ile Arg Arg His Leu Ala Asn Ala Thr Thr Asp Leu
 180 185 190
 Met Lys Leu Asp His Glu Glu Glu Pro Gln Leu Ser Glu Pro Tyr Leu
 195 200 205
 Ser Lys Gln Lys Lys Leu Met Ala Lys Ile Leu Glu His Asp Asp Val
 210 215 220
 Ser Tyr Leu Lys Lys Ile Leu Gly Glu Leu Ala Met Val Leu Asp Gln
 225 230 235 240
 Ile Glu Ala Glu Leu Glu Lys Arg Lys Leu Glu Asn Glu Gly Gln Lys
 245 250 255
 Cys Glu Leu Trp Leu Cys Gly Cys Ala Phe Thr Leu Ala Asp Val Leu
 260 265 270
 Leu Gly Ala Thr Leu His Arg Leu Lys Phe Leu Gly Leu Ser Lys Lys
 275 280 285
 Tyr Trp Glu Asp Gly Ser Arg Pro Asn Leu Gln Ser Phe Phe Glu Arg
 290 295 300
 Val Gln Arg Arg Phe Ala Phe Arg Lys Val Leu Gly Asp Ile His Thr
 305 310 315 320
 Thr Leu Leu Ser Ala Val Ile Pro Asn Ala Phe Arg Leu Val Lys Arg
 325 330 335
 Lys Pro Pro Ser Phe Phe Gly Ala Ser Phe Leu Met Gly Ser Leu Gly

340 345 350
 Gly Met Gly Tyr Phe Ala Tyr Trp Tyr Leu Lys Lys Lys Tyr Ile
 355 360 365

<210> 404
 <211> 20
 <212> PRT
 <213> Homo sapiens

<400> 404
 Met Ala Ala Ala Arg Pro Ser Leu Gly Arg Val Leu Pro Gly Ser Ser
 1 5 10 15
 Pro Val Pro Val
 20

<210> 405
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 405
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
 1 5 10 15
 Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val
 20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn Phe Trp Glu
 35 40 45
 Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys
 50 55 60
 Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala
 65 70 75 80
 Arg Gly Leu Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met
 85 90 95
 Met Ala Ile Leu Gly Met Lys Cys Thr Arg Cys Thr Gly Asp Asn Glu
 100 105 110
 Lys Val Lys Ala His Ile Leu Leu Thr Ala Gly Ile Ile Phe Ile Ile
 115 120 125
 Thr Gly Met Val Val Leu Ile Pro Val Ser Trp Val Ala Asn Ala Ile
 130 135 140
 Ile Arg Asp Phe Tyr Asn Ser Ile Val Asn Val Ala Gln Lys Arg Glu
 145 150 155 160
 Leu Gly Glu Ala Leu Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile
 165 170 175
 Val Gly Gly Ala Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser
 180 185 190
 Ser Ser Tyr Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser
 195 200 205
 Tyr His Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr
 210 215 220
 Val
 225

<210> 406
 <211> 378
 <212> PRT
 <213> Homo sapiens

<400> 406

Met Asp Pro Gly Asp Asp Trp Leu Val Glu Ser Leu Arg Leu Tyr Gln
1 5 10 15
Asp Phe Tyr Ala Phe Asp Leu Ser Gly Ala Thr Arg Val Leu Glu Trp
20 25 30
Ile Asp Asp Lys Gly Val Phe Val Ala Gly Tyr Glu Ser Leu Lys Lys
35 40 45
Asn Glu Ile Leu His Leu Lys Leu Pro Leu Arg Leu Ser Val Lys Glu
50 55 60
Asn Lys Gly Leu Phe Pro Glu Arg Asp Phe Lys Val Arg His Gly Gly
65 70 75 80
Phe Ser Asp Arg Ser Ile Phe Asp Leu Lys His Val Pro His Thr Arg
85 90 95
Leu Leu Val Thr Ser Gly Leu Pro Gly Cys Tyr Leu Gln Val Trp Gln
100 105 110
Val Ala Glu Asp Ser Asp Val Ile Lys Ala Val Ser Thr Ile Ala Val
115 120 125
His Glu Lys Glu Glu Ser Leu Trp Pro Arg Val Ala Val Phe Ser Thr
130 135 140
Leu Ala Pro Gly Val Leu His Gly Ala Arg Leu Arg Ser Leu Gln Val
145 150 155 160
Val Asp Leu Glu Ser Arg Lys Thr Thr Tyr Thr Ser Asp Val Ser Asp
165 170 175
Ser Glu Glu Leu Ser Ser Leu Gln Val Leu Asp Ala Asp Thr Phe Ala
180 185 190
Phe Cys Cys Ala Ser Gly Arg Leu Gly Leu Val Asp Thr Arg Gln Lys
195 200 205
Trp Ala Pro Leu Glu Asn Arg Ser Pro Gly Pro Gly Ser Gly Gly Glu
210 215 220
Arg Trp Cys Ala Glu Val Gly Ser Trp Gly Gln Gly Pro Gly Pro Ser
225 230 235 240
Ile Ala Ser Leu Ser Ser Asp Gly Arg Leu Cys Leu Leu Asp Pro Arg
245 250 255
Asp Leu Cys His Pro Val Ser Ser Val Gln Cys Pro Val Ser Val Pro
260 265 270
Ser Pro Asp Pro Glu Leu Leu Arg Val Thr Trp Ala Pro Gly Leu Lys
275 280 285
Asn Cys Leu Ala Ile Ser Gly Phe Asp Gly Thr Val Gln Val Tyr Asp
290 295 300
Ala Thr Ser Trp Asp Gly Thr Arg Ser Gln Asp Gly Thr Arg Ser Gln
305 310 315 320
Val Glu Pro Leu Phe Thr His Arg Gly His Ile Phe Leu Asp Gly Asn
325 330 335
Gly Met Asp Pro Ala Pro Leu Val Thr Thr His Thr Trp His Pro Cys
340 345 350
Arg Pro Arg Thr Leu Leu Ser Ala Thr Asn Asp Ala Ser Leu His Val
355 360 365
Trp Asp Trp Val Asp Leu Cys Ala Pro Arg
370 375

<210> 407

<211> 43

<212> PRT

<213> Homo sapiens

<400> 407

Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly Val
1 5 10 15
Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp Arg Val

20 25 30
 Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe
 35 40

<210> 408
 <211> 345
 <212> PRT
 <213> Homo sapiens

<400> 408
 Met Ala Trp Arg Gly Trp Ala Gln Arg Gly Trp Gly Cys Gly Gln Ala
 1 5 10 15
 Trp Gly Ala Ser Val Gly Gly Arg Ser Cys Glu Glu Leu Thr Ala Val
 20 25 30
 Leu Thr Pro Pro Gln Leu Leu Gly Arg Arg Phe Asn Phe Phe Ile Gln
 35 40 45
 Gln Lys Cys Gly Phe Arg Lys Ala Pro Arg Lys Val Glu Pro Arg Arg
 50 55 60
 Ser Asp Pro Gly Thr Ser Gly Glu Ala Tyr Lys Arg Ser Ala Leu Ile
 65 70 75 80
 Pro Pro Val Glu Glu Thr Val Phe Tyr Pro Ser Pro Tyr Pro Ile Arg
 85 90 95
 Ser Leu Ile Lys Pro Leu Phe Phe Thr Val Gly Phe Thr Gly Cys Ala
 100 105 110
 Phe Gly Ser Ala Ala Ile Trp Gln Tyr Glu Ser Leu Lys Ser Arg Val
 115 120 125
 Gln Ser Tyr Phe Asp Gly Ile Lys Ala Asp Trp Leu Asp Ser Ile Arg
 130 135 140
 Pro Gln Lys Glu Gly Asp Phe Arg Lys Glu Ile Asn Lys Trp Trp Asn
 145 150 155 160
 Asn Leu Ser Asp Gly Gln Arg Thr Val Thr Gly Ile Ile Ala Ala Asn
 165 170 175
 Val Leu Val Phe Cys Leu Trp Arg Val Pro Ser Leu Gln Arg Thr Met
 180 185 190
 Ile Arg Tyr Phe Thr Ser Asn Pro Ala Ser Lys Val Leu Cys Ser Pro
 195 200 205
 Met Leu Leu Ser Thr Phe Ser His Phe Ser Leu Phe His Met Ala Ala
 210 215 220
 Asn Met Tyr Val Leu Trp Ser Phe Ser Ser Ser Ile Val Asn Ile Leu
 225 230 235 240
 Gly Gln Glu Gln Phe Met Ala Val Tyr Leu Ser Ala Gly Val Ile Ser
 245 250 255
 Asn Phe Val Ser Tyr Val Gly Lys Val Ala Thr Gly Arg Tyr Gly Pro
 260 265 270
 Ser Leu Gly Ala Ala Leu Lys Ala Ile Ile Ala Met Asp Thr Ala Gly
 275 280 285
 Met Ile Leu Gly Trp Lys Phe Phe Asp His Ala Ala His Leu Gly Gly
 290 295 300
 Ala Leu Phe Gly Ile Trp Tyr Val Thr Tyr Gly His Glu Leu Ile Trp
 305 310 315 320
 Lys Asn Arg Glu Pro Leu Val Lys Ile Trp His Glu Ile Arg Thr Asn
 325 330 335
 Gly Pro Lys Lys Gly Gly Gly Ser Lys
 340 345

<210> 409
 <211> 236
 <212> PRT

<213> Homo sapiens

<400> 409

Met	Lys	Arg	Ser	Gly	Asn	Pro	Gly	Ala	Glu	Val	Thr	Asn	Ser	Ser	Val
1				5					10					15	
Ala	Gly	Pro	Asp	Cys	Cys	Gly	Gly	Leu	Gly	Asn	Ile	Asp	Phe	Arg	Gln
			20					25					30		
Ala	Asp	Phe	Cys	Val	Met	Thr	Arg	Leu	Leu	Gly	Tyr	Val	Asp	Pro	Leu
		35					40					45			
Asp	Pro	Ser	Phe	Val	Ala	Ala	Val	Ile	Thr	Ile	Thr	Phe	Asn	Pro	Leu
	50					55					60				
Tyr	Trp	Asn	Val	Val	Ala	Arg	Trp	Glu	His	Lys	Thr	Arg	Lys	Leu	Ser
65					70					75					80
Arg	Ala	Phe	Gly	Ser	Pro	Tyr	Leu	Ala	Cys	Tyr	Ser	Leu	Ser	Ile	Thr
				85					90					95	
Ile	Leu	Leu	Leu	Asn	Phe	Leu	Arg	Ser	His	Cys	Phe	Thr	Gln	Ala	Met
			100					105					110		
Leu	Ser	Gln	Pro	Arg	Met	Glu	Ser	Leu	Asp	Thr	Pro	Ala	Ala	Tyr	Ser
		115					120					125			
Leu	Val	Leu	Ala	Leu	Leu	Gly	Leu	Gly	Val	Val	Leu	Val	Leu	Ser	Ser
	130					135					140				
Phe	Phe	Ala	Leu	Gly	Phe	Ala	Gly	Thr	Phe	Leu	Gly	Asp	Tyr	Phe	Gly
145					150					155					160
Ile	Leu	Lys	Glu	Ala	Arg	Val	Thr	Val	Phe	Pro	Phe	Asn	Ile	Leu	Asp
				165					170					175	
Asn	Pro	Met	Tyr	Trp	Gly	Ser	Thr	Ala	Asn	Tyr	Leu	Gly	Trp	Ala	Ile
			180					185					190		
Met	His	Ala	Ser	Pro	Thr	Gly	Leu	Leu	Leu	Thr	Val	Leu	Val	Ala	Leu
		195					200					205			
Thr	Tyr	Ile	Val	Ala	Leu	Leu	Tyr	Glu	Glu	Pro	Phe	Thr	Ala	Glu	Ile
	210				215						220				
Tyr	Arg	Gln	Lys	Ala	Ser	Gly	Ser	His	Lys	Arg	Ser				
225					230					235					

<210> 410

<211> 121

<212> PRT

<213> Homo sapiens

<400> 410

Met	Asn	Thr	Glu	Ala	Glu	Gln	Gln	Leu	Leu	His	His	Ala	Arg	Asn	Gly
1				5					10					15	
Asn	Ala	Glu	Glu	Val	Arg	Gln	Leu	Leu	Glu	Thr	Met	Ala	Ser	Asn	Glu
			20					25					30		
Val	Ile	Ala	Asp	Ile	Asn	Cys	Lys	Gly	Arg	Ser	Lys	Ser	Asn	Leu	Gly
		35					40					45			
Trp	Thr	Pro	Leu	His	Leu	Ala	Gly	Ala	Glu	Val	Asn	Val	Leu	Asn	Asp
	50					55					60				
Gln	Asp	Leu	Leu	Lys	Ala	Gly	Ala	Glu	Val	Asn	Val	Leu	Asn	Asp	Met
65					70					75					80
Gly	Asp	Thr	Pro	Leu	His	Arg	Ala	Ala	Phe	Thr	Gly	Arg	Lys	Val	Lys
				85					90					95	
Ile	Ile	Leu	Cys	Ser	Met	Phe	Val	Ser	Glu	Val	Phe	Gly	Gly	Val	Val
			100					105					110		
Thr	Ile	Val	Phe	Ser	Val	Ile	Thr	Ile							
	115						120								

<210> 411

<211> 170
 <212> PRT
 <213> Homo sapiens

<400> 411

Met	Arg	Leu	Gln	Gly	Ala	Ile	Phe	Val	Leu	Leu	Pro	His	Leu	Gly	Pro
1			5						10					15	
Ile	Leu	Val	Trp	Leu	Phe	Thr	Arg	Asp	His	Met	Ser	Gly	Trp	Cys	Glu
		20					25						30		
Gly	Pro	Arg	Met	Leu	Ser	Trp	Cys	Pro	Phe	Tyr	Lys	Val	Leu	Leu	Leu
	35					40					45				
Val	Gln	Thr	Ala	Ile	Tyr	Ser	Val	Val	Gly	Tyr	Ala	Ser	Tyr	Leu	Val
	50				55					60					
Trp	Lys	Asp	Leu	Gly	Gly	Gly	Leu	Gly	Trp	Pro	Leu	Ala	Leu	Pro	Leu
65				70					75					80	
Gly	Leu	Tyr	Ala	Val	Gln	Leu	Thr	Ile	Ser	Trp	Thr	Val	Leu	Val	Leu
			85					90					95		
Phe	Phe	Thr	Val	His	Asn	Pro	Gly	Leu	Ala	Leu	Leu	His	Leu	Leu	Leu
			100					105					110		
Leu	Tyr	Gly	Leu	Val	Val	Ser	Thr	Ala	Leu	Ile	Trp	His	Pro	Ile	Asn
		115					120					125			
Lys	Leu	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Tyr	Leu	Ala	Trp	Leu	Thr	Val
	130					135					140				
Thr	Ser	Ala	Leu	Thr	Tyr	His	Leu	Trp	Arg	Asp	Ser	Leu	Cys	Pro	Val
145					150					155					160
His	Gln	Pro	Gln	Pro	Thr	Glu	Lys	Ser	Asp						
			165						170						

<210> 412
 <211> 236
 <212> PRT
 <213> Homo sapiens

<400> 412

Met	Leu	Ser	Lys	Gly	Leu	Lys	Arg	Lys	Arg	Glu	Glu	Glu	Glu	Glu	Lys
1				5					10					15	
Glu	Pro	Leu	Ala	Val	Asp	Ser	Trp	Trp	Leu	Asp	Pro	Gly	His	Thr	Ala
		20					25						30		
Val	Ala	Gln	Ala	Pro	Pro	Ala	Val	Ala	Ser	Ser	Ser	Leu	Phe	Asp	Leu
	35					40					45				
Ser	Val	Leu	Lys	Leu	His	His	Ser	Leu	Gln	Gln	Ser	Glu	Pro	Asp	Leu
	50				55					60					
Arg	His	Leu	Val	Leu	Val	Val	Asn	Thr	Leu	Arg	Arg	Ile	Gln	Ala	Ser
65				70					75					80	
Met	Ala	Pro	Ala	Ala	Ala	Leu	Pro	Pro	Val	Pro	Ser	Pro	Pro	Ala	Ala
			85					90						95	
Pro	Ser	Val	Ala	Asp	Asn	Leu	Leu	Ala	Ser	Ser	Asp	Ala	Ala	Leu	Ser
		100					105						110		
Ala	Ser	Met	Ala	Ser	Leu	Leu	Glu	Asp	Leu	Ser	His	Ile	Glu	Gly	Leu
		115					120					125			
Ser	Gln	Ala	Pro	Gln	Pro	Leu	Ala	Asp	Glu	Gly	Pro	Pro	Gly	Arg	Ser
	130					135					140				
Ile	Gly	Gly	Ala	Ala	Pro	Ser	Leu	Gly	Ala	Leu	Asp	Leu	Leu	Gly	Pro
145					150				155					160	
Ala	Thr	Gly	Cys	Leu	Leu	Asp	Asp	Gly	Leu	Glu	Gly	Leu	Phe	Glu	Asp
			165					170						175	
Ile	Asp	Thr	Ser	Met	Tyr	Asp	Asn	Glu	Leu	Trp	Ala	Pro	Ala	Ser	Glu
			180					185					190		

Gly Leu Lys Pro Gly Pro Glu Asp Gly Pro Gly Lys Glu Glu Ala Pro
 195 200 205
 Glu Leu Asp Glu Ala Glu Leu Asp Tyr Leu Met Asp Val Leu Val Gly
 210 215 220
 Thr Gln Ala Leu Glu Arg Pro Pro Gly Pro Gly Arg
 225 230 235

<210> 413
 <211> 191
 <212> PRT
 <213> Homo sapiens

<400> 413
 Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
 1 5 10 15
 Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn Phe
 20 25 30
 Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn Thr Lys
 35 40 45
 Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val Gly Arg
 50 55 60
 Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser Phe Phe
 65 70 75 80
 Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser Glu Asp
 85 90 95
 Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu Val His
 100 105 110
 Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile Arg Asp
 115 120 125
 Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu Ser Pro
 130 135 140
 Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly Thr Ile
 145 150 155 160
 Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Phe Gln Gln His
 165 170 175
 Ala Ala Leu Lys Ile Ser Ser Ala Leu Lys Asp Ser Asp Leu Pro
 180 185 190

<210> 414
 <211> 389
 <212> PRT
 <213> Homo sapiens

<400> 414
 Met Ala Glu Pro Asp Pro Ser His Pro Leu Glu Thr Gln Ala Gly Lys
 1 5 10 15
 Val Gln Glu Ala Gln Asp Ser Asp Ser Asp Ser Glu Gly Gly Ala Ala
 20 25 30
 Gly Gly Glu Ala Asp Met Asp Phe Leu Arg Asn Leu Phe Ser Gln Thr
 35 40 45
 Leu Ser Leu Gly Ser Gln Lys Glu Arg Leu Leu Asp Glu Leu Thr Leu
 50 55 60
 Glu Gly Val Ala Arg Tyr Met Gln Ser Glu Arg Cys Arg Arg Val Ile
 65 70 75 80
 Cys Leu Val Gly Ala Gly Ile Ser Thr Ser Ala Gly Ile Pro Asp Phe
 85 90 95
 Arg Ser Pro Ser Thr Gly Leu Tyr Asp Asn Leu Glu Lys Tyr His Leu
 100 105 110

Pro Tyr Pro Glu Ala Ile Phe Glu Ile Ser Tyr Phe Lys Lys His Pro
 115 120 125
 Glu Pro Phe Phe Ala Leu Ala Lys Glu Leu Tyr Pro Gly Gln Phe Lys
 130 135 140
 Pro Thr Ile Cys His Tyr Phe Met Arg Leu Leu Lys Asp Lys Gly Leu
 145 150 155 160
 Leu Leu Arg Cys Tyr Thr Gln Asn Ile Asp Thr Leu Glu Arg Ile Ala
 165 170 175
 Gly Leu Glu Gln Glu Asp Leu Val Glu Ala His Gly Thr Phe Tyr Thr
 180 185 190
 Ser His Cys Val Ser Ala Ser Cys Arg His Glu Tyr Pro Leu Ser Trp
 195 200 205
 Met Lys Glu Lys Ile Phe Ser Glu Val Thr Pro Lys Cys Glu Asp Cys
 210 215 220
 Gln Ser Leu Val Lys Pro Asp Ile Val Phe Phe Gly Glu Ser Leu Pro
 225 230 235 240
 Ala Arg Phe Phe Ser Cys Met Gln Ser Asp Phe Leu Lys Val Asp Leu
 245 250 255
 Leu Leu Val Met Gly Thr Ser Leu Gln Val Gln Pro Phe Ala Ser Leu
 260 265 270
 Ile Ser Lys Ala Pro Leu Ser Thr Pro Arg Leu Leu Ile Asn Lys Glu
 275 280 285
 Lys Ala Gly Gln Ser Asp Pro Phe Leu Gly Met Ile Met Gly Leu Gly
 290 295 300
 Gly Gly Met Asp Phe Asp Ser Lys Lys Ala Tyr Arg Asp Val Ala Trp
 305 310 315 320
 Leu Gly Glu Cys Asp Gln Gly Cys Leu Ala Leu Ala Glu Leu Leu Gly
 325 330 335
 Trp Lys Lys Glu Leu Glu Asp Leu Val Arg Arg Glu His Ala Ser Ile
 340 345 350
 Asp Ala Gln Ser Gly Ala Gly Val Pro Asn Pro Ser Thr Ser Ala Ser
 355 360 365
 Pro Lys Lys Ser Pro Pro Pro Ala Lys Asp Glu Ala Arg Thr Thr Glu
 370 375 380
 Arg Glu Lys Pro Gln
 385

<210> 415

<211> 481

<212> PRT

<213> Homo sapiens

<400> 415

Met Ser Leu Asn Leu Pro Glu Ala Ser Leu Leu Ser Arg Ala Ser Trp
 1 5 10 15
 Pro Glu Gln Ala Lys Glu Pro Arg Arg Glu Gly His Thr Asp Lys Gln
 20 25 30
 Gln Thr Glu Asp Val Leu Ala Ala Gly Leu Arg Cys Leu Pro His Leu
 35 40 45
 Pro Ala Ile Cys Ala Arg Arg Met Ser Pro Ala Phe Arg Ala Met Asp
 50 55 60
 Val Glu Pro Arg Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln
 65 70 75 80
 Val Gly Gly His Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys
 85 90 95
 Lys Pro Leu Val Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ala
 100 105 110
 Glu Met Arg Lys Phe Thr Pro Gln Tyr Lys Gly Val Val Ser Val Arg

Ala	Glu	Thr	Leu	Asp	Met	Ala	Ser	His	Thr	Trp	Leu	Ala	Leu	Ala	Pro
50						55					60				
Leu	Pro	Thr	Ala	Arg	Ala	Gly	Ala	Ala	Ala	Val	Val	Leu	Gly	Lys	Gln
65					70					75					80
Val	Leu	Val	Val	Gly	Gly	Val	Asp	Glu	Val	Gln	Ser	Pro	Val	Ala	Ala
				85					90					95	
Val	Glu	Ala	Phe	Leu	Met	Asp	Glu	Gly	Arg	Trp	Glu	Arg	Arg	Ala	Thr
			100					105					110		
Leu	Pro	Gln	Ala	Ala	Met	Gly	Val	Ala	Thr	Val	Glu	Arg	Asp	Gly	Met
		115					120					125			
Val	Tyr	Ala	Leu	Gly	Gly	Met	Gly	Pro	Asp	Thr	Ala	Pro	Gln	Ala	Gln
		130				135					140				
Val	Arg	Val	Tyr	Glu	Pro	Arg	Arg	Asp	Cys	Trp	Leu	Ser	Leu	Pro	Ser
145					150					155					160
Met	Pro	Thr	Pro	Cys	Tyr	Gly	Ala	Ser	Thr	Phe	Leu	His	Gly	Asn	Lys
				165					170					175	
Ile	Tyr	Val	Leu	Gly	Gly	Arg	Gln	Gly	Lys	Leu	Pro	Val	Thr	Ala	Phe
			180				185						190		
Glu	Ala	Phe	Asp	Leu	Glu	Ala	Arg	Thr	Trp	Thr	Arg	His	Pro	Ser	Leu
		195				200						205			
Pro	Ser	Arg	Arg	Ala	Phe	Ala	Gly	Cys	Ala	Met	Ala	Glu	Gly	Ser	Val
		210				215					220				
Phe	Ser	Leu	Gly	Gly	Leu	Gln	Gln	Pro	Gly	Pro	His	Asn	Phe	Tyr	Ser
225					230					235					240
Arg	Pro	His	Phe	Val	Asn	Thr	Val	Glu	Met	Phe	Asp	Leu	Glu	His	Gly
				245					250					255	
Ser	Trp	Thr	Lys	Leu	Pro	Arg	Ser	Leu	Arg	Met	Arg	Asp	Lys	Arg	Ala
			260					265					270		
Asp	Phe	Val	Val	Gly	Ser	Leu	Gly	Gly	His	Ile	Val	Ala	Ile	Gly	Gly
		275					280					285			
Leu	Gly	Asn	Gln	Pro	Cys	Pro	Leu	Gly	Ser	Val	Glu	Ser	Phe	Ser	Leu
		290				295					300				
Ala	Arg	Arg	Arg	Trp	Glu	Ala	Leu	Pro	Ala	Met	Pro	Thr	Ala	Arg	Cys
305					310					315					320
Ser	Cys	Ser	Ser	Leu	Gln	Ala	Gly	Pro	Arg	Leu	Phe	Val	Ile	Gly	Gly
				325				330						335	
Val	Ala	Gln	Gly	Pro	Ser	Gln	Ala	Val	Glu	Ala	Leu	Cys	Leu	Arg	Asp
			340					345					350		

<210> 417

<211> 20

<212> PRT

<213> Homo sapiens

<400> 417

Met	Lys	Gly	Leu	Tyr	Phe	Gln	Gln	Ser	Ser	Thr	Asp	Glu	Glu	Ile	Thr
1				5					10					15	

Phe	Val	Phe	Gln
			20

<210> 418

<211> 320

<212> PRT

<213> Homo sapiens

<400> 418

Met Lys Gly Leu Tyr Phe Gln Gln Ser Ser Thr Asp Glu Glu Ile Thr
1 5 10 15
Phe Val Phe Gln Glu Lys Glu Asp Leu Pro Val Thr Glu Asp Asn Phe
20 25 30
Val Lys Leu Gln Val Lys Ala Cys Ala Leu Ser Gln Ile Asn Thr Lys
35 40 45
Leu Leu Ala Glu Met Lys Met Lys Lys Asp Leu Phe Pro Val Gly Arg
50 55 60
Glu Ile Ala Gly Ile Val Leu Asp Val Gly Ser Lys Val Ser Phe Phe
65 70 75 80
Gln Pro Asp Asp Glu Val Val Gly Ile Leu Pro Leu Asp Ser Glu Asp
85 90 95
Pro Gly Leu Cys Glu Val Val Arg Val His Glu His Tyr Leu Val His
100 105 110
Lys Pro Glu Lys Val Thr Trp Thr Glu Ala Ala Gly Ser Ile Arg Asp
115 120 125
Gly Val Arg Ala Tyr Thr Ala Leu His Tyr Leu Ser His Leu Ser Pro
130 135 140
Gly Lys Ser Val Leu Ile Met Asp Gly Ala Ser Ala Phe Gly Thr Ile
145 150 155 160
Ala Ile Gln Leu Ala His His Arg Gly Ala Lys Val Ile Ser Thr Ala
165 170 175
Cys Ser Leu Glu Asp Lys Gln Cys Leu Glu Arg Phe Arg Pro Pro Ile
180 185 190
Ala Arg Val Ile Asp Val Ser Asn Gly Lys Val His Val Ala Glu Ser
195 200 205
Cys Leu Glu Glu Thr Gly Gly Leu Gly Val Asp Ile Val Leu Asp Ala
210 215 220
Gly Val Arg Leu Tyr Ser Lys Asp Asp Glu Pro Ala Val Lys Leu Gln
225 230 235 240
Leu Leu Pro His Lys His Asp Ile Ile Thr Leu Leu Gly Val Gly Gly
245 250 255
His Trp Val Thr Thr Glu Glu Asn Leu Gln Leu Asp Pro Pro Asp Ser
260 265 270
His Cys Leu Phe Leu Lys Gly Ala Thr Leu Ala Phe Leu Asn Asp Glu
275 280 285
Val Trp Asn Leu Ser Asn Val Gln Gln Gly Lys Tyr Leu Tyr Leu Lys
290 295 300
Gly Cys Asp Gly Glu Val Ile Asn Trp Cys Phe Gln Thr Ser Val Gly
305 310 315 320

<210> 419
<211> 159
<212> PRT
<213> Homo sapiens

<400> 419
Met Glu Lys Leu Arg Arg Val Leu Ser Gly Gln Asp Asp Glu Glu Gln
1 5 10 15
Gly Leu Thr Ala Gln Val Leu Asp Ala Ser Ser Leu Ser Phe Asn Thr
20 25 30
Arg Leu Lys Trp Phe Ala Ile Cys Phe Val Cys Gly Val Phe Phe Ser
35 40 45
Ile Leu Gly Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe
50 55 60
Ala Val Phe Tyr Thr Leu Gly Asn Leu Ala Ala Leu Ala Ser Thr Cys
65 70 75 80
Phe Leu Met Gly Pro Val Lys Gln Leu Lys Lys Met Phe Glu Ala Thr

				85				90					95				
Arg	Leu	Leu	Ala	Thr	Ile	Val	Met	Leu	Leu	Cys	Phe	Ile	Phe	Thr	Leu		
			100					105					110				
Cys	Ala	Ala	Leu	Trp	Trp	His	Lys	Lys	Gly	Leu	Ala	Val	Leu	Phe	Cys		
		115					120					125					
Ile	Leu	Gln	Phe	Leu	Ser	Met	Thr	Trp	Tyr	Ser	Leu	Ser	Tyr	Ile	Pro		
	130					135					140						
Tyr	Ala	Arg	Asp	Ala	Val	Ile	Lys	Cys	Cys	Ser	Ser	Leu	Leu	Ser			
145					150					155							

<210> 420

<211> 183

<212> PRT

<213> Homo sapiens

<400> 420

Met	Glu	Gln	Arg	Leu	Ala	Glu	Phe	Arg	Ala	Ala	Arg	Lys	Arg	Ala	Gly		
1			5					10				15					
Leu	Ala	Ala	Gln	Pro	Pro	Ala	Ala	Ser	Gln	Gly	Ala	Gln	Thr	Pro	Gly		
		20						25				30					
Glu	Lys	Ala	Glu	Ala	Ala	Ala	Thr	Leu	Lys	Ala	Ala	Pro	Gly	Trp	Leu		
	35						40					45					
Lys	Arg	Phe	Leu	Val	Trp	Lys	Pro	Arg	Pro	Ala	Ser	Ala	Arg	Ala	Gln		
	50					55					60						
Pro	Gly	Leu	Val	Gln	Glu	Ala	Ala	Gln	Pro	Gln	Gly	Ser	Thr	Ser	Glu		
65				70						75					80		
Thr	Pro	Trp	Asn	Thr	Ala	Ile	Pro	Leu	Pro	Ser	Cys	Trp	Asp	Gln	Ser		
			85					90						95			
Phe	Leu	Thr	Asn	Ile	Thr	Phe	Leu	Lys	Val	Leu	Leu	Trp	Leu	Val	Leu		
		100					105						110				
Leu	Gly	Leu	Phe	Val	Glu	Leu	Glu	Phe	Gly	Leu	Ala	Tyr	Phe	Val	Leu		
	115						120					125					
Ser	Leu	Phe	Tyr	Trp	Met	Tyr	Val	Gly	Thr	Arg	Gly	Pro	Glu	Glu	Lys		
	130					135					140						
Lys	Glu	Gly	Glu	Lys	Ser	Ala	Tyr	Ser	Val	Phe	Asn	Pro	Gly	Cys	Glu		
145				150						155				160			
Ala	Ile	Gln	Gly	Thr	Leu	Thr	Ala	Glu	Gln	Leu	Glu	Arg	Glu	Leu	Gln		
			165					170						175			
Leu	Arg	Pro	Leu	Ala	Gly	Arg											
			180														

<210> 421

<211> 143

<212> PRT

<213> Homo sapiens

<400> 421

Met	Ala	Ala	Pro	Arg	Arg	Gly	Arg	Gly	Ser	Ser	Thr	Val	Leu	Ser	Ser		
1			5					10					15				
Val	Pro	Leu	Gln	Met	Leu	Phe	Tyr	Leu	Ser	Gly	Thr	Tyr	Tyr	Ala	Leu		
		20						25					30				
Tyr	Phe	Leu	Ala	Thr	Leu	Leu	Met	Ile	Thr	Tyr	Lys	Ser	Gln	Val	Phe		
	35						40					45					
Ser	Tyr	Pro	His	Arg	Tyr	Leu	Val	Leu	Asp	Leu	Ala	Leu	Leu	Phe	Leu		
	50					55					60						
Met	Gly	Ile	Leu	Glu	Ala	Val	Arg	Leu	Tyr	Leu	Gly	Thr	Arg	Gly	Asn		
65				70						75					80		
Leu	Thr	Glu	Ala	Glu	Arg	Pro	Leu	Ala	Ala	Ser	Leu	Ala	Leu	Thr	Ala		

85 90 95
 Gly Thr Ala Leu Leu Ser Ala His Phe Leu Leu Trp Gln Ala Leu Val
 100 105 110
 Leu Trp Ala Asp Trp Ala Leu Ser Ala Thr Leu Leu Ala Leu His Gly
 115 120 125
 Leu Glu Ala Val Leu Gln Val Val Ala Ile Ala Ala Phe Thr Arg
 130 135 140

<210> 422
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 422
 Met Ser Gly Val Pro Ala Glu Met Thr Gly Ala Val Glu Ala Phe Leu
 1 5 10 15
 Pro Val Val Ser Ser Ser Arg Arg Leu Pro Arg Phe Val His Met Val
 20 25 30
 Ala Gly Val Ser Ser Lys Gln Glu Arg Ala Arg Ser Asn Thr Glu Ala
 35 40 45
 Leu Phe Lys Leu Cys Phe His His Ile Cys Gln Cys Leu Thr Asp Glu
 50 55 60
 His Lys Phe His Gly Gln Val Gln Phe
 65 70

<210> 423
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 423
 Met Pro Pro Phe Gly Gly His Pro Leu Ser Gln Glu Glu Asp Gly Ser
 1 5 10 15
 Gln Arg Cys Cys Cys Leu Ser Ser Leu Arg Ser Val Asp Asp Ser Asn
 20 25 30
 Gly Glu Thr Val Val Ile Met Ala Leu Phe Leu Ala Val Ser Tyr His
 35 40 45
 His Lys Thr Gln Ser Lys Arg Trp Pro Gly Leu Thr Pro Pro His Ser
 50 55 60
 Ser Leu Leu Cys Arg Pro Leu Gln Leu Ser Phe Leu Val Ile Gln Ser
 65 70 75 80
 Val Arg Met Arg Ala Cys Gly Cys Asp Ser Gly His Cys Arg Ile Leu
 85 90 95
 Gly Arg Tyr Ser Leu Leu Gly Trp Ser Gln Gly His Arg Ala Arg Gly
 100 105 110
 Arg Gly Gly Val Ser Leu Arg Asp Asn Thr Phe Phe Gln Glu Ala Ser
 115 120 125
 Glu Gly Gln Gly Gln Trp Leu Met Pro Val Ile Pro Ala Phe
 130 135 140

<210> 424
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 424
 Met Leu Ser Ile Leu Lys Pro Arg Arg Ser Gln Glu Trp Arg Thr Ala
 1 5 10 15

Leu Arg Arg Tyr Cys Cys Pro Thr Asp Leu Gln Ala Pro Arg Ser Pro
 20 25 30
 Val Pro Pro Ile Arg Lys Val Gly Ile Ser Asp Val Ile Val His Ala
 35 40 45
 Asn Leu Ala Thr Ser Leu Lys Lys Asn Thr Cys Asn Cys Gln Ala Asp
 50 55 60
 Leu Leu Ser Trp Arg Ser Trp Val Asn Gly Ile Ser Cys His Cys Pro
 65 70 75 80
 Asn Leu Arg Pro Leu Ser Lys Ser Ile Phe Arg Asp Ser Thr Ser Leu
 85 90 95
 Cys Ser Leu Ser Gln Gln Arg Leu Cys Pro Leu His Ser Lys Pro Glu
 100 105 110
 Ala Cys Trp Gly Leu Phe Val Ser Val His Ala His Phe Arg Val Gln
 115 120 125
 Ala Gly Gly Arg Gly Asn Arg Val Gly Lys Lys Thr Arg Val Ser Arg
 130 135 140
 Asn Asp Glu Thr Leu
 145

<210> 425
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 425
 Met Tyr Leu Pro Pro Asn Arg Ser Glu Leu Cys Asn Phe Ala Leu Ser
 1 5 10 15
 Leu Asn Leu Tyr Gly Lys Gly Phe Phe Ser Leu Val Glu Lys His Asn
 20 25 30
 Ser Arg Asp Leu Glu Asp Arg Ala Ser Ser Gly Pro Ser Leu Ser Ser
 35 40 45
 Pro Ser His Pro Asp Trp Gly Tyr Ile Val Leu Ile Leu Val Ala Thr
 50 55 60
 Leu Gly Glu Leu Asp Thr Gln Val Gly Gly His
 65 70 75

<210> 426
 <211> 168
 <212> PRT
 <213> Homo sapiens

<400> 426
 Met Arg Leu Thr Glu Lys Ser Glu Gly Glu Gln Gln Leu Lys Pro Asn
 1 5 10 15
 Asn Ser Asn Ala Pro Asn Glu Asp Gln Glu Glu Glu Ile Gln Gln Ser
 20 25 30
 Glu Gln His Thr Pro Ala Arg Gln Arg Thr Gln Arg Ala Asp Thr Gln
 35 40 45
 Pro Ser Arg Cys Arg Leu Pro Ser Arg Arg Thr Pro Thr Thr Ser Ser
 50 55 60
 Asp Arg Thr Ile Asn Leu Leu Glu Val Leu Pro Trp Pro Thr Glu Trp
 65 70 75 80
 Ile Phe Asn Pro Tyr Arg Leu Pro Ala Leu Phe Glu Leu Tyr Pro Glu
 85 90 95
 Phe Leu Leu Val Phe Lys Glu Ala Phe His Asp Ile Ser His Cys Leu
 100 105 110
 Lys Ala Gln Met Glu Lys Ile Gly Leu Pro Ile Ile Leu His Leu Phe
 115 120 125

Ala Leu Ser Thr Leu Tyr Phe Tyr Lys Phe Phe Leu Pro Thr Ile Leu
 130 135 140
 Ser Leu Ser Phe Phe Ile Leu Leu Val Leu Leu Leu Leu Phe Ile
 145 150 155 160
 Ile Val Phe Ile Leu Ile Phe Phe
 165

<210> 427
 <211> 160
 <212> PRT
 <213> Homo sapiens

<400> 427
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
 1 5 10 15
 Asp Val Ala His Asn Pro Arg Pro Arg Arg Ile Ala Gln Arg Gly Arg
 20 25 30
 Asn Thr Ser Arg Met Ala Glu Asp Thr Ser Pro Asn Met Asn Asp Asn
 35 40 45
 Ile Leu Leu Pro Val Arg Asn Asn Asp Gln Ala Leu Gly Leu Thr Gln
 50 55 60
 Cys Met Leu Gly Cys Val Ser Trp Phe Thr Cys Phe Ala Cys Ser Leu
 65 70 75 80
 Arg Thr Gln Ala Gln Gln Val Leu Phe Asn Thr Cys Arg Asp Arg Val
 85 90 95
 Ser Pro Cys Cys Pro Gly Trp Ser Gln Thr Pro Val Ile Leu Pro Pro
 100 105 110
 Gln Pro Ser Glu Val Leu Gly Leu Gln Met Gln Ala Ala Val Pro Glu
 115 120 125
 Ala His Gly Glu Asp Arg His Ser Ala Pro Leu Cys Phe Arg Cys Val
 130 135 140
 Pro Gly Pro Cys Pro Val Pro Gly Gly Gly Ile Pro Gly Pro Trp His
 145 150 155 160

<210> 428
 <211> 94
 <212> PRT
 <213> Homo sapiens

<400> 428
 Met Asn Lys Glu Ile Asp Ser Leu Asn Leu Ala Tyr Ser Phe Pro Phe
 1 5 10 15
 Leu Leu Pro Ala Phe Leu Asp Thr Pro Trp Thr Asp Pro Phe Pro Ser
 20 25 30
 Gly Phe Met Val Arg Ser Arg Val Leu Leu Ile Gln Leu Leu Ser Arg
 35 40 45
 Pro Arg Ser Ser Gln Glu Ser Arg Gly His Ser Leu Pro Cys Ser Pro
 50 55 60
 Ser Ala Leu His Lys Pro Gly Gly Ile Cys Pro Ala Ala Leu Gly Arg
 65 70 75 80
 Ser His Leu Leu Val Trp Glu Gln Pro Ser Leu Arg Asp Ser
 85 90

<210> 429
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 429

Met	Lys	Ala	Ser	Gly	Pro	Asp	Leu	Ser	Asp	Gly	Leu	His	Cys	Pro	Ser
1				5					10					15	
Leu	Ile	Arg	His	Leu	Arg	Thr	Phe	Ser	Ala	Ala	Ala	Ala	Leu	Ala	Pro
			20					25					30		
Arg	Tyr	Pro	Thr	Arg	Leu	Pro	Ser	Ser	Leu	Leu	Leu	Trp	His	Leu	Cys
		35					40					45			
Gln	Cys	Leu	His	Leu	Leu	Tyr	Ala	Val	Ser	Thr	Ser	Cys	Asn	Ser	His
	50					55					60				
Gly	Lys	Arg	Ser	Ala	Ala	Trp	Ala	Met	Thr	Arg	Thr	Glu	Asp	Thr	Asp
65					70					75					80
Ala	Leu	Thr	Asp	Ser	Phe	Asp	Asp	Ser	Phe	Ile	Ser	Ser	Ala	Asp	
			85						90					95	

<210> 430

<211> 99

<212> PRT

<213> Homo sapiens

<400> 430

Met	Lys	Lys	Lys	Glu	Glu	Thr	Thr	Leu	Ser	Glu	Met	Glu	Pro	Val	Glu
1				5					10					15	
Pro	Gln	Tyr	Gln	Leu	Val	Asn	Ala	Glu	Ser	Thr	Ser	Pro	Phe	Leu	His
			20					25					30		
Cys	Leu	Arg	Glu	Val	Ile	Gly	Glu	Tyr	Ser	Val	His	Glu	Phe	Ser	Leu
		35					40					45			
Leu	Gly	Lys	Thr	Glu	Ser	Gln	Gly	Ile	Gly	Leu	Trp	Ile	Ala	Leu	Val
	50					55					60				
Val	Phe	Leu	Ser	Phe	Leu	Ile	Phe	Ser	Thr	Ser	Phe	Tyr	Ile	Ser	Asn
65					70					75					80
Ala	Glu	Gln	Pro	Phe	Phe	Lys	Glu	Pro	Pro	Thr	Glu	Ala	Ala	Lys	Glu
			85						90					95	

Leu Ser Leu

<210> 431

<211> 122

<212> PRT

<213> Homo sapiens

<400> 431

Ile	Arg	Ala	Thr	Met	Val	Ala	Arg	Val	Trp	Ser	Leu	Met	Arg	Phe	Leu
1				5					10					15	
Ile	Lys	Gly	Ser	Val	Ala	Gly	Gly	Ala	Val	Tyr	Leu	Val	Tyr	Asp	Gln
			20					25					30		
Glu	Leu	Leu	Gly	Pro	Ser	Asp	Lys	Ser	Gln	Ala	Ala	Leu	Gln	Lys	Ala
		35					40					45			
Gly	Glu	Val	Val	Pro	Pro	Ala	Met	Tyr	Gln	Phe	Ser	Gln	Tyr	Val	Cys
	50					55					60				
Gln	Gln	Thr	Gly	Leu	Gln	Ile	Pro	Gln	Leu	Pro	Ala	Pro	Pro	Lys	Ile
65					70					75					80
Tyr	Phe	Pro	Ile	Arg	Asp	Ser	Trp	Asn	Ala	Gly	Ile	Met	Thr	Val	Met
			85						90					95	
Ser	Ala	Leu	Ser	Val	Ala	Pro	Ser	Lys	Ala	Arg	Glu	Tyr	Ser	Lys	Glu
			100					105					110		
Gly	Trp	Glu	Tyr	Val	Lys	Ala	Arg	Thr	Lys						
		115						120							

<210> 432

<211> 118
 <212> PRT
 <213> Homo sapiens

<400> 432
 Met Gln Pro Ser Leu Leu Arg Ser Tyr Arg Leu Lys Ala Gln Leu Ser
 1 5 10 15
 Leu Ser Ser Thr Val Pro Arg Arg Ile Thr Asp Lys Pro Ala Thr Lys
 20 25 30
 Ser Trp Glu Gly Gly Arg Arg Glu Leu Cys Pro Arg Val Leu Phe Thr
 35 40 45
 Gln Leu Leu Leu Trp Val Trp Pro Gly Asp Pro Gly Pro Glu Leu Gln
 50 55 60
 Glu Thr Gly Phe Pro Gly Pro Pro Arg Pro Ala His Leu Lys Thr Asp
 65 70 75 80
 Arg Ala Ile Met Val Gly Val Lys Gly Ile Glu Glu Lys Ser Gly Ile
 85 90 95
 Gly Ala Gly Val Cys Arg Val Ser Val Glu Lys Leu Ala Ser Thr Gln
 100 105 110
 Glu Arg Thr Ser Ser Leu
 115

<210> 433
 <211> 49
 <212> PRT
 <213> Homo sapiens

<400> 433
 Met Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Pro
 1 5 10 15
 Val Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe
 20 25 30
 Thr Ala Trp Phe Phe Val Tyr Pro Phe Thr Glu Gln Pro Glu Asp Gln
 35 40 45
 His

<210> 434
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 434
 Met Leu Ala Leu Phe His Phe His Leu Pro Pro Trp Asp Asp Ala Val
 1 5 10 15
 Arg Arg Pro Ser Val Asp Ala Ser Pro Ser Thr Leu Asn Phe Pro Asp
 20 25 30
 Ala Glu Leu Tyr Ala Ser Ile Phe Leu Cys Cys Met Ala Pro Gly Glu
 35 40 45
 Ile Leu Ile Ser Phe Leu Thr Leu Val Gln Ile Ala His Ala Asn Gly
 50 55 60
 Arg Gly Cys Asn Thr Pro Ala Cys Gly Ala Ala Cys Val Trp His
 65 70 75 80
 Glu Asn Ser Gln Glu Arg Lys Tyr
 85

<210> 435
 <211> 87
 <212> PRT

<213> Homo sapiens

<400> 435

```

Met Ser Gln Gln His Arg Arg Lys Arg Pro Ser Ser Glu Arg Lys Ser
1          5          10          15
Thr Arg Lys Met Asp Thr Trp Gln Ser Leu Lys Val Lys Glu Val Phe
          20          25          30
Cys Lys His Asn Ser Ser Tyr Glu Cys Leu Leu Tyr Lys Glu Val Glu
          35          40          45
Ala Arg Gln Val Ser Lys Thr Ala Thr Asp Gly Ser Tyr Leu Leu Val
          50          55          60
Phe Thr Ser Tyr Val Ile Ser Ser Pro Val Trp Thr Gly Pro Gly Asp
65          70          75          80
Leu Leu Pro Val Asn Arg Ile
          85

```

<210> 436

<211> 45

<212> PRT

<213> Homo sapiens

<400> 436

```

Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
1          5          10          15
Asp Gly Pro Gln Ser Gln Thr Pro Glu Asp Cys Pro Ala Arg Pro Glu
          20          25          30
His Gln Gln Asp Gly Arg Gly His Leu Pro Lys His Glu
          35          40          45

```

<210> 437

<211> 65

<212> PRT

<213> Homo sapiens

<400> 437

```

Met Ala Tyr Leu Asp Asp Lys Gly Ser Leu Leu Ala Ile His Ser His
1          5          10          15
Ala Arg Gln His Ser His Glu Thr Asn Gln Val His Gln Trp Leu Pro
          20          25          30
Arg Asn Thr Phe Ala Phe Leu Ile Lys Glu Asp Arg Cys Ser Cys Arg
          35          40          45
Ser Thr Cys Ala Ser Phe Ser Phe Ser Ser Ser Phe Ser Phe Leu Ile
          50          55          60
Ser
65

```

<210> 438

<211> 112

<212> PRT

<213> Homo sapiens

<400> 438

```

Met Arg Lys Lys Cys Lys Cys Phe Thr Ile Lys Lys Thr Asn Thr Tyr
1          5          10          15
Glu Glu Ser Asn Ala Gly Asn Glu Gly Gln Lys Glu Ala Ile Ser Ile
          20          25          30
Cys Ile Cys Arg Arg Asp Gly Leu Leu Pro Leu Trp Val Thr Arg Leu
          35          40          45

```

Ser Asp Leu Val Phe Ser Lys Glu Lys Ala His Gly Met Ile Pro Leu
50 55 60
Leu Gly Ser His Arg Glu Lys Lys Thr Ser Lys Glu Met Lys Thr Ser
65 70 75 80
Ser Arg Asn Leu Arg Tyr Phe Ile Val Cys Arg Asp Ala Ser Ser Tyr
85 90 95
Thr Pro Gln Ser Leu Ile Ser Gly Tyr Ile Gly Pro Cys Gln His Gln
100 105 110

<210> 439

<211> 110

<212> PRT

<213> Homo sapiens

<400> 439

Met Val Phe Gly Ala Met Val Leu Leu Val Gly Leu Glu Glu Leu Thr
1 5 10 15
Asn Ile Arg Asn Val Glu Arg Leu Lys Asp Leu Arg Ala Ser Tyr
20 25 30
Cys Leu Ile Asp Ser Phe Leu Gly Asp Ser Glu Leu Ile Gly Asp Leu
35 40 45
Thr Gln Cys Val Asp Cys Val Ile Pro Pro Glu Gly Ser Leu Leu Gln
50 55 60
Ile Ser Ser Tyr Leu Tyr Leu Asn Thr Ala Leu Val Asp Leu Pro Gly
65 70 75 80
Val Ala Ala Ser Gln Ala Cys Asp Ser Gln Gln Val Thr Trp Leu Leu
85 90 95
Tyr Val Ala Asn Gly Ala Tyr Ser Ala Cys Asn Arg Pro Gly
100 105 110

<210> 440

<211> 121

<212> PRT

<213> Homo sapiens

<400> 440

Thr Ser Ser Ser Gly Ala Glu Val Thr Met Ala Ala Ala Leu Ala Arg
1 5 10 15
Leu Gly Leu Arg Pro Val Lys Gln Val Arg Val Gln Phe Cys Pro Phe
20 25 30
Glu Lys Asn Val Glu Ser Thr Arg Thr Phe Leu Gln Thr Val Ser Ser
35 40 45
Glu Lys Val Arg Ser Thr Asn Leu Asn Cys Ser Val Ile Ala Asp Val
50 55 60
Arg His Asp Gly Ser Glu Pro Cys Val Asp Val Leu Phe Gly Asp Gly
65 70 75 80
His Arg Leu Ile Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu
85 90 95
Thr Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ala Gly Ser Gly
100 105 110
Asp Lys Pro Gly Ala Asp Thr Gly Arg
115 120

<210> 441

<211> 99

<212> PRT

<213> Homo sapiens

<400> 441

Met Leu Ala Arg Ala Thr Phe Arg Ala Ala Ser Ala Pro Thr Leu Val
 1 5 10 15
 Ala Arg Arg Gly Phe Gln Ser Thr Arg Ala Gln Met Ala Ser Pro Tyr
 20 25 30
 His Tyr Pro Glu Gly Pro Arg Ser Asn Leu Pro Phe Asp Pro Leu Lys
 35 40 45
 Lys Gly Phe Ala Phe Lys Tyr Trp Gly Phe Met Gly Thr Gly Phe Ala
 50 55 60
 Leu Pro Phe Leu Leu Ala Val Trp Gln Thr Glu Gln Ala Val Asn Ala
 65 70 75 80
 Leu Arg His Gly Val Asp Met Arg Ile Gly Ile Pro Gly Asn Thr Ala
 85 90 95
 Phe Val Asp

<210> 442

<211> 183

<212> PRT

<213> Homo sapiens

<400> 442

Arg Glu Gly Ala Arg Ala Arg Pro Ser Pro Thr Met Ser Asp Glu Ala
 1 5 10 15
 Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe
 20 25 30
 Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu
 35 40 45
 Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys Gln Leu Ser Ser Cys
 50 55 60
 His Arg Thr Asp Pro Leu His Arg Phe His Thr Asn Arg Trp Asn Leu
 65 70 75 80
 Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu Gly Ser Glu Glu Leu
 85 90 95
 Phe Ser Ser Val Ser Val Gly Asp Gln Asp Asp Cys Tyr Ser Leu Leu
 100 105 110
 Asp Asp Gln Asp Phe Thr Ser Phe Asp Leu Phe Pro Glu Gly Ser Val
 115 120 125
 Cys Ser Asp Val Ser Ser Ser Ile Ser Thr Tyr Trp Asp Trp Ser Asp
 130 135 140
 Ser Glu Phe Glu Trp Gln Leu Pro Gly Ser Asp Ile Ala Ser Gly Ser
 145 150 155 160
 Asp Val Leu Ser Asp Val Ile Pro Ser Ile Pro Ser Ser Pro Cys Leu
 165 170 175
 Leu Pro Lys Lys Lys Lys Lys
 180

<210> 443

<211> 94

<212> PRT

<213> Homo sapiens

<400> 443

Met Ser Asp Glu Ala Ser Ala Ile Thr Ser Tyr Glu Lys Phe Leu Thr
 1 5 10 15
 Pro Glu Glu Pro Phe Pro Leu Leu Gly Pro Pro Arg Gly Val Gly Thr
 20 25 30
 Cys Pro Ser Glu Glu Pro Gly Cys Leu Asp Ile Ser Asp Phe Gly Cys
 35 40 45

Gln Leu Ser Ser Cys His Arg Thr Asp Pro Leu His Arg Phe His Thr
 50 55 60
 Asn Arg Trp Asn Leu Thr Ser Cys Gly Thr Ser Val Ala Ser Ser Glu
 65 70 75 80
 Gly Ser Glu Glu Leu Phe Ser Ser Val Cys Trp Arg Ser Arg
 85 90

<210> 444
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 444
 Ile Gly Pro Arg Ala Pro Ser Pro Ser Phe Ser Val Arg Asp Val Glu
 1 5 10 15
 Leu Ser Asp Pro Ala Arg Glu Arg Gly Glu Met Pro Val Ala Val Gly
 20 25 30
 Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe Asp Arg Val Lys Met Gly
 35 40 45
 Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Gly Ala Leu Phe Gly
 50 55 60
 Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly
 65 70 75 80
 Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe
 85 90 95
 Met Ala Ile Gly Met Gly Ile Arg Cys
 100 105

<210> 445
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 445
 Met Pro Arg Ser Ser Arg Ser Pro Gly Asp Pro Gly Ala Leu Leu Glu
 1 5 10 15
 Asp Val Ala His Asn Pro Arg Pro Arg Arg Ile Ala Gln Arg Gly Arg
 20 25 30
 Asn Thr Ser Arg Met Ala Glu Asp Thr Ser Pro Asn Met Asn Asp Asn
 35 40 45
 Ile Leu Leu Pro Val Arg Asn Asn Asp Gln Ala Leu Gly Leu Thr Gln
 50 55 60
 Cys Met Leu Gly Cys Val Ser Trp Phe Thr Cys Phe Ala Cys Ser Leu
 65 70 75 80
 Arg Thr Gln Ala Gln Gln Val Leu Phe Asn Thr Cys Arg Cys Lys Leu
 85 90 95
 Leu Cys Gln Lys Leu Met Glu Lys Thr Gly Ile Leu Leu Leu Cys Ala
 100 105 110
 Phe Gly Val Ser Gln Gly Pro Ala Gln Ser Gln Val Glu Val Ser Leu
 115 120 125
 Gly Pro Gly Thr Asp Tyr Arg Thr Leu Gly Lys Thr Leu His Cys His
 130 135 140
 Val Thr Gln Phe Pro His Leu Pro Asp Gly Cys Cys Glu Asn Tyr
 145 150 155 160
 Glu Met Lys

<210> 446
 <211> 128

<212> PRT
<213> Homo sapiens

<400> 446
Met Glu Asp Lys Glu Ile Pro Ile Lys Ser Glu Pro Leu Pro Lys Pro
1 5 10 15
Pro Ala Ser Ala Pro Pro Ser Ile Leu Val Lys Pro Glu Asn Ser Arg
20 25 30
Asn Gly Ile Glu Lys Gln Val Lys Thr Val Arg Phe Gln Asn Tyr Ser
35 40 45
Pro Pro Pro Thr Lys His Tyr Thr Ser His Pro Thr Ser Gly Lys Pro
50 55 60
Glu Gln Pro Ala Thr Leu Lys Ala Ser Gln Pro Glu Ala Ala Ser Leu
65 70 75 80
Gly Pro Glu Met Thr Val Leu Phe Ala His Arg Ser Gly Cys His Ser
85 90 95
Gly Gln Gln Thr Asp Leu Arg Arg Lys Ser Ala Leu Ala Lys Ala Thr
100 105 110
Thr Leu Val Ser Thr Ala Ser Gly Thr Gln Thr Val Phe Pro Ser Lys
115 120 125

<210> 447
<211> 96
<212> PRT
<213> Homo sapiens

<400> 447
Met Leu Thr Arg Val Glu Glu Gln Lys Lys Met Val Lys Ala Cys Arg
1 5 10 15
Tyr Arg Cys Ser Ala Cys His Leu Lys Tyr Ser Pro Gln Arg Gln Lys
20 25 30
Glu Arg Lys Leu Ser Leu Lys Arg Gly Arg Thr Ser Gln Gln Asn Met
35 40 45
Ser Met Phe Trp Leu Lys Lys Leu Leu Glu Ser Gly Leu Phe Cys Ala
50 55 60
Met Cys Ser Pro Arg Ala Ser Thr Lys Lys Gly Phe Trp Cys Arg Pro
65 70 75 80
Lys Thr Thr Ile Ile Ile Ile Asp Tyr Ser Ser Pro Arg Gln Cys Leu
85 90 95

<210> 448
<211> 160
<212> PRT
<213> Homo sapiens

<220> .
<221> UNSURE
<222> 114
<223> Xaa = Glu,Val

<220>
<221> UNSURE
<222> 113
<223> Xaa = His,Gln

<220>
<221> UNSURE
<222> 115

<223> Xaa = Ile,Val

<400> 448

```

Met Gly Lys Ile Ala Leu Gln Leu Lys Ala Thr Leu Glu Asn Ile Thr
1          5          10          15
Asn Leu Arg Pro Val Gly Glu Asp Phe Arg Trp Tyr Leu Lys Met Lys
          20          25          30
Cys Gly Asn Cys Gly Glu Ile Ser Asp Lys Trp Gln Tyr Ile Arg Leu
          35          40          45
Met Asp Ser Val Ala Leu Lys Gly Gly Arg Gly Ser Ala Ser Met Val
          50          55          60
Gln Lys Cys Lys Leu Cys Ala Arg Glu Asn Ser Ile Glu Ile Leu Ser
65          70          75          80
Ser Thr Ile Lys Pro Tyr Asn Ala Glu Asp Asn Glu Asn Phe Lys Thr
          85          90          95
Ile Val Glu Phe Glu Cys Arg Gly Leu Glu Pro Val Asp Phe Gln Pro
          100          105          110
Xaa Xaa Xaa Leu Leu Leu Lys Val Trp Ser Gln Gly Gln Pro Ser Val
          115          120          125
Thr Leu Ile Cys Arg Arg Arg Thr Gly Thr Asp Tyr Asp Glu Lys Ala
          130          135          140
Gln Glu Ser Val Gly Ile Tyr Glu Val Thr His Gln Phe Val Lys Cys
145          150          155          160

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<210> 449

<211> 117

<212> PRT

<213> Homo sapiens

<400> 449

```

Met Asp Ser Leu Ala Ala Gly Glu Leu Asn Ala Ser His Gln Pro Trp
1          5          10          15
Val Pro Glu Phe Val Ala Tyr Trp Arg Lys Thr His Gln Asp His Leu
          20          25          30
Cys Ser Leu His Ser Arg Ala Phe Gly Leu Leu Asp Ala Arg Val Thr
          35          40          45
Trp Ala Leu Arg Arg Ala Pro Glu Pro Val Pro Gly Lys Asp Arg Leu
          50          55          60
Leu Leu Ala Ala Phe Pro Ala Glu Ala Ser Pro Val Asp Thr Ala Ser
65          70          75          80
Val Ser Val Tyr Gly Arg Ala Pro Arg Tyr Met His Lys Gly Val Lys
          85          90          95
Lys Cys Val Cys Thr Pro Val Ser Lys Asn Ser Thr Ala Trp Leu Leu
          100          105          110
Leu Gly Gly Ile Ser
          115

```

<210> 450

<211> 335

<212> PRT

<213> Homo sapiens

<400> 450

```

Met Cys Cys Gln Val Cys Glu Ala Val Arg Ser Gly Asn Glu Glu Val
1          5          10          15
Leu Ala Asp Val Arg Thr Ile Val Asn Gln Ile Ser Tyr Thr Pro Gln
          20          25          30
Asp Pro Arg Asp Leu Cys Gly Arg Ile Leu Thr Thr Cys Tyr Met Ala

```


35 40 45
 Ser Lys Asn Ser Ser Gln Glu Thr Cys Thr Arg Ala Arg Glu Leu Ala
 50 55 60
 Gln Gln Ile Gly Ser His Ile Ser Leu Asn Ile Asp Pro Ala Val
 65 70 75 80
 Lys Ala Val Met Gly Ile Phe Ser Leu Val Thr Gly Lys Ser Pro Leu
 85 90 95
 Phe Ala Ala His Gly Gly Ser Ser Arg Glu Asn Leu Ala Leu Gln Asn
 100 105 110
 Val Gln Ala Arg Ile Arg Met Val Leu Ala Tyr Leu Phe Ala Gln Leu
 115 120 125
 Ser Leu Trp Ser Arg Gly Val His Gly Gly Leu Leu Val Leu Gly Ser
 130 135 140
 Ala Asn Val Asp Glu Ser Leu Leu Gly Tyr Leu Thr Lys Tyr Asp Cys
 145 150 155 160
 Ser Ser Ala Asp Ile Asn Pro Ile Gly Gly Ile Ser Lys Thr Asp Leu
 165 170 175
 Arg Ala Phe Val Gln Phe Cys Ile Gln Arg Phe Gln Leu Pro Ala Leu
 180 185 190
 Gln Ser Ile Leu Leu Ala Pro Ala Thr Ala Glu Leu Glu Pro Leu Ala
 195 200 205
 Asp Gly Gln Val Ser Gln Thr Asp Glu Glu Asp Met Gly Met Thr Tyr
 210 215 220
 Ala Glu Leu Ser Val Tyr Gly Lys Leu Arg Lys Val Ala Lys Met Gly
 225 230 235 240
 Pro Tyr Ser Met Phe Cys Lys Leu Leu Gly Met Trp Arg His Ile Cys
 245 250 255
 Thr Pro Arg Gln Val Ala Asp Lys Val Lys Arg Phe Phe Ser Lys Tyr
 260 265 270
 Ser Met Asn Arg His Lys Met Thr Thr Leu Thr Pro Ala Tyr His Ala
 275 280 285
 Glu Asn Tyr Ser Pro Glu Asp Asn Arg Phe Asp Leu Arg Pro Phe Leu
 290 295 300
 Tyr Asn Thr Ser Trp Pro Trp Gln Phe Arg Cys Ile Glu Asn Gln Val
 305 310 315 320
 Leu Gln Leu Glu Arg Ala Glu Pro Gln Ser Leu Asp Gly Val Asp
 325 330 335

<210> 451

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> 76

<223> Xaa = Lys, Asn

<400> 451

Met Cys Trp Val Ile Asn His Ala Ile Leu Pro Arg Met Arg Met His
 1 5 10 15
 Ser Lys Arg Gln Thr Ile Thr Arg His Ser Ala Ser Leu Ser Phe His
 20 25 30
 Ala Leu Pro Arg Ser Ala Phe Leu Gln Leu Cys Leu Leu Arg Gln Ile
 35 40 45
 His Gln Ile Pro Cys Leu Ser Ile Phe Ser Ser Thr Leu Arg Ala Gln
 50 55 60
 Thr His Asp Ser Gly Ile Gly Cys Thr Thr Ala Xaa Pro Gly Gly Arg

65 70 75 80
Arg Gln Glu Gln Leu Arg
85

<210> 452
<211> 93
<212> PRT
<213> Homo sapiens

<400> 452
Met Lys Ile Ala Leu Cys Gln Arg Glu Leu Pro Ser Pro Arg Ser Cys
1 5 10 15
Leu Leu Ser Arg Asp Val Thr Gly Val Ile Cys Thr Arg Met Pro Arg
20 25 30
Leu Ala Ile Cys Ser Lys Thr Ala Gln Lys Ala Leu Pro Cys Ile Pro
35 40 45
Leu Leu His Thr Ser Pro Leu Cys Leu Gln Leu Leu Ser Ala Gly Leu
50 55 60
His Ile Tyr Ala Thr Leu Cys Lys Ser Cys Ala Ser Arg Asn His Lys
65 70 75 80
Asn Ile Phe Leu His Leu Leu His Ser Leu Ser Ala Ala
85 90

<210> 453
<211> 108
<212> PRT
<213> Homo sapiens

<400> 453
Met Ala Val Arg Ala Ser Phe Glu Asn Asn Cys Glu Ile Gly Cys Phe
1 5 10 15
Ala Lys Leu Thr Asn Thr Tyr Cys Leu Val Ala Ile Gly Gly Ser Glu
20 25 30
Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro Val
35 40 45
Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys Val
50 55 60
Gly Asp Arg Arg Asn Ser Gly Arg Cys Ala Gln Gly Gly Ser Leu Gln
65 70 75 80
Thr Asp Ser Gly Arg Pro Gly Ala Ser Arg Lys Leu Leu Cys Leu Gln
85 90 95
Gln Ser Gly Arg Ala Gly Ala Ser Gln Asp Phe Asn
100 105

<210> 454
<211> 277
<212> PRT
<213> Homo sapiens

<400> 454
Met Ser Leu Cys Glu Asp Met Leu Leu Cys Asn Tyr Arg Lys Cys Arg
1 5 10 15
Ile Lys Leu Ser Gly Tyr Ala Trp Val Thr Ala Cys Ser His Ile Phe
20 25 30
Cys Asp Gln His Gly Ser Gly Glu Phe Ser Arg Ser Pro Ala Ile Cys
35 40 45
Pro Ala Cys Asn Ser Thr Leu Ser Gly Lys Leu Asp Ile Val Arg Thr
50 55 60

Glu Leu Ser Pro Ser Glu Glu Tyr Lys Ala Met Val Leu Ala Gly Leu
65 70 75 80
Arg Pro Glu Ile Val Leu Asp Ile Ser Ser Arg Ala Leu Ala Phe Trp
85 90 95
Thr Tyr Gln Val His Gln Glu Arg Leu Tyr Gln Glu Tyr Asn Phe Ser
100 105 110
Lys Ala Glu Gly His Leu Lys Gln Met Glu Lys Ile Tyr Thr Gln Gln
115 120 125
Ile Gln Ser Lys Asp Val Glu Leu Thr Ser Met Lys Gly Glu Val Thr
130 135 140
Ser Met Lys Lys Val Leu Glu Glu Tyr Lys Lys Lys Phe Ser Asp Ile
145 150 155 160
Ser Glu Lys Leu Met Glu Arg Asn Arg Gln Tyr Gln Lys Leu Gln Gly
165 170 175
Leu Tyr Asp Ser Leu Arg Leu Arg Asn Ile Thr Ile Ala Asn His Glu
180 185 190
Gly Thr Leu Glu Pro Ser Met Ile Ala Gln Ser Gly Val Leu Gly Phe
195 200 205
Pro Leu Gly Asn Asn Ser Lys Phe Pro Leu Asp Asn Thr Pro Val Arg
210 215 220
Asn Arg Gly Asp Gly Asp Gly Asp Phe Gln Phe Arg Pro Phe Phe Ala
225 230 235 240
Gly Ser Pro Thr Ala Pro Glu Pro Ser Asn Ser Phe Phe Ser Phe Val
245 250 255
Ser Pro Ser Arg Glu Leu Glu Gln Gln Val Ser Ser Arg Ala Phe
260 265 270
Lys Val Lys Arg Ile
275

<210> 455

<211> 173

<212> PRT

<213> Homo sapiens

<400> 455

Met Leu Val Met Tyr Leu Leu Ala Ala Leu Phe Gly Tyr Leu Thr Phe
1 5 10 15
Tyr Gly Glu Val Glu Asp Glu Leu Leu His Ala Tyr Ser Lys Val Tyr
20 25 30
Thr Leu Asp Ile Pro Leu Leu Met Val Arg Leu Ala Val Leu Val Ala
35 40 45
Val Thr Leu Thr Val Pro Ile Val Leu Phe Pro Ile Arg Thr Ser Val
50 55 60
Ile Thr Leu Leu Phe Pro Lys Arg Pro Phe Ser Trp Ile Arg His Phe
65 70 75 80
Leu Ile Ala Ala Val Leu Ile Ala Leu Asn Asn Val Leu Val Ile Leu
85 90 95
Val Pro Thr Ile Lys Tyr Ile Phe Gly Phe Ile Gly Ala Ser Ser Ala
100 105 110
Thr Met Leu Ile Phe Ile Leu Pro Ala Val Phe Tyr Leu Lys Leu Val
115 120 125
Lys Lys Glu Thr Phe Arg Ser Pro Gln Lys Val Gly Ala Leu Ile Phe
130 135 140
Leu Val Val Gly Ile Phe Phe Met Ile Gly Ser Met Ala Leu Ile Ile
145 150 155 160
Ile Asp Trp Ile Tyr Asp Pro Pro Asn Ser Lys His His
165 170

<210> 456
 <211> 370
 <212> PRT
 <213> Homo sapiens

<400> 456

Met	Ser	Ala	Ser	Ala	Ala	Thr	Gly	Val	Phe	Val	Leu	Ser	Leu	Ser	Ala
1			5						10					15	
Ile	Pro	Val	Thr	Tyr	Val	Phe	Asn	His	Leu	Ala	Ala	Gln	His	Asp	Ser
		20					25					30			
Trp	Thr	Ile	Val	Gly	Val	Ala	Ala	Leu	Ile	Leu	Phe	Leu	Val	Ala	Leu
		35					40					45			
Leu	Ala	Arg	Val	Leu	Val	Lys	Arg	Lys	Pro	Pro	Arg	Asp	Pro	Leu	Phe
		50				55					60				
Tyr	Val	Tyr	Ala	Val	Phe	Gly	Phe	Thr	Ser	Val	Val	Asn	Leu	Ile	Ile
65					70					75				80	
Gly	Leu	Glu	Gln	Asp	Gly	Ile	Ile	Asp	Gly	Phe	Met	Thr	His	Tyr	Leu
			85					90						95	
Arg	Glu	Gly	Glu	Pro	Tyr	Leu	Asn	Thr	Ala	Tyr	Gly	His	Met	Ile	Cys
			100					105				110			
Tyr	Trp	Asp	Gly	Ser	Ala	His	Tyr	Leu	Met	Tyr	Leu	Val	Met	Val	Ala
		115					120					125			
Ala	Ile	Ala	Trp	Glu	Glu	Thr	Tyr	Arg	Thr	Ile	Gly	Leu	Tyr	Trp	Val
		130				135					140				
Gly	Ser	Ile	Ile	Met	Ser	Val	Val	Val	Phe	Val	Pro	Gly	Asn	Ile	Val
145				150					155					160	
Gly	Lys	Tyr	Gly	Thr	Arg	Ile	Cys	Pro	Ala	Phe	Phe	Leu	Ser	Ile	Pro
				165					170					175	
Tyr	Thr	Cys	Leu	Pro	Val	Trp	Ala	Gly	Phe	Arg	Ile	Tyr	Asn	Gln	Pro
			180					185					190		
Ser	Glu	Asn	Tyr	Asn	Tyr	Pro	Ser	Lys	Val	Ile	Gln	Glu	Ala	Gln	Ala
		195					200				205				
Lys	Asp	Leu	Leu	Arg	Arg	Pro	Phe	Asp	Leu	Met	Leu	Val	Val	Cys	Leu
		210				215					220				
Leu	Leu	Ala	Thr	Gly	Phe	Cys	Leu	Phe	Arg	Gly	Leu	Ile	Ala	Leu	Asp
225				230					235					240	
Cys	Pro	Ser	Glu	Leu	Cys	Arg	Leu	Tyr	Thr	Gln	Phe	Gln	Glu	Pro	Tyr
				245					250					255	
Leu	Lys	Asp	Pro	Ala	Ala	Tyr	Pro	Lys	Ile	Gln	Met	Leu	Ala	Tyr	Met
			260					265					270		
Phe	Tyr	Ser	Val	Pro	Tyr	Phe	Val	Thr	Ala	Leu	Tyr	Gly	Leu	Val	Val
			275				280					285			
Pro	Gly	Cys	Ser	Trp	Met	Pro	Asp	Ile	Thr	Leu	Ile	His	Ala	Gly	Gly
			290			295					300				
Leu	Ala	Gln	Ala	Gln	Phe	Ser	His	Ile	Gly	Ala	Ser	Leu	His	Ala	Arg
305					310					315					320
Thr	Ala	Tyr	Val	Tyr	Arg	Val	Pro	Glu	Glu	Ala	Lys	Ile	Leu	Phe	Leu
				325					330					335	
Ala	Leu	Asn	Ile	Ala	Tyr	Gly	Val	Leu	Pro	Gln	Leu	Leu	Ala	Tyr	Arg
			340					345					350		
Cys	Ile	Tyr	Lys	Pro	Glu	Phe	Phe	Ile	Lys	Thr	Lys	Ala	Glu	Glu	Lys
		355					360					365			
Val	Glu														
															370

<210> 457
 <211> 393
 <212> PRT

<213> Homo sapiens

<400> 457

Met Thr Tyr Arg Trp Gly Thr Leu Leu Met Lys Arg Lys Phe Glu Glu
1 5 10 15
Pro Arg Pro Gly Phe His Gly Val Leu Gly Ile Asn Ser Ile Thr Gly
20 25 30
Lys Glu Glu Pro Leu Tyr Pro Ser Tyr Lys Arg Gln Leu Arg Ile Tyr
35 40 45
Leu Val Ser Leu Pro Phe Val Cys Leu Cys Leu Tyr Phe Ser Leu Tyr
50 55 60
Val Met Met Ile Tyr Phe Asp Met Glu Val Trp Ala Leu Gly Leu His
65 70 75 80
Glu Asn Ser Gly Ser Glu Trp Thr Ser Val Leu Leu Tyr Val Pro Ser
85 90 95
Ile Ile Tyr Ala Ile Val Ile Glu Ile Met Asn Arg Leu Tyr Arg Tyr
100 105 110
Ala Ala Glu Phe Leu Thr Ser Trp Glu Asn His Arg Leu Glu Ser Ala
115 120 125
Tyr Gln Asn His Leu Ile Leu Lys Val Leu Val Phe Asn Phe Leu Asn
130 135 140
Cys Phe Ala Ser Leu Phe Tyr Ile Ala Phe Val Leu Lys Asp Met Lys
145 150 155 160
Leu Leu Arg Gln Ser Leu Ala Thr Leu Leu Ile Thr Ser Gln Ile Leu
165 170 175
Asn Gln Ile Met Glu Ser Phe Leu Pro Tyr Trp Leu Gln Arg Lys His
180 185 190
Gly Val Arg Val Lys Arg Lys Val Gln Ala Leu Lys Ala Asp Ile Asp
195 200 205
Ala Thr Leu Tyr Glu Gln Val Ile Leu Glu Lys Glu Met Gly Thr Tyr
210 215 220
Leu Gly Thr Phe Asp Asp Tyr Leu Glu Leu Phe Leu Gln Phe Gly Tyr
225 230 235 240
Val Ser Leu Phe Ser Cys Val Tyr Pro Leu Ala Ala Ala Phe Ala Val
245 250 255
Leu Asn Asn Phe Thr Glu Val Asn Ser Asp Ala Leu Lys Met Cys Arg
260 265 270
Val Phe Lys Arg Pro Phe Ser Glu Pro Ser Ala Asn Ile Gly Val Trp
275 280 285
Gln Leu Ala Phe Glu Thr Met Ser Val Ile Ser Val Val Thr Asn Cys
290 295 300
Ala Leu Ile Gly Met Ser Pro Gln Val Asn Ala Val Phe Pro Glu Ser
305 310 315 320
Lys Ala Asp Leu Ile Leu Ile Val Val Ala Val Glu His Ala Leu Leu
325 330 335
Ala Leu Lys Phe Ile Leu Ala Phe Ala Ile Pro Asp Lys Pro Arg His
340 345 350
Ile Gln Met Lys Leu Ala Arg Leu Glu Phe Glu Ser Leu Glu Ala Leu
355 360 365
Lys Gln Gln Gln Met Lys Leu Val Thr Glu Asn Leu Lys Glu Glu Pro
370 375 380
Met Glu Ser Gly Lys Glu Lys Ala Thr
385 390

<210> 458

<211> 116

<212> PRT

<213> Homo sapiens

<400> 458

Met Val Gly Gly Glu Ala Ala Ala Ala Val Glu Glu Leu Val Ser Gly
 1 5 10 15
 Val Arg Gln Ala Ala Asp Phe Ala Glu Gln Phe Arg Ser Tyr Ser Glu
 20 25 30
 Ser Glu Lys Gln Trp Lys Ala Arg Met Glu Phe Ile Leu Arg His Leu
 35 40 45
 Pro Asp Tyr Arg Asp Pro Pro Asp Gly Ser Gly Arg Leu Asp Gln Leu
 50 55 60
 Leu Ser Leu Ser Met Val Trp Ala Asn His Leu Phe Leu Gly Cys Ser
 65 70 75 80
 Tyr Asn Lys Asp Leu Leu Asp Lys Val Met Glu Met Ala Asp Gly Ile
 85 90 95
 Glu Val Glu Asp Leu Pro Gln Phe Thr Arg Ser Glu Leu Met Lys
 100 105 110
 Lys His Gln Ser
 115

<210> 459

<211> 163

<212> PRT

<213> Homo sapiens

<400> 459

Met Glu His Tyr Arg Lys Ala Gly Ser Val Glu Leu Pro Ala Pro Ser
 1 5 10 15
 Pro Met Pro Gln Leu Pro Pro Asp Thr Leu Glu Met Arg Val Arg Asp
 20 25 30
 Gly Ser Lys Ile Arg Asn Leu Leu Gly Leu Ala Leu Gly Arg Leu Glu
 35 40 45
 Gly Gly Ser Ala Arg His Val Val Phe Ser Gly Ser Gly Arg Ala Ala
 50 55 60
 Gly Lys Ala Val Ser Cys Ala Glu Ile Val Lys Arg Arg Val Pro Gly
 65 70 75 80
 Leu His Gln Leu Thr Lys Leu Arg Phe Leu Gln Thr Glu Asp Ser Trp
 85 90 95
 Val Pro Ala Ser Pro Asp Thr Gly Leu Asp Pro Leu Thr Val Arg Arg
 100 105 110
 His Val Pro Ala Val Trp Val Leu Leu Ser Arg Asp Pro Leu Asp Pro
 115 120 125
 Asn Glu Cys Gly Tyr Gln Pro Pro Gly Ala Pro Pro Gly Leu Gly Ser
 130 135 140
 Met Pro Ser Ser Ser Cys Gly Pro Arg Ser Arg Arg Ala Arg Asp
 145 150 155 160
 Thr Arg Ser

<210> 460

<211> 230

<212> PRT

<213> Homo sapiens

<400> 460

Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro Arg Asp Ser Gly
 1 5 10 15
 Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val Phe Lys Met Ala
 20 25 30
 Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala
 1 5 10 15
 Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu
 20 25 30
 Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg
 35 40 45
 Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Ala Thr Leu
 50 55 60
 Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp
 65 70 75 80
 Met Val Gly Gly Glu Gly Gly Ala Gly Gly Arg Ser Pro
 85 90

<210> 463
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 463
 Met Gly His Gly Asp Glu Ile Val Leu Ala Asp Leu Asn Phe Pro Ala
 1 5 10 15
 Ser Ser Ile Cys Gln Cys Gly Pro Met Glu Ile Arg Ala Asp Gly Leu
 20 25 30
 Gly Ile Pro Gln Leu Leu Glu Ala Val Leu Lys Leu Leu Pro Leu Asp
 35 40 45
 Thr Tyr Val Glu Ser Pro Ala Ala Val Met Glu Leu Val Pro Ser Asp
 50 55 60
 Lys Glu Arg Gly Leu Gln Thr Pro Val Trp Thr Glu Tyr Glu Ser Ile
 65 70 75 80
 Leu Arg Arg Ala Gly Cys Val Arg Ala Leu Ala Lys Ile Glu Arg Phe
 85 90 95
 Glu Phe Tyr Glu Arg Ala Lys Lys Ala Phe Ala Val Val Ala Thr Gly
 100 105 110
 Glu Thr Ala Leu Tyr Gly Asn Leu Ile Leu Arg Lys Gly Val Leu Ala
 115 120 125
 Leu Asn Pro Leu Leu
 130

<210> 464
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 464
 Met Gly His Gly Asp Glu Ile Val Leu Ala Asp Leu Asn Phe Pro Ala
 1 5 10 15
 Ser Ser Ile Cys Gln Cys Gly Pro Met Glu Ile Arg Ala Asp Gly Leu
 20 25 30
 Gly Ile Pro Gln Leu Leu Glu Ala Val Leu Ala Ala Ala Pro Gly His
 35 40 45
 Leu Cys Gly Glu Ser Gly Cys Ser His Gly Ala Gly Ala Gln Arg Gln
 50 55 60
 Gly Glu Gly Pro Ala Asp Pro Ser Val Asp Gly Val Arg Val His Pro
 65 70 75 80
 Thr Gln Gly Arg Leu Cys Glu Ser Pro Gly Lys Asp Arg Glu Val
 85 90 95

<210> 465

<211> 93
 <212> PRT
 <213> Homo sapiens

<400> 465
 Met Thr Pro Ile Lys Leu Leu Asn Leu Thr Ser Arg Tyr Asn Phe Arg
 1 5 10 15
 Arg Thr Phe Gly Ile Glu Leu Ser Ser Asn Ser Ser Tyr Cys Lys Arg
 20 25 30
 Gly Asn Gly Tyr Arg Ser Arg Val Pro Lys Glu Cys Glu Cys Asn Trp
 35 40 45
 Leu His Leu Glu Ser Asp Thr Leu Lys Lys Leu Pro Ile Ile Ser Pro
 50 55 60
 Ser Trp Thr Cys Arg Ile Ile Leu Phe Leu Tyr Phe Ser Gly Gln Leu
 65 70 75 80
 Leu Gln Leu Ser Leu Ser Cys Leu Gln Leu Ile Lys Leu
 85 90

<210> 466
 <211> 500
 <212> PRT
 <213> Homo sapiens

<400> 466
 Met Glu Val Ser Thr Asn Pro Ser Ser Asn Ile Asp Pro Gly Asn Tyr
 1 5 10 15
 Val Glu Met Asn Asp Ser Ile Thr His Leu Pro Ser Lys Val Val Ile
 20 25 30
 Gln Asp Ile Thr Met Glu Leu His Cys Pro Leu Cys Asn Asp Trp Phe
 35 40 45
 Arg Asp Pro Leu Met Leu Ser Cys Gly His Asn Phe Cys Glu Ala Cys
 50 55 60
 Ile Gln Asp Phe Trp Arg Leu Gln Ala Lys Glu Thr Phe Cys Pro Glu
 65 70 75 80
 Cys Lys Met Leu Cys Gln Tyr Asn Asn Cys Thr Phe Asn Pro Val Leu
 85 90 95
 Asp Lys Leu Val Glu Lys Ile Lys Lys Leu Pro Leu Leu Lys Gly His
 100 105 110
 Pro Gln Cys Pro Glu His Gly Glu Asn Leu Lys Leu Phe Ser Lys Pro
 115 120 125
 Asp Gly Lys Leu Ile Cys Phe Gln Cys Lys Asp Ala Arg Leu Ser Val
 130 135 140
 Gly Gln Ser Lys Glu Phe Leu Gln Ile Ser Asp Ala Val His Phe Phe
 145 150 155 160
 Met Glu Glu Leu Ala Ile Gln Gln Gly Gln Leu Glu Thr Thr Leu Lys
 165 170 175
 Glu Leu Gln Thr Leu Arg Asn Met Gln Lys Glu Ala Ile Ala Ala His
 180 185 190
 Lys Glu Asn Lys Leu His Leu Gln Gln His Val Ser Met Glu Phe Leu
 195 200 205
 Lys Leu His Gln Phe Leu His Ser Lys Glu Lys Asp Ile Leu Thr Glu
 210 215 220
 Leu Arg Glu Glu Gly Lys Ala Leu Asn Glu Glu Met Glu Leu Asn Leu
 225 230 235 240
 Ser Gln Leu Gln Glu Gln Cys Leu Leu Ala Lys Asp Met Leu Val Ser
 245 250 255
 Ile Gln Ala Lys Thr Glu Gln Gln Asn Ser Phe Asp Phe Leu Lys Asp
 260 265 270

Ile Thr Thr Leu Leu His Ser Leu Glu Gln Gly Met Lys Val Leu Ala
 275 280 285
 Thr Arg Glu Leu Ile Ser Arg Lys Leu Asn Leu Gly Gln Tyr Lys Gly
 290 295 300
 Pro Ile Gln Tyr Met Val Trp Arg Glu Met Gln Asp Thr Leu Cys Pro
 305 310 315 320
 Gly Leu Ser Pro Leu Thr Leu Asp Pro Lys Thr Ala His Pro Asn Leu
 325 330 335
 Val Leu Ser Lys Ser Gln Thr Ser Val Trp His Gly Asp Ile Lys Lys
 340 345 350
 Ile Met Pro Asp Asp Pro Glu Arg Phe Asp Ser Ser Val Ala Val Leu
 355 360 365
 Gly Ser Arg Gly Phe Thr Ser Gly Lys Trp Tyr Trp Glu Val Glu Val
 370 375 380
 Ala Lys Lys Thr Lys Trp Thr Val Gly Val Val Arg Glu Ser Ile Ile
 385 390 395 400
 Arg Lys Gly Ser Cys Pro Leu Thr Pro Glu Gln Gly Phe Trp Leu Leu
 405 410 415
 Arg Leu Arg Asn Gln Thr Asp Leu Lys Ala Leu Asp Leu Pro Ser Phe
 420 425 430
 Ser Leu Thr Leu Thr Asn Asn Leu Asp Lys Val Gly Ile Tyr Leu Asp
 435 440 445
 Tyr Glu Gly Gly Gln Leu Ser Phe Tyr Asn Ala Lys Thr Met Thr His
 450 455 460
 Ile Tyr Thr Phe Ser Asn Thr Phe Met Glu Lys Leu Tyr Pro Tyr Phe
 465 470 475 480
 Cys Pro Cys Leu Asn Asp Gly Arg Glu Asn Lys Glu Pro Leu His Ile
 485 490 495
 Leu His Pro Gln
 500

<210> 467
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 467
 Met Val Leu Thr Lys Pro Leu Gln Arg Asn Gly Ser Met Met Ser Phe
 1 5 10 15
 Glu Asn Val Lys Glu Lys Ser Arg Glu Gly Gly Pro His Ala His Thr
 20 25 30
 Pro Glu Glu Glu Leu Cys Phe Val Val Thr His Tyr Pro Gln Val Gln
 35 40 45
 Thr Thr Leu Asn Leu Phe Phe His Ile Phe Lys Val Leu Thr Gln Pro
 50 55 60
 Leu Ser Leu Leu Trp Gly Cys Asp Gln Lys Pro Arg Thr Val Pro Thr
 65 70 75 80
 Leu Gly Asn Gly Ala Trp Asp Thr Cys Gln Gln His Ile Arg Thr Ser
 85 90 95
 Ser Trp Thr Ala Asn Thr Leu Val Ile Gln Asn Gln His Ser Arg Glu
 100 105 110
 Ser Thr Val Ser Val Cys Leu Phe Met Leu Ile Arg Met Gln His Ile
 115 120 125
 Leu Lys Thr Asp Thr Leu Gln Gln Phe Arg Ile Cys
 130 135 140

<210> 468
 <211> 100

<212> PRT

<213> Homo sapiens

<400> 468

Met Tyr Met Leu Leu Ser Pro His Arg Leu Arg Glu Gln Ala Gly Val
1 5 10 15
Arg Gly Ser Ile Arg Thr Ala Asn Arg Thr Glu Asp Gly Leu Lys Ile
20 25 30
Arg Glu Ala Glu Ser Leu Pro Gln Ser Asn Thr Ala Asp Phe Lys Cys
35 40 45
Leu His Ser Ala Ser Leu Gln Gln Ala Pro Gly Gly Ile Leu Met Gly
50 55 60
Pro Ala Ser Ser Pro Trp Thr Leu Ala Val Glu Gly Glu Lys Arg Thr
65 70 75 80
Ser Ala Pro Pro Leu Arg Glu Ser Leu Met Pro Thr Lys Gly Leu Gly
85 90 95
Trp Trp Thr Gln
100

<210> 469

<211> 119

<212> PRT

<213> Homo sapiens

<400> 469

Met Ala Ser Tyr Ser Gly Phe Ser Gly Leu Leu Glu Ile Arg Tyr Gly
1 5 10 15
Pro Gly His Arg Ser Cys Leu Pro Gln Phe Ala Phe Phe Pro Gln Pro
20 25 30
Pro Leu Pro Arg Pro Arg Ile Cys Met Trp Val Leu Ala Glu Leu Leu
35 40 45
Glu Leu Gly Cys Pro Glu Gln Ser Leu Arg Asp Ala Ile Thr Leu Asp
50 55 60
Leu Phe Cys His Ala Leu Ile Phe Cys Arg Gln Gln Gly Phe Ser Leu
65 70 75 80
Glu Gln Thr Ser Ala Ala Cys Ala Leu Leu Gln Asp Leu His Lys Ala
85 90 95
Cys Ile Gly Glu Arg Gly Gln Leu Pro Gly Leu Ser Pro Arg Glu Lys
100 105 110
Arg Asn Arg Ala Trp His Lys
115

<210> 470

<211> 140

<212> PRT

<213> Homo sapiens

<400> 470

Met Arg Ser Glu Cys Val Leu Gly Ala Ala Ser Asp Ser Gly Gln Glu
1 5 10 15
Ala Pro Arg Asp Thr Trp Phe Leu Gln Gly Trp Lys Ala Ser Arg Arg
20 25 30
Phe Leu Ile Lys Gly Ser Val Ala Gly Gly Ala Val Tyr Leu Val Tyr
35 40 45
Asp Gln Glu Leu Leu Gly Pro Ser Asp Lys Ser Gln Ala Ala Leu Gln
50 55 60
Lys Ala Gly Glu Val Val Pro Pro Ala Met Tyr Gln Phe Ser Gln Tyr
65 70 75 80

098765097 060801

Val Cys Gln Gln Thr Gly Leu Gln Ile Pro Gln Leu Pro Ala Pro Pro
85 90 95
Lys Ile Tyr Phe Pro Ile Arg Asp Ser Trp Asn Ala Gly Ile Met Thr
100 105 110
Val Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu Tyr Ser
115 120 125
Lys Glu Gly Trp Glu Tyr Val Lys Ala Arg Thr Lys
130 135 140

<210> 471
<211> 109
<212> PRT
<213> Homo sapiens

<400> 471
Met Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala
1 5 10 15
Ser Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg
20 25 30
Thr Phe Gln Gln Ile Arg Cys Tyr Ser Ala Pro Val Ala Ala Glu Pro
35 40 45
Phe Leu Ser Gly Thr Ser Ser Asn Tyr Val Glu Glu Met Tyr Cys Ala
50 55 60
Trp Leu Glu Asn Pro Lys Ser Val His Lys Thr Gly Ser His Cys Cys
65 70 75 80
Pro Gly Trp Ser Ala Val Ala Gly Ser Arg Leu Ala Ala Thr Ser Asp
85 90 95
Ser Trp Val Gln Val Ile Leu Met Pro Gln Pro Pro Glu
100 105

<210> 472
<211> 100
<212> PRT
<213> Homo sapiens

<400> 472
Met Phe His Leu Arg Thr Cys Ala Ala Lys Leu Arg Pro Leu Thr Ala
1 5 10 15
Ser Gln Thr Val Lys Thr Phe Ser Gln Asn Arg Pro Ala Ala Ala Arg
20 25 30
Thr Phe Gln Gln Ile Arg Ala Ile Leu His Leu Leu Leu Leu Ser Pro
35 40 45
Phe Ser Val Gly Leu Val Arg Thr Met Trp Arg Arg Cys Thr Val Leu
50 55 60
Gly Trp Lys Thr Pro Lys Val Tyr Ile Arg Gln Gly Pro Thr Val Val
65 70 75 80
Gln Ala Gly Val Gln Trp Arg Asp Leu Gly Leu Leu Gln Pro Pro Thr
85 90 95
Pro Gly Phe Lys
100

<210> 473
<211> 141
<212> PRT
<213> Homo sapiens

<400> 473
Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile Pro Asp Gly Thr

1 5 10 15
 Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile Ala Ser Val Ala
 20 25 30
 Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn Pro Pro Gly Thr
 35 40 45
 Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
 50 55 60
 Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
 65 70 75 80
 Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala
 85 90 95
 Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala
 100 105 110
 Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu Val Lys Met Gly
 115 120 125
 Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys Val
 130 135 140

<210> 474
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 474
 Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu Gly Pro Leu Ala Ala
 1 5 10 15
 Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr Glu Gly Pro Val Arg
 20 25 30
 Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn Thr Met Ala Ala Ala
 35 40 45
 Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
 50 55 60
 Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu
 65 70 75 80
 Ser Gly Pro Arg Gly Pro Thr Gly Arg Ser Phe Ala Val His Thr Arg
 85 90 95
 Arg Glu Asn Pro Ala Glu Pro Gly Ala Val Thr Gly Ser Ala Thr Val
 100 105 110
 Thr Ala Phe Trp Arg Ser Leu Leu Ala Cys Cys Gln Leu Pro Ser Arg
 115 120 125
 Pro Gly Ile His Leu Cys
 130

<210> 475
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 475
 Met Ala Thr His Pro Asp Gly Phe Arg Leu Glu Gly Pro Leu Ala Ala
 1 5 10 15
 Ala His Ser Pro Gly Pro Cys Thr Val Leu Tyr Glu Gly Pro Val Arg
 20 25 30
 Gly Leu Cys Pro Phe Ala Pro Arg Asn Ser Asn Thr Met Ser Ala Ala
 35 40 45
 Ala Leu Ala Ala Pro Ser Leu Gly Phe Asp Gly Val Ile Gly Val Leu
 50 55 60
 Val Ala Asp Thr Ser Leu Thr Asp Met His Val Val Asp Val Glu Leu

[illegible][illegible]

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<400> 477
Met Gly Arg Pro Trp Met Val Met Ile Leu Glu Ser Lys Ser Glu Glu
1          5          10          15
Lys Met Trp Tyr Gly Val Phe Leu Trp Ala Leu Val Ser Ser Leu Phe
          20          25          30
Phe His Val Pro Ala Gly Leu Leu Ala Leu Phe Thr Leu Arg His His
          35          40          45
Lys Tyr Gly Arg Phe Met Ser Val Ser Ile Leu Leu Met Gly Ile Val
          50          55          60
Gly Pro Ile Thr Ala Gly Ile Leu Thr Ser Ala Ala Ile Ala Gly Val
65          70          75          80
Tyr Arg Ala Ala Gly Lys Glu Met Ile Pro Phe Glu Ala Leu Thr Leu
          85          90          95
Gly Thr Gly Gln Thr Phe Cys Val Leu Val Val Ser Phe Leu Arg Ile
          100          105          110
Leu Ala Thr Leu
          115

```

<400> 478

Met Asn Arg Tyr Cys Gly Lys Ile Phe Val Ser Val Met Val Lys Leu
 1 5 10 15
 Gln Lys Asn Lys Leu Thr Ser Phe Pro Arg Gln Pro Leu Leu Thr Phe
 20 25 30
 Phe Glu Tyr Leu Glu Lys Val Leu Cys Ser Gly Leu Phe Ser His Ser
 35 40 45
 Ala Lys Ser His His Asp Leu Leu Thr Arg His Pro Tyr Glu Thr Ala
 50 55 60
 Ala Pro Leu Leu Ser Ser His Leu Ile Leu Thr Glu Ala Leu Arg Asn
 65 70 75 80
 Gly Leu Gly Lys Cys His Asp Pro His Phe Thr Gly Glu Glu Thr Glu
 85 90 95
 Ala Gln Arg Gly Lys Leu Thr Thr
 100

<210> 479
 <211> 439
 <212> PRT
 <213> Homo sapiens

<400> 479
 Leu Gly Asp His Gly Trp Glu Leu Ser Leu Glu Glu Asp Ala Gln Leu
 1 5 10 15
 Trp Gly Gly Val Val Lys Ser Cys Phe Glu Gly Lys Gly Pro Gln Arg
 20 25 30
 Glu Ala Gln Pro Ala Ser Pro Gln Ala Ala Pro Pro Gly Pro Thr Asn
 35 40 45
 Glu Ala Gln Met Ala Ala Ala Ala Leu Ala Arg Leu Glu Gln Lys
 50 55 60
 Gln Ser Arg Ala Trp Gly Pro Thr Ser Gln Asp Thr Ile Arg Asn Gln
 65 70 75 80
 Val Arg Lys Glu Leu Gln Ala Glu Ala Thr Val Ser Gly Ser Pro Glu
 85 90 95
 Ala Pro Gly Thr Asn Val Val Ser Glu Pro Arg Glu Glu Gly Ser Ala
 100 105 110
 His Leu Ala Val Pro Gly Val Tyr Phe Thr Cys Pro Leu Thr Gly Ala
 115 120 125
 Thr Leu Arg Lys Asp Gln Arg Asp Ala Cys Ile Lys Glu Ala Ile Leu
 130 135 140
 Leu His Phe Ser Thr Asp Pro Val Ala Ala Ser Ile Met Lys Ile Tyr
 145 150 155 160
 Thr Phe Asn Lys Asp Gln Asp Arg Val Lys Leu Gly Val Asp Thr Ile
 165 170 175
 Ala Lys Tyr Leu Asp Asn Ile His Leu His Pro Glu Glu Glu Lys Tyr
 180 185 190
 Arg Lys Ile Lys Leu Gln Asn Lys Val Phe Gln Glu Arg Ile Asn Cys
 195 200 205
 Leu Glu Gly Thr His Glu Phe Glu Ala Ile Gly Phe Gln Lys Val
 210 215 220
 Leu Leu Pro Ala Gln Asp Gln Glu Asp Pro Glu Glu Phe Tyr Val Leu
 225 230 235 240
 Ser Glu Thr Thr Leu Ala Gln Pro Gln Ser Leu Glu Arg His Lys Glu
 245 250 255
 Gln Leu Leu Ala Ala Glu Pro Val Arg Ala Lys Leu Asp Arg Gln Arg
 260 265 270
 Arg Val Phe Gln Pro Ser Pro Leu Ala Ser Gln Phe Glu Leu Pro Gly
 275 280 285
 Asp Phe Phe Asn Leu Thr Ala Glu Glu Ile Lys Arg Glu Gln Arg Leu

290 295 300
 Arg Ser Glu Ala Val Glu Arg Leu Ser Val Leu Arg Thr Lys Ala Met
 305 310 315 320
 Arg Glu Lys Glu Glu Gln Arg Gly Leu Arg Lys Tyr Asn Tyr Thr Leu
 325 330 335
 Leu Arg Val Arg Leu Pro Asp Gly Cys Leu Leu Gln Gly Thr Phe Tyr
 340 345 350
 Ala Arg Glu Arg Leu Gly Ala Val Tyr Gly Phe Val Arg Glu Ala Leu
 355 360 365
 Gln Ser Asp Trp Leu Pro Phe Glu Leu Leu Ala Ser Gly Gly Gln Lys
 370 375 380
 Leu Ser Glu Asp Glu Asn Leu Ala Leu Asn Glu Cys Gly Leu Val Pro
 385 390 395 400
 Ser Ala Leu Leu Thr Phe Ser Trp Asp Met Ala Val Leu Glu Asp Ile
 405 410 415
 Lys Ala Ala Gly Ala Glu Pro Asp Ser Ile Leu Lys Pro Glu Leu Leu
 420 425 430
 Ser Ala Ile Glu Lys Leu Leu
 435

<210> 480
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 480
 Met Trp Ala Arg Leu Pro His Thr Pro Glu Gln Met Gly His Arg Leu
 1 5 10 15
 Ile Gly Pro Lys Glu Ala Ser Leu His Val Val Pro Ser Trp Pro Ala
 20 25 30
 Arg Lys Met Glu Gly Leu Leu Ala Gly Leu Ser Ser Ser Pro Arg Lys
 35 40 45
 Ser Cys Trp Pro Phe Trp Val His Gly Pro Lys Val His Glu Gly Gly
 50 55 60
 Ser Ala Cys Glu Thr Ser Ser Ser Trp Val Glu Gly Leu Gly Leu Arg
 65 70 75 80
 Arg Val Thr Ser Val His Ser Leu Cys Gln Gly Leu Gly Ala Ser Val
 85 90 95
 Gln Leu Leu Pro Gly Pro Pro Pro Thr Thr Thr Ser Asp Lys Asn Asn
 100 105 110
 Tyr Thr Ser Gly
 115

<210> 481
 <211> 171
 <212> PRT
 <213> Homo sapiens

<400> 481
 Met Gln Pro Ala Glu Arg Ser Arg Val Pro Arg Ile Asp Pro Tyr Gly
 1 5 10 15
 Phe Glu Arg Pro Glu Asp Phe Asp Asp Ala Ala Tyr Glu Lys Phe Phe
 20 25 30
 Ser Ser Tyr Leu Val Thr Leu Thr Arg Arg Ala Ile Lys Trp Ser Arg
 35 40 45
 Leu Leu Gln Gly Gly Gly Val Pro Arg Ser Arg Thr Val Lys Arg Tyr
 50 55 60
 Val Arg Lys Gly Val Pro Leu Glu His Arg Ala Arg Val Trp Met Val

65					70					75					80
Leu	Ser	Gly	Ala	Gln	Ala	Gln	Met	Asp	Gln	Asn	Pro	Gly	Tyr	Tyr	His
			85						90					95	
Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu	Glu	Asp	Ala	Ile	Arg
			100					105					110		
Thr	Asp	Leu	Asn	Arg	Thr	Phe	Pro	Asp	Asn	Val	Lys	Phe	Arg	Lys	Thr
		115						120					125		
Thr	Asp	Pro	Cys	Leu	Gln	Arg	Thr	Leu	Tyr	Asn	Val	Leu	Leu	Ala	Tyr
		130				135					140				
Gly	His	His	Asn	Gln	Gly	Val	Gly	Tyr	Cys	Gln	Gly	Met	Asn	Phe	Ile
145					150					155					160
Ala	Gly	Tyr	Leu	Ile	Leu	Ile	Thr	Asn	Asn	Glu					
				165						170					

<210> 482
 <211> 177
 <212> PRT
 <213> Homo sapiens

<400> 482

Met	Gln	Pro	Ala	Glu	Arg	Ser	Arg	Val	Pro	Arg	Ile	Asp	Pro	Tyr	Gly
1				5					10					15	
Phe	Glu	Arg	Pro	Glu	Asp	Phe	Asp	Asp	Ala	Ala	Tyr	Glu	Lys	Phe	Phe
			20					25					30		
Ser	Ser	Tyr	Leu	Val	Thr	Leu	Thr	Arg	Arg	Ala	Ile	Lys	Trp	Ser	Arg
		35					40					45			
Leu	Leu	Gln	Gly	Gly	Gly	Val	Pro	Arg	Ser	Arg	Thr	Val	Lys	Arg	Tyr
	50					55					60				
Val	Arg	Lys	Gly	Val	Pro	Leu	Glu	His	Arg	Ala	Arg	Val	Trp	Met	Val
65					70					75					80
Leu	Ser	Gly	Ala	Gln	Ala	Gln	Met	Asp	Gln	Asn	Pro	Gly	Tyr	Tyr	His
			85						90					95	
Gln	Leu	Leu	Gln	Gly	Glu	Arg	Asn	Pro	Arg	Leu	Glu	Asp	Ala	Ile	Arg
			100					105					110		
Thr	Asp	Leu	Asn	Arg	Thr	Phe	Pro	Asp	Asn	Val	Lys	Phe	Arg	Lys	Thr
		115						120					125		
Thr	Asp	Pro	Cys	Leu	Gln	Arg	Thr	Leu	Tyr	Asn	Val	Leu	Leu	Ala	Tyr
		130				135					140				
Gly	His	His	Asn	Gln	Gly	Val	Gly	Tyr	Cys	Gln	Gly	Met	Asn	Phe	Ile
145					150					155					160
Ala	Gly	Tyr	Leu	Ile	Leu	Ile	Thr	Asn	Asn	Asp	Lys	Asn	Leu	Phe	Gly
				165					170					175	

Cys